

## STIC Search Report Biotech-Chem Library

## STIC Database Tracking Number: 133719

To: Jeffrey Parkin Location: rem/3d39/3c18

Art Unit: 1648

Wednesday, September 29, 2004

Case Serial Number: 10/084813

From: Beverly Shears Location: Remsen Bldg.

**RM 1A54** 

Phone: 571-272-2528

beverly.shears@uspto.gov

Search Notes		2 (1997)	
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Sequence 11, Appli
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Sequence 52, Appli
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Sequence 13, Appli
Sequence 2, Appli
Sequence 13, Appli
Sequence 13, Appli
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                                                              3 , Search time 16.2 Seconds (without alignments) 57.362 Million cell updates/sec
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-833-752-11
US-08-863-31D-2
US-08-861-105-14
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US-08-575-957A-2
US-09-534-185-52
US-09-534-185-52
US-09-534-185-52
US-09-534-185-52
US-09-796-202-1
US-08-883-752-5
US-09-796-202-1
US-08-886-319A-2
US-09-886-319A-2
US-09-686-319A-2
US-09-686-319A-2
US-09-686-319A-2
US-09-686-319A-2
US-09-686-319A-2
US-09-686-319A-2
US-09-686-319A-2
US-09-681-192-2
US-08-934-185-53
US-08-934-185-4
US-08-934-185-4
US-08-934-185-4
US-08-934-185-4
US-09-540-233-3033
US-09-540-235-6593
                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                    389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                               September 28, 2004, 09:00:23
                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                             - protein search, using sw model
                                                                                                    US-10-084-813-13
96
1 SOYQFWKNFQTLKIVILG 18
                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match
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Perfect score:
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                                                                Run on:
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US-08-833-752-11

US-08-833-752-11

Sequence 11, Application US/08833752

Patent No. 6448375

GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: PARABUTIER, MAC
APPLICANT: PARABUTIER, MAC
APPLICANT: LIBERT

TITLE OF INVENTION: AND NUCLEIC ACTIVE AND MICHELS ENCODING SAID RECEPTOR

TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
ADDRESSES: Knowbort Center Drive 16th Floor
CITY: Newport Beach

STATE: OA

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                        Sequence 2, Appli
Sequence 5, Appli
Sequence 1, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 26013, Ap
Sequence 5538, Ap
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 53, Ap
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ZIP: 92660

COMPUTER READABLE FORM:

MEDLUM TYPE: Floppy disk

COMPUTER: PROPY disk

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                                                                                                                                     US-09-239-938-1
US-08-813-752-9
US-09-886-313A-14
PCT-US55-00476-5
US/08/622
US-09-165-922A-10
US-09-252-931A-26013
US-09-328-352-5171
US-09-134-000C-3794
US-09-134-000C-6031
US-08-134-00C-6031
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US-08-134-00C-6031
                                US-08-012-988A-2
US-08-450-393A-5
US-08-446-669-5
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Best Local Similarity 100.'
Matches 18, Conservative
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RESULT

US-09-252-991A-25052 US-09-134-001C-4582 US-09-134-001C-5171

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1 SQYQFWKNFQTLKIVILG 18
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INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear; MOLECULE TYPE: protein US-09-087-232A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
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CITY: Ha
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US-09-087-232A-13

US-09-087-232A-13

US-09-087-232A-13

Sequence 13, Application US/09087232A

Patent No. 6153431

TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR

TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INTERPRESONDENCE ADDRESS: 23

CORRESPONDENCE ADDRESS: 23

CORRESPONDENCE ADDRESS: 24

CONTENT: New York

STREET: 30 Rockefeller Plaza

CITY: New York

COUNTRY: USA

ZIP: 10112

COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: PatentIn Release #1.0, Version #1.30 (BPO)

SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)

CURRENT APPLICATION NUMBER: US/09/087,232A

FILING DATE: 28 MAY 1998

FILING DATE: 28 MAY 1998
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0
Sequence 2, Application US/08466343D
Patent No. 6025154
GENERAL INFORMATION:
PAPPLICANT: L1, Yil
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
ADDRESSEE: STERNE, KESSIER, GOLDSTEIN & FOX P.L.L.C.
STREED: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 96; DB 3; Length 352; Best Local Similarity 100.0%; Pred. No. 3.8e-08; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 2000
ZIP: 2000
COUNTRY: U.S. 2000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Plopy disk
COMPUTER: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,343D
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY AGENT INPORMATION:
NAME: STEPE, ERIC K.
REGISTRATION NUMBER: 1488.1150000/EKS/KLM
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 SQYQFWKNPQTLKIVILG 202
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-466-343D-2
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PRIOR APPLICATION DRIVE.

APPLICATION WYMER: 60/046,057

ATTORNAY, GREY INCOMPATION:
AND ATTORNAY, GREAT INCOMPATION:
AND ATTOR
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Sequence 52, Application US/09045583
Patent No. 6287805
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
COUNTESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State & COCKFIELD, LLP
STREET: 28 STATE:
MASSACHUSELE FORM:
MEDIUM TYPE READABLE FORM:
MEDIUM TYPE PROCOMPATION
COMPUTER READABLE FORM:
MEDIUM TYPE PROCOMPATION
COMPUTER: 13M PC COMPATION
COMPUTER: 13M PC COMPATION
COMPUTER: 13M PC COMPATION
SOFTARE: PRESETTION DATA:
APPLICATION NUMBER:
FILING DATE: 20-MAR-98
CLASSIFICATION NUMBER: 36,207
REGISTRATION NUMBER: 36,207
REGISTRATION NUMBER: 36,207
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
REGISTRATION NUMB
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100.0%; Score 96; DB 3; I
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-045-583-52
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Patent No. 6265184

GENERAL INFORMATION:

TITLE OF INVENTION: Chemokine Receptor Materials and Methods NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 4300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 96; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels
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CONDUTER: USA

CONDUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: LBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT DEDICATION DATA:

APPLICATION NUMBER: US/08/575,967A

FLING DATE: NOFMATION:

NAME: NO. 2555184and, Greta E.

REFERRACE/DOCKET NUMBER: 32918

TELEPRATION NUMBER: 35,302

REFERRACE/DOCKET NUMBER: 32918

TELEPRACE TOOR SEQ ID NO: 2:

SEQUENCE CHARACTER: 100

INFORMATION SEQ ID NO: 2:

SEQUENCE CHARACTER: STORE:

INFORMATION CAID ACIDS

TYPE: CHARACTER: STORE:

TOPOLOGY: Linear

MODELCULE TYPE: protein
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): OTHER INFORMATION: /= "88C amino acid sequence"
US-08-575-967A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; STRANDEDNESS: single
; POPOLOGY: linear
MOLECTUE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-861-105-14
                   SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 6300 Sear
CITY: Chicago
STATE: Illinois
COUNTRY: USA
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US-08-575-967A-2
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US-09-517-605-5

US-09-517-605-5

Sequence 5. 34pplication US/09517605

Patent No. 6391567

GENERAL INFORMATION:

APPLICANT: Litteman, Dan R.

APPLICANT: Wan Kooyk, Yvette

APPLICANT: Wan Kooyk, Yvette

APPLICANT: Geliptenbeck, Theo

TITLE OF INVENTION: GELLS

FILE REFERENCE: 1049-1-017

CURRENT APPLICATION NUMBER: US/09/517,605

CURRENT APPLICATION NUMBER: US/09/517,605

CURRENT FILING DATE: 2000-03-02

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentln Ver. 2.0

SEQ ID NO 5

LENGTH: 352

MANDER OF SEQ ID NOS: 17

SEQ ID NO 5

LENGTH: 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 352;
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ORGANISM: Homo sapiens
US-09-517-605-5
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Gaps .. 0

0; Indels

Length 352;

: 352 amino acids amino acids

TOPOLOGY:

18-10-084-818-12:181

Query Match 100.0%; Score 96; DB 3; Length 352; Best Local Similarity 100.0%; Pred. No. 3.8e-08; Matches 18; Conservative 0; Mismatches 0; Indels

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RESULT 6 US-09-045-583-52

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TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
STREET: Knobbe, Martens, Olson & Bear STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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0
                                                                                                                                                                                              COUNTRY:

(COUNTRY:
(1) 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER:
(COMPUTER: IBM PC compatible
OPERATING SYSTEM:
(CURRENT APPLICATION DATA:
(CURRENT APPLICATION DATA:
(CURRENT APPLICATION NUMBER: US/08/833,752
(CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
(CLASSIFICATION: DATA:
(CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 352;
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100.0%; Score 96, DB 4, I
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0;
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ilarity 100.0%; Pred. No. 3.8e-08;
Conservative 0; Mismatches 0;
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US-09-796-202-1
; Sequence 1, Application US/09796202
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-833-752-5
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US-09-534-185-52

i Sequence 52, Application US/09534185

; Patent No. 6403767

; GENERAL INPORMATION:

APPLICANT: Graham, Gerard J. et al.

APPLICANT: Graham, Gerard J. et al.

TITLE OF INVENTION: No. 640376761 Molecules of the G Protein-Coupled

; TITLE OF INVENTION: No. Heptahelical Receptor Superfamily and Uses
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Patent No. 6448375
CENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: PARMENTIER, MARC
APPLICANT: PASSART, GILBERT
APPLICANT: LIEBRY: FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOXINES RECEPTOR
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                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                       Pred. No. 3.8e-08;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/534,185
FILING DATE: 24-Mar-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/045,583
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: MANGAGOLICA: AMY E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: poptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 352 amino acids TYPE: amino acid
  100.08; Fr.
                                                                                                                                                     185 SQYQFWKNFQTLKIVILG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 SQYQFWKNFQTLKIVILG 202
                                                                                                        1 SOYOFWKNFOTLKIVILG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 18; Conservative
                                                  18; Conservative
                    Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-534-185-52
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US-08-833-752-5
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Patent No. 6548636
GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/61010/JPW/SHS
CURRENT APPLICATION NUMBER: US/09/796,202
CURRENT FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 96; DB 4; Length 352; 100.0%; Pred. No. 3.8e-08; Ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-907-468-11

| Sequence | I. Application US/08907468
| Patent No. 6057102
| GENERAL INFORMATION:
| APPLICANT: Landau, Nathaniel R. APPLICANT: Liu, Rong
| TILLE OF INVENTION: HIV CORECEPTOR MUTANTS
| NUMBER OF SEQUENCES: 13
| CORRESPONDENCE ADDRESS:
| ADDRESSE: David A. Jackson, Esq.
| STREET: Floor
| CITY: Hackensack
| STREET: Hackensack
| STREET: Naw Jersey
| COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
COMPOTER: BATENTIN Release #1.0, Version #1.30
SOFTWARE: PatentIN Release #1.0, Version #1.30
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FLING DATE:
FLING DATE:
FLING DATE:
FLING DATE:
FLING PATENTIN:
NAME: Jackson Esq., David A.
REGISTATION NUMBER: 26,742
REFERENCE/ODCKET NUMBER: 1049-1-005 N
TELEFRAX: 201-487-580
INFORMATION FROUND: 201-487-580
INFORMATION FROUND: 201-487-580
INFORMATION FOR EQUID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TTPE: TYPE: amino acids
TTPE: TYPE: amino acids
TTPE: TYPE: amino acids
TTPE: TYPE: TYPE: Amino acids
TTPE: TYPE: Amino acids
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Best Local Similarity 100.0
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
; ORGANISM: human
US-09-796-202-1
                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 1
LENGTH: 352
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Query Match Best Local Similarity

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MESSULT 1944.2

Sequence 2, Application US/0872494A

Sequence 2, Application US/0872494A

Sequence 2, Application US/0872494A

Sequence 2, Application US/0872494A

SETEMET NOTAWATHORN TO SEQUENCES.

SEQUENCE SEQUENCES.

CORRESCONDENCE SEQUENCES.

STREET 709 Swedland Road, P.O. Box 1539

CORRESCONDENCE SEQUENCES.

STREET 709 Swedland Road, P.O. Box 1539

CONTINE BY MEDICATION NUMBER: USA

COUNTINE WEB-BALLOWING THE WASHINGTON TO SETEME SEQUENCE SEQUENCES.

SOFTWARE: MISCOSTY WORD THE SEQUENCE SEQUENCES.

CONTRERY ADDRESS: MISCOSTY WORD THE SEQUENCE SEQUENCES.

CONTRERY ADDRESS: WASHINGTON TO SEQUENCES.

CONTRERY ADDRESS: WASHINGTON THE SEQUENCE SEQUENCES.

CONTRERY ADDRESS: WASHINGTON TO SEQUENCES.

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Gaps

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Indels

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Mismatches

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15; Conservative

Matches

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CITY: Boston
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US-09-489-039A-13500
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Patent No. 6287805
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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46.9%; Score 45; DB 3; Length 355;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 8; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                   49.0%; Score 47; DB 4; Length 355; ilarity 61.5%; Pred. No. 5; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
CURRENT APPLICATION NUMBER: US/09/886,319A;
CURRENT FILING DATE: 2001-06-20;
PRIOR APPLICATION NUMBER: US 60/222,081
PRIOR FILING DATE: 2000-06-01;
PRIOR APPLICATION NUMBER: DE 10030149.5;
PRIOR FILING DATE: 2000-06-20;
NUMBER OF SEQ ID NOS: 84
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURKELL AFFLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MANDARGOURS: AMY E.
REGISTRATION NUMBER: 36,207
REGISTRATION NUMBER: 36,207
REFENCE/COCKET NUMBER: MNI-044
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: LAHIVE & COCKFIELD, LLP STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 53:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 FQQWKLFQALKLNLFG 207
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amino acid
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195 WKRFQALKINILG 207
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                                                                                                                                                                                                                                                                                                                                                                      6 WKNFOTLKIVILG 18
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internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                             TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 8; Conserv
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FRAGMENT TYPE:
                                                                                                                                                                                                                                                 US-09-886-319A-13
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US-09-045-583-53
                                                                                                                                                                                          355
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Sequence 13500, Application US/09489039A

Factor No. 6610836

GENERAL INFORMATION:
APPLICANT: GATY Breton et. al
APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
FILE REPERENCE: 2709.2004001
FURRENT APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
S-09-534-185-53
Sequence 53, Application US/09534185
Sequence 53, Application US/09534185
Batent No. 6403767
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 640376701 Molecules of the G Protein-Coupled
TITLE OF INVENTION: Heptahelical Receptor Superfamily and Uses
Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                             STATE: BOSCOL

STATE: MASSACHUSELTS

COUNTRY: USA

ZIP: 02109

COMPUTER READBLE FORM:

COMPUTER: ISA FO Compatible

COMPUTER: ISA FO Compatible

COMPUTER: ISA FO Compatible

COMPUTER: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/09/534,185

FILING DATE: 24-Mar-2000

CLASSIFICATION: ADMINER: US/09/5583

FILING DATE: CURROWN-

APPLICATION NUMBER: 09/045,583

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 34,207

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: MAI-044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.9%; Score 45; DB 4; Length 355; 50.0%; Pred. No. 11; 51.00%; Pred. 3; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 53:
                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD,
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 355 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192 FQQWKLFQALKLNLFG 207
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                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.03
Matches 8; Conservative
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Schreck, Patricia A.
REGISTRATION NUMBER: 33,777
REFERENCE/DOCKET NUMBER: ATG50014
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5031
TELEFAX: 610-270-4026
TELEX.
                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 344 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-terminal
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                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Kurthia sp.
US-08-935-263-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FRACHENT TYPE: NO ; ORIGINAL SOURCE: US-08-681-192-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 460
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US-09-594-185-4
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                                                                                                                                 Query Match
45.3%; Score 43.5; DB 4; Length 352;
Best Local Similarity 43.5%; Pred. No. 19;
Matches 10; Conservative 3; Mismatches 3; Indels .
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| Sequence 2, Application US/08681192
| Sequence 2, Application US/08681192
| Patent No. 6287801
| PATENT No. 6287801
| APPLICANT BERGEMA, DERK
| APPLICANT BERGEMA, HENRY
| APPLICANT SAKAU, HENRY
| APPLICANT SAKAU, HENRY
| TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR HNPDS78
| NUMBER OF SEQUENCES: G-CORRESPONDENCES: G-CORRESPONDENCES: G-CORRESPONDENCES: G-CORRESPERSEE: SmithKilne Beecham Corporation
| STREET 709 Swedeland Road | CORPORATION CONTRIBUTED CONTRIBUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 44.8%; Score 43; DB 4; Length 172; Best Local Similarity 57.1%; Pred. No. 11; Matches 8; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-61-976-4131

Sequence 4131, Application US/09621976

Fatefit No. 6639063;
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
ITILE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICANT: NOS: 1930-07-21
NUMBER OF SEQ ID NOS: 19335
SEQ ID NO 4131
LENGTH: 172
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COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASISEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/681,192
                                                                                                                                                                                                                                                                                                                2 QYQFW-----KNFQTLKIVIL 17
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 OFWKNFOTLKIVIL 17
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: SIGNAL
; LOCATION: -30..-1
US-09-621-976-4131
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                                                                                                                                           Gaps
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Query Match

44.8%; Score 43; DB 3; Length 344;
Best Local Similarity 66.7%; Pred. No. 22;
Matches 8; Conservative 2; Mismatches 2; Indels
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Pred. No. 45;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WESULT 20
US-08-935-263-4

Sequence 4, Application US/08935263A

Patent No. 611769

GENERAL INFORMATION:
APPLICANT: FUTLICH: Tatsuo
APPLICANT: Kimura, Hitcshi
APPLICANT: Kimura, Hitcshi
APPLICANT: Kiyasu, Tatsuo
TITLE COF INVENTION: BIOCIN GENES
FILE REPREBNCE: Biocin Genes
CURRENT FILING DATE: 1997-09-22

EARLIER PILING DATE: 1996-09-27

NUMBER: OF SEQ ID NOS: 23

SOFTWARE: Patentin Ver: 2.1

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Patent No. 6365388
GENERAL INFORMATION:
APPLICANT: Furuichi, Tatsuo
APPLICANT: Hoshino, Tatsuo
APPLICANT: Kimura, Hitoshi
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Sequence 25052, Application US/09252991A, Patent No. 6551795, GENERAL INFORMATION:
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PLILING DATE: 1999-02-18
PRIOR PLILING DATE: 1999-02-18
PRIOR PLILING DATE: 1999-07-37
NUMBER OF SEQ ID NOS: 33142
SEGO ID NO 25552
                                                                                                                                                                                                                                            Sequence 2, Application US/09491577
Parent No. 6610511
Parent No. 6610511
Parent No. 6610511
APPLICANT: Varies on John R. APPLICANT: Carleson, John R. APPLICANT: Carleson, John R. APPLICANT: Carleson, John R. APPLICANT: Clyne, Peter J. APPLICANT: Warleson, John R. G. CORRENT FILLS OF THE REFERENCE: 44574-5061-US FILLS REFERENCE: 44574-5061-US CURRENT FILLING DATE: 2000-01-25 EARLIER APPLICATION NUMBER: US 60/117,132 EARLIER FILLING DATE: 1999-01-25 NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity 53.3%; Pred. No. 35;
Matches 8; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
42.7%; Score 41; DB 4; Length 363;
Best Local Similarity 60.0%; Pred. No. 51;
Matches 9; Conservative 2; Mismatches 0; Indels
                             1; Indels
                          1; Mismatches
     Best Local Similarity 75.0%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Drosophila melanogaster US-09-491-577-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 YOFWKNFOTLKIVIL 17
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                             6; Conservative
                                                                                                                           146 YVFWKNYO 153
                                                                             3 YOFWKONFO 10
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US-09-252-991A-25052
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                                                                                                                                                                                                                                 US-09-491-577-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                Matches
                                                                                                                                                                                                      RESULT 24
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Patent No. 6673910
GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 2709, 2005-001
CURRENT APPLICATION NUMBER: US/09/540, 236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
NUMBER OF SEQ ID NOS: 3840
LENGTH: 727
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Patent No. 6562588
Patent No. 6562586
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BADVANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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Pred. No. 45;
2; Mismatches 3; Indels
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43.8%; Score 42; DB 4; Length 727;
Best Local Similarity 37.5%; Pred. No. 74;
Matches 6; Conservative 5; Mismatches 5; Indels
APPLICANT: Kiyasu, Tatsuya
APPLICANT: Nagahashi, Yoshie
TILE OP INVENTION: BIOTIN BIOSYNTHETIC GENES
FILE REFERENCE: BIOTIN BIOSYNTHETIC GENES
FILE REFERENCE: BIOTIN GENES
CURRENT APPLICATION NUMBER: US/09/594,185
CURRENT FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: 08/335,263
PRIOR PILING DATE: 1997-09-22
PRIOR PILING DATE: 1996-09-27
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PATENTIN OF 1996-09-27
SEQ ID NO 4
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LENGTH: 160
LYPE: PRT
ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 OLEYWKNOTTLSLITI 182
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Best Local Similarity 54.5%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT; CRGANISM: M.catarrhalis
US-09-540-236-3023
                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT

ORGANISM: Kurthia sp.

US-09-594-185-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-540-236-3023
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42.7%; Score 41; DB 4; Length 160;

Query Match

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us-10-084-813-13.rai

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-012-988A-2

Sequence 2, Application US/08012988A

Patent No. 5652133

GENERAL INFORMATION:
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                                                                                                                  TYPE: PRT;
CRGANISM: Klebsiella pneumoniae
US-09-489-039A-8904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                             Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
              1999-01-29
           PRIOR FILING DATE: 1999-01-2
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 8904
LENGTH: 316
                                                                                                                                                                                                                                                                                                                                                                                         226 WINVOGLKVEILG 238
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Best Local Similarity 53.84
....hes 7; Conservative
                                                                                                                                                                                                                                                                                                                                          6 WKNFQTLKIVILG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94610
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US-09-134-001C-4582
Sequence 4582, Application US/09134001C
Sequence 4582, Application US/09134001C
GENERAL INPORMATION:
TILLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: WUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
SEQ ID NOS: 5674
LENGTH: 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: LYAIN DOUGETEE-Stamm et al
APPLICANT: LYAIN DOUGETEE-STAMM et al
APPLICANT: LYAIN DOUGETEE-STAMM MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-10-08
PRIOR APPLICATION NUMBER: US 60/065,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-10-08
PRIOR FILING DATE: 1997-10-08
PRIOR FILING DATE: 1997-10-08-14
SEQUID NOS: 5674
LENGTH: 311
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; Sequence 8061, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
    APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: NUMBER: 2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 41.7%; Score 40; DB 4; Length 311; Best Local Similarity 38.5%; Pred. No. 63; Matches 5; Conservative 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 27
20-09-134-001C-5171
; Sequence 5171, Application US/09134001C
; Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5171
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Matches
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Gaps
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TITLE OF INVENTION: Cloning and Expression of Human
TITLE OF INVENTION: Cloning and Expression of Human
TITLE OF INVENTION: Appropriate Inflammatory Protein-1 alpha (MIP-1
TITLE OF INVENTION: alpha)/RANTES Receptor.
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
Score 40; DB 4; Length 316;
Pred. No. 64;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.7%; Score 40; DB 1; Length 355; 53.8%; Pred. No. 73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/012,988A
FILING DATE: 19930128
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 15280-118
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
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US-09-239-938-1
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US-09-239-938-1
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41.7%; Score 40; DB 1; Length 355;
Best Local Similarity 53.8%; Pred. No. 73;
Matches 7; Conservative 2; Mismatches 4; Indels
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Patent No. 6132987
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Charc, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MANCALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADRESS:
ADDRESSE: COALey Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE FLORY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOGTWARE: Patentin Release #1.0, Version #1.25

CURREWT APPLICATION DATA:

APPLICATION NUMBER: US/00/450,393A

FILING DATE: May 25, 1995

CLASSIFICATION NUMBER: 31,825

REPREMENCE/DOCKET NUMBER: 31,822

RESPREMCE/DOCKET NUMBER: 31,822

RESPREMCE/DOCKET NUMBER: 31,822

RESPREMCE/DOCKET NUMBER: 31,822

REJEPHONE: 415-843-5165

TELEPHONE: 415-843-5165

TELEPHONE: 415-843-5165

TELEPHONE: 415-843-5165

TELEPHONE: 415-843-5165

TELEPHONE: 308016COOlePyA

INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:

LENGTH: 355 amino acids

TYPE: amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/446,669 FILING DATE: May 25, 1995 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                        CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Palo Alto
California
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ZIP: 94306-2155
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US-08-450-393A-5
                                                                                                                                                                                                                             USA
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| Patent No. 6448375
| GENERAL INFORMATION:
| APPLICANT: SANSON, MICHEL
| APPLICANT: MASSART, GILBERT
| APPLICANT: LIBERT, REDESICK
| TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR ITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR NUMBER OF SEQUENCES:
| CORRESPONDENCE ADDRESS:
| ADDRESSED: Knobbe, Martens, Olson & Bear
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Faterix No. 6329510
Faterix No. 6329510
GENERAL INFORMATION:
APPLICANT: Stassam, Nasim
APPLICANT: Assam, Nasim
APPLICANT: Leukoštte, Inc.
TITLE OF INVENTION: THEREFOR
FILE OF INVENTION: THEREFOR
FILE REFERENCE: LESS97-13
CURRENT APPLICATION NUMBER: US/09/239,938
CURRENT PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                               41.7%; Score 40; DB 3; Length 355; 53.8%; Pred. No. 73; tive 2; Mismatches 4; Indels
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                  NAME: Neeley, Richard
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAL-237/01US
TELECOMMUNICATION INFORMATION:
TELEFRONE: 415-484-5000
TELEFAX: 415-485-0663
TELEFAX: 380816CooleyPA
INFORMATION FOR SEQ ID NO: 5:
SECUROR CHARACTERISTICS:
LENGTH: 355 amino acids
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                         : 355 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195 WKLFOALKLNLFG 207
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Best Local Similarity 53.8%
Best Local 7; Conservative
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                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
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Query Match
Best Local Similarity 40.0%
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Best Local Similarity 53.8
Matches 7; Conservative
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   RESULT 35
PCT-US95-00476-5
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Patent No. 6586185

GENERAL INFORMATION:
APPLICANT:
APPLICANT: Wolf, Eckard
APPLICANT: Regenbeen, Johannes
TITLE OF INVENTION: the Jagnosis or Treatment of Skin Disorders and Wound
TITLE OF INVENTION: Active Substances
TITLE OF INVENTION: Active Substances
FILE REFERENCE: 50125/014002
CURRENT APPLICATION NUMBER: US/09/886,319A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 60/222,081
PRIOR APPLICATION NUMBER: DE 10030149.5
PRIOR PILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR PILING DATE: 2000-06-20
PRIOR PILING DATE: 2000-06-20
PRIOR PILING DATE: 2000-06-20
SOFTWARE: FastsEQ for Windows Version 4.0
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                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
CMBUTHER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
FILING DATE: 9-APR-1997
CLASSIFICATION NUMBER: 18/08/833,752
CLASSIFICATION NUMBER: 34,115
REGISTRATION NUMBER: 34,115
REGISTRATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
CLENGTH: 355 amino acid
STRANDEDBESS: single
TOPOLOGY: linear
MOLECULE TYPE: No: 6448375e
US-08-833-752-9

41.7%; SCOIF 40; DB 4; Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 4; Length 355;
Pred. No. 73;
2; Mismatches 4; Indels
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Pred. No. 73;
2; Mismatches 4; Indels
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Best Local Similarity 53.8-
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Best Local Similarity 53.8
Matches 7; Conservative
Newport Beach
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                                 U.S.A.
                               COUNTRY: U.ZIP: 92660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-886-319A-14
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Gaps
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SENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
ATILE OF INVENTION: MANALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson
STREET: 201 N. Figueroa Street, 5th Floor
CITY: Los Angeles
STREET: California
COUNTRY: USA
ZIP: 90012-2628
COUNTRY: USA
ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURSENT PAPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00476
FILING DATE:
CLASSIFICATION:
APPLICATION:
APPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 5; Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 3;
Pred. No. 77;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 73;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid residue:

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cunknown>
DESCRIPTION: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US/08/622,679D-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: BETLINEY, ROBERT
REGISTRATION NUMBER: 20.121
REFERENCE/DOCKET NUMBER: 5555
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-977-1001
TELEPHAX: 310-977-1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 36
US/08/622
; INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.78;
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Sequence 5538, Application US/09543681A

Sequence 5538, Application US/09543681A

Patel No. 6605709

GENERAL INFORMATION:
APPLICANT: GARY BRETON:
APPLICANT: GARY BRETON:
TITLE OF INVENTION: ULAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001

TITLE OF INVENTION: UNMER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR APPLICATION NUMBER: US 60/128,706

NUMBER OF 553

INVERT OF 538

LENGTH: 2037

MANDER OF 5538

LENGTH: 2037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6562956;
Serent No. 6562956;
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTOS9-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
NUMBER OF SEQ ID NOS: 8252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                               Length 659;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Indels
                                                                                               Score 40; DB 4; Length 659
Pred. No. 1.4e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 4; I
Pred. No. 4.9e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  core 39; DB 4;
red. No. 25;
Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: September 28, 2004, 09:21:32 Job time : 17.2 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

40.6%; Score 39;
Best Local Similarity 43.8%; Pred. No.
Matches 7; Conservative 4; Mismatc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT; ORGANISM: Acinetobacter baumannii
US-09-328-352-5171
                                         ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||| : :|:|: ||
25 YQFTRYIRTIKVAQLG 40
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75.0%;
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                                                                                                   Query Match
Best Local Similarity 71.4%;
Matches 10; Conservative
                                                                                                                                                                                                                                   401 OYKTFWKNFGOVLK 414
                                                                                                                                                                                           2 OYO-FWKNF-OTLK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Proteus mirabilis
US-09-543-681A-5538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283 SAYOYWKN 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SQYQFWKN 8
                                                ; ORGANISM: Pseudo
US-09-252-991A-26013
                                                                                                                                                                                                                                                                                                                           US-09-543-681A-5538
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US-09-328-352-5171
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LENGTH: 92
TENGIH: 659
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US-09-252-991A-26013
; Sequence 26013, Application US/09252991A
; Sequence 26013, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: NARUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: 007196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT APPLICATION NUMBER: US 60/074,788
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                            Sequence 10, Application US/09165922A
Sequence 10, Application US/09165922A
Patent No. 6348641
GENERAL INFORMATION:
APPLICANT: STILES, JOHN I.
MOISYADI, ISTEFO
NEUPANE, KABI R.
TITLE OF INVENTION: PURIFIED PROTEINS,
PRODUCING CAFFEINE FREE BEVERAGES
PRODUCING CAFFEINE FREE BEVERAGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER . DISS...

STOTAGE COMPUTER: DISS...

STOTAGE COMPUTER: DISP COMPATIBLE COMPUTER: TBM PC compatible
OPERATING SYSTEM: MS-DOS V. 5.1
SOFTWARE WOORDEFECT for Windows V. 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,922A
FILING DATE: O2-Oct-1998
CIASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: GRIFFITH, CALVIN P.
REGISTRATION NUMBER: 34,831
REFERENCE/DOCKET NUMBER: 265036600003
TELEFAX: (216) 579-0212
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acid residues
TWPE: amino acid
TC... single
                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
STREET: NORTH POINT, 901 LAKESIDE AVENUE
CITY: CLEVELAND
STATE: OHIO
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 44114
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DESCRIPTION: protein
;
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-165-922A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           319 NQYYFWDDFHPSEVV 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SOYOFWKNFOTLKIV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 6; Conserv
           RESULT 37
US-09-165-922A-10
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Gaps

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September 28, 2004, 08:51:21; Search time 52.525 Seconds (without alignments) 118.345 Million cell updates/sec Run on:

Title: Perfect score:

US-10-084-813-12 126 1 QWDFGNTMCQLLTGLYFIGFFS 22 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq léngth: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A Geneseq 29Jan04:\*

1: geneseqp1980s:\*
2: geneseqp2000s:\*
4: geneseqp2001s:\*
5: geneseqp2001s:\*
6: geneseqp2003s:\*
7: geneseqp2003bs:\*
8: geneseqp2003bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	D88994 HIV gp12	Aaw27406 Inactive	Aaw27408 Inactive	Aaw88238 HIV-1 CO	Adc10142 Human NOV	Adc10144 Human NOV	Aaw26766 Human che	Aaw27407 Human CCR	Aaw27123 Human che	Aaw27125 Macaque c	Aaw07602 Human G-p	Aaw23835 Human CC	Aaw88232 HIV-1 CO-	89	Amino	6 Human	Aae07048 Human G-p		Aae04321 Human che	Aae07037 Human G-p	Aae07039 Human G-p	8 Human	Abb56342 Non-endog	Aab83354 Human CCR	****
ID	B8	AAW27406	AAW27408	AAW88238	ADC10142	ADC10144	AAW26766	AAW27407	AAW27123	AAW27125	AAW07602	AAW23835	AAW88232	AAY80128	AAG79089	AAE07046	AAE07048	AAG80111	AAE04321	AAE07037	AAE07039	AAB46858	ABB56342	AAB83354	ŀ
DB	4	N	N	7	7	_		~	7	7	N	7	~	m	4	4	4	4	4	4	4	4	4	4	
Length	22	184	215	215	268	268	332	352	352	352	352	352	352	352	352	352	352	352	352	352	352	352	352	352	
Query	100.0	100.0	00	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0		00	100.0	ö	100.0	100.0	100.0	100.0	100.0	100.0	100.0	
Score	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126	
Result No.	н	8	٣	4	Ŋ	9	7	œ	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	

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1 QWDFGNTMCQLLTGLYFIGFFS 22

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Aau97150 Human G-p Aau97152 Human G-p Aam52829 Human CCR		Human Human G-prot Human	Abg75540 Human G-p Abr58602 Human G-n Aao29514 Human G-C Abu61654 Human G-D Abr04773 Amino aci	Human Human Macaqu Human
AAU97150 AAU97152 AAM52829	AAM52828 ABG70597 ABG92883 ABG92880	AAE25808 AAE25811 ABB81054 ABB08343	ABG75540 ABR58602 AAC29514 ABU61654	ABP81933 ABC03341 ADC03359 AAW23834
222	2222	352 352 352 352 5	3325 3352 3352 3352 3352 3352 3352 3352	352 6 352 7 371 2
			126 100.0 126 100.0 126 100.0 126 100.0	4444
	0 0 H 0	8888 8488 6486	78884. 78890-	4 C/ C// 4" L/

## ALIGNMENTS

	HIV; glycoprotein 120; gp120; antagonist; STRL33.	fection, have homology to rs CCR5, CXCR4 and STRL33, nditions.	peptides which are able to are similar to the human as well as CD4. These are ent replication of the virus. ide of the invention 4; Length 22; -12; 0; Indels 0; Gaps 0;
andard; peptide; 22 (first entry) rotein binding pepti	kine receptor; CD4; ; CCR5; CXCR4; CD4; s. -A2. ; 2000WO-US023505.	27-AUG-1999; 99US-0151270P.  (USSH ) US DEPT HEALTH & HUMAN SERVICES.  Saxinger C;  WPI; 2001-244398/25.  Where polypeptides useful for treating HIV infection, regions of domains of human chemokine receptors CCRS, and binds to HIV gp120 under physiological conditions.	; Page 38; 114pp; English.  ent invention describes a number of HIV glycoprotein 120 (gp120). These erceptors CCRS, CCR4 and STR133, n the treatment of HIV, as they prevent sequence is an example of a pept 22 AA;  100.0%; Score 126; DE Similarity 100.0%; Pred. No. 1.26 2; Conservative 0; Mismatches
3UL 888	XX		2ue Mat

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Homo sapiens.
                                                                                                                                                                                                                               28-FEB-1997;
                                                                                                                                                                        WO9732019-A2.
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                                                                                                                                                                                                                                                            01-MAR-1996;
                                                                                                                                                                                                                                                                         06-AUG-1996;
                                                                                                                                                                                                    04-SEP-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW88238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW88238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is an inactive human CC (Cys-Cys) chemokine receptor C CCRS), which is not a receptor of human immundeficiency virus type 1 or type 2 (HIV-1 or HIV-2). CCRS or its CDNA can used to diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid arthritis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis, viral infections, especially HIV-1 or HIV-2 infection, cancer, atherosclerosis and autoimmune disorders. Subjects that express the inactive receptor have a predisposition, or resistance to HIV-1 and/or
                                                                                                                                                                                                  Inactive; human Cys-Cys chemokine receptor-5; CCR5; human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2; predisposition; resistance; diagnosis; treatment; prevention; inflammatory disease; rheumatorid arthritis; glomerulonephritis; asthma; idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer; atherosclerosis; autoimmune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Active and inactive forms of human CC chemokine receptor CCR-5 - useful to diagnose, prevent and/or treat inflammatory disorders, autoimmune disease and viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 126; DB 2; Length 184; 100.0%; Pred. No. 1.2e-11; tive 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vassart G, Libert F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                       AAW27406 standard; protein; 184 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW27408 standard; protein; 215 AA.
OWDFGNIMCOLLIGLYFIGFFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 1a; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       97WO-BE000023.
                                                                                                                                                                                                                                                                                                                                                                                                                 96EP-00870021
96EP-00870102
                                                                                                                                             14-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Simitaricy
nes 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Samson M, Parmentier M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EURO-) EUROSCREEN SA.
                                                                                                                                                                          Inactive human CCR5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-479829/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT90116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 184 AA;
                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-1996;
06-AUG-1996;
                                                                                                                                                                                                                                                                                                                                 WO9732019-A2
                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                             04-SEP-1997.
                                                                                                                  AAW27406;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
                                                           RESULT 2
                                                                           AAW27406
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                                                Inactive; human Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2; predisposition; resistance; diagnosis; treatment; prevention; inflammatory disease; theumatorid arthritis; glomerulonephritis; asthma; idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer; atherosclerosis; autoimmune disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Active and inactive forms of human CC chemokine receptor CCR-5 - usel to diagnose, prevent and/or treat inflammatory disorders, autoimmune disease and viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIV-1; CCR5; CCR5-delta32; co-receptor; infection; diagnosis; AIDS; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 126; DB 2; Length 215; 100.0%; Pred. No. 1.5e-11; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32. .56
/note= "transmembrane domain 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Libert F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIV-1 co-receptor CCR5 variant CCR5-delta32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vassart G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 QWDFGNTMCQLLTGLYFIGFPS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW88238 standard; protein; 215 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Fig 1d-e; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-BE000023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96EP-00870021.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Samson M, Parmentier M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EURO-) EUROSCREEN SA.
Inactive human CCR5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-479829/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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WO2003000842-A2

03-JAN-2003

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This is the amino acid sequence of a CCR5 variant protein, designated CCR5-delta12, that includes the first 4 transmembrane domains of wild-type CCR5 (see AAW88121), but lacks transmembrane domains of wild-type CCR5 (see AAW88122), but lacks transmembrane domains 5-7. CCR5 serves as a co-receptor for infection by macrophage-tropic (M-tropic) are individuals homozygous for the CCR5-delta23 mutation are resistant to HIV-1 infection, but hererozygous individuals are susceptible. The invention additionally relates to the identification of variant CCR5mil (See AAW88211), which lacks transmembrane domains 3-7 of CCR5. The detection of CCR5 variants may be used to identify individuals at lower risk of infection relative to the general population who, if infected, may exhibit slower progression to AINS. Probes and primers (see AAW84127-36) are provided for use in diagnostic methods for detecting the presence of such variants. A method is provided for inhibiting HIV-1 infection of a cell expressing the CCR5 receptor. This involves introducing a nucleic acid encoding a CCR5 variant into the cell thereby references.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New CCR5 variant protein of the HIV-1 co-receptor - useful in developing resistance of CCR5-expressing cells to HIV-1 infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quillent C, Arenzana Siesdedos F, Braun J;
67. .87
/note= "transmembrane domain 2"
103. .124
/note= "transmembrane domain 3"
142. .167
/note= "transmembrane domain 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MOND-) FOND MONDIALE RECH & PREVENTION SIDA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 38-39; 55pp; English.
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        Domain
                                                                                    Domain
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100.0%; Score 126; DB 2; Length 215;
100.0%; Pred. No. 1.5e-11;
live 0; Mismatches 0; Indels 0; Gaps
                                                                      1 QWDFGNTMCQLLTGLYFIGFFS 22
                   Local Similarity 100.0
   Query Match
                                      Matches
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93 QWDFGNTWCQLLIGLYFIGFFS 114

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RESULT 5
 ADC10142
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ADC10142 standard; protein; 268 AA.

ADC10142;

18-DEC-2003 (first entry)

Human NOVX polypeptide SEQ ID NO: 162

cytostatic, antidiabetic; anorectic, cerebroprotective, neuroprotective, antiinflammatory; gene therapy; antisense therapy; thyromimetic; NOVX; pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder; inflammatory disorder; chromosome mapping; tissue typing; predictive medicine.

Homo sapiens

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04-JUN-2001, 2001US-0295607P.
04-JUN-2001, 2001US-0295604P.
06-JUN-2001, 2001US-0295614P.
06-JUN-2001, 2001US-0295614P.
11-JUN-2001, 2001US-0295614P.
12-JUN-2001, 2001US-029573P.
12-JUN-2001, 2001US-029573P.
14-JUN-2001, 2001US-029582P.
15-JUN-2001, 2001US-029828P.
19-JUN-2001, 2001US-02993P.
21-JUN-2001, 2001US-02993P.
22-JUN-2001, 2001US-02993P.
22-JUN-2001, 2001US-03093P.
23-JUN-2001, 2001US-0301S9P.
23-JUN-2001, 2001US-0301S9P.
24-JUN-2001, 2001US-0301S9P.
25-JUN-2001, 2001US-0301S9P.
26-JUN-2001, 2001US-0301S9P.
27-JUN-2001, 2001US-0301S9P.
28-JUN-2001, 2001US-0301S9P.
                                                                                                                                                                                                                                                                                                                            2002US-0358978P.
; 2002US-0359034P.
; 2002US-0359035P.
; 2002US-0359121P.
; 2002US-0359964P.
                                                                                                                                                                                                                                                                                      2001US-0337477P.
2001US-0341562P.
2002US-0358656P.
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27-FEB-2002; 2002US-035964P.
01-MAR-2002; 2002US-0360858P.
                                                 04-JUN-2002; 2002WO-US017443
                                                                                                                                                                                                                                                                                                                     2002US-0359122P
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12-MAR-2002; 2002US-0363676P.
                                                                                                                                                                                                                                                                                                                                                                                                                                  04-JUN-2002; 2002US-00379444
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(CURA-) CURAGEN CORP.

Kekuda R; Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;
Diptpo VR, Edinger SR, Elsen A, Ellerman K, Gangolli EA;
Gerlach VL, Gorman L, Guo X, Hermann JL, Hjalt T, Vi W, Kekuda F
Khramtsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;
Ort T, Padigaru M, Patturajan M, Pena CEA, Rascelli L, Rieger DK;
Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G, Spaderna SK;
Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP; Stone DJ, V Lepley DM; Spytek KA, Burgess CE,

WPI; 2003-210149/20. N-PSDB; ADC10141.

New isolated NOVX polypeptides and nucleic acid molecules useful for treating, preventing and diagnosing pathological conditions with NOVX-associated disorders, such as cancer, obesity, diabetes and inflammatory or CNS diseases.

Claim 1; SEQ ID NO 162; 772pp; English.

The invention relates to novel isolated polypeptides, mature form of the polypeptide, a sequence that is 95% identical to the polypeptide or the polypeptide comprising one or more conservative substitutions. The NOVX polypeptide is useful for treating or preventing a pathology associated with the polypeptide e.g. disorders associated with aberrant expression or activity of the polypeptide, such as cancer, diabetees, obesity, and endocrine, CNS and inflammatory disorders. They can also be used in various detection and screening assays, chromosome mapping, tissue typing

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04-JUN-2002; 2002US-00379444.
              (CURA-) CURAGEN CORP.
                                                                                           WPI; 2003-210149/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 121
                                                                                                  N-PSDB; ADC10143.
                                                                                                                                                                                                                                             Sequence 268 AA;
                                                                                                                                     or CNS diseases.
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                                                                                                                                                                                                                                                                                                                                                     AAW26766;
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                                                                                                                                                                      cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective; antilitammatory; gene therapy; antisense therapy; thyrominetic; NOVX; pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder; inflammatory disorder; chromosome mapping; tissue typing;
                                                 Gaps
and predictive medicine. This sequence corresponds to one of the polypeptides of the invention.
                                                 ö
                                   100.0%; Score 126; DB 7; Length 268; 100.0%; Pred. No. 1.9e-11;
                                                 0; Indels
                                                 0; Mismatches
                                                                                                                                                          Human NOVX polypeptide SEQ ID NO: 164.
                                                                      93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                               ADC10144 standard; protein; 268 AA.
                                                              1 OWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                              2001US-0296418P.
2001US-0296575P.
                                                                                                                                                                                                                                                           04-JUN-2002; 2002WO-US017443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-MAY-2002; 2002US-0379444P
                                                                                                                                          18-DEC-2003 (first entry)
                                       Local Similarity 100.
                                                                                                                                                                                                  predictive medicine.
                     Sequence 268 AA;
                                                                                                                                                                                                                               WO2003000842-A2.
                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                     07-JUN-2001;
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                                                                                                                             ADC10144;
                                   Query Match
                                                 Matches
                                                                                                 RESULT 6
                                                                                                        ADC10144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated NOVX polypeptides and nucleic acid molecules useful for treating, preventing and diagnosing pathological conditions with NOVX-associated disorders, such as cancer, obesity, diabetes and inflammatory
                                                                                          Kekuda R;
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121"
Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;
Dipipo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;
Gerlach VL, Gorman L, Guo X, Herrnann JL, Hialt T, Ji W, Kekuda R
Khramtsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;
Ort T, Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK;
Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G, Spaderna SK;
Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chediak-Higashi syndrome; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107. .128 /note= "conserved peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 164; 772pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 OWDFGNTMCOLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 OWDFGNIMCQLLIGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW26766 standard; protein; 332 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
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                                                                                                                                                                                                                                                                                                  Burgess CE, Lepley DM;
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This protein comprises human MMLR-CCR, a novel C-C chemokine receptor associated with monocyte/macrophage infiltration and chemotaxis and haematopoiesis. The amino acid sequence was deduced from a cDNA clone (see AAT99542) obtained from a cDNA library made from a cDNA clone collected on day 2 of a mixed lymphocyte culture, i.e. cells associated with inflammation and immunomdulation. Another novel chemokine receptor, MPHG-CCR (see AAN36767), is also claimed. MMLR-CCR contains 7 transmembrane spanning segments connected by a serives of intracellular and extracellular loops. MMLR-CCR and MPHG-CCR can be used to study, diagnose and treat disease states in which normal leukocyte function is perturbed by normal leukopoiesis or inappropriate activation via proliferative disease, tumourigenesis, autoimmune disease, abnormal proliferative, solid tumours, cardiovascular disease, abnormal cell proliferation, solid tumours, cardiovascular disease, abnormal cell arthritis, alveolitis, atherosclerosis, chronic granulomatous disease, asthma, myasthenia gravis, diabetes, inflammatory bowel disease, toxic shock syndrome, septic shock and Chediak-Higashi syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                       Polynucleotide encoding MMLR-CCR or MPHG-CCR chemokine receptor - useful to study, diagnose and treat, e.g. infection, inflammation, solid tumour and proliferative and cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention; inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma; idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer; atherosclerosis; autoimmune disorder.
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Best Local Similarity 100.0%; Pred. No. 2.4e-11;
Matches 22; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                Coleman R, Wilde CG;
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                                                                                                                                                                                                                                                                                                                                   Claim 8; Page 37-38; 59pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW27407 standard; protein; 352 AA
                                                    97WO-US006993
                                                                                        96US-0063B0B1
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                                                                                                                            (INCY-) INCYTE PHARM INC
                                                                                                                                                                Au-Young J, Bandman O,
                                                                                                                                                                                                    WPI; 1997-549729/50.
N-PSDB; AAT99542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 332 AA;
                                                    25-APR-1997;
                                                                                          26-APR-1996;
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                  06-NOV-1997
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Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour; asthma; viral infection, AIDS; inflammation; autoimmune disease; therapy; diagnosis; leukocyte trafficking; G protein coupled receptor; ligand; modulator; antibody; human.
                                                                                                                                                                                                                           The present sequence is human CC (Cys-Cys) chemokine receptor 5 (CCR5), which is stimulated by MIP-1 alpha, MIP-1 beta or RAWTES chemokines, but not by monocyte chemoattractant protein 1 (MCP-1), MCP-2, MCP-3, MCP-3, interleukin-6 (IL-8) or growth related gene product alpha (GRO alpha) chemokines. Active CGR-5 is also a receptor of human immundeficiency virus type 1 or type 2 (HIV-1 or HIV-2). CGR5 or its cDNA can used to diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid psoriasis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and atherosclerosis and autoimmune disorders
                                                                                                                                           Active and inactive forms of human CC chemokine receptor CCR-5 - useful to diagnose, prevent and/or treat inflammatory disorders, autoimmune disease and viral infection.
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                                                                        Vassart G, Libert F;
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259. 280
/label= Extracellular_domain
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label= Extracellular_domain
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/label= Intracellular_domain
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/label= Extracellular_domain
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|abel= Intracellular_domain
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/label= Intracellular_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW27123 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 OWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                     Claim 4; Fig 1b-c; 94pp; English.
96EP-00870021.
96EP-00870102.
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/label= Ert
113.
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Best Local Similarity 100.
Matches 22; Conservative
                                                                        Samson M, Parmentier M,
                                           (EURO-) EUROSCREEN SA
                                                                                                  WPI; 1997-479829/44.
                                                                                                                  N-PSDB; AAT90117.
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 352 AA;
01-MAR-1996;
06-AUG-1996;
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This polypeptide sequence comprises macaque chemokine receptor 88C, a G protein coupled receptor that is involved in laukocyte trafficking. Its amnion sequence in the from a 88C DNA (AATS163) isolated by PCR amplification. It shows 97% identity to human 88C (AAM27123). 88C receptors and their polypeptide fragments can be produced in transformed host cells. The receptors of peptides comprising one or more of the extracellular or intracellular domains, and anti-receptor antibodies can be used to modulate receptor activities, particularly ligand and G protein binding, and are potentially potentially useful in the treatment of atheroslerosis, rheumatoid arthritis, tumours, asthma, viral infection, AIDS, inflammatory conditions, pathological immune response, antibody that specifically binds to macaque 88C is claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G-protein chemokine receptor; HDGNR10; signal transduction; haematopoiesis; leukaemia; inflammation; rheumatoid arthritis; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human G-protein chemokine receptor, HDGNR10 - useful to identify (ant)agonists, for treatment of haematopoiesis, leukaemia, chronic and acute inflammation, rheumatoid arthritis, etc.
                                                                                                                                                        New nucleic acid encoding chemokine receptors 88-2B and 88C - used modulate leukocyte trafficking, e.g. for treatment of inflammation, tumours, viral infections, auto-immune diseases, etc.
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                                                Raport CJ;
                                                                                                                                                                                                                                                 Claim 36; Page 57-58; 65pp; English.
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                                             Gray PW, Schweickart VL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-1997 (first entry)
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                                                                                         WPI; 1997-341689/31
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(ICOS-) ICOS CORP.
                                                                                                               N-PSDB; AAT85163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 352 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This polypeptide sequence comprises novel human chemokine receptor 88C, a givetein coupled receptor that is involved in leukocyte trafficking. Its amino sequence was deduced from a cDNA clone (AAT851G) isolated from a macrophage library. It shows 62% identity to CCCKR1. Chemokine receptor 89.2B (see AAW27124) has also been identified. 88C and 88.2B receptors and their polypeptide fragments can be produced in transformed host cells. The receptors, peptides comprising one or more of the extracellular or intracellular domains, and anti-receptor antibodies can be used to modulate receptor activities, particularly ligand and G protein binding, and are potentially potentially useful in the treatment of atheroslerosis, rheumatoid arthritis, tumours, asthma, viral infection, AIDS, inflammatory conditions, pathological immune response, abnormal haematopoietic processes etc
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                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding chemokine receptors 88-2B and 88C - used to modulate leukocyte trafficking, e.g. for treatment of inflammation, tumours, viral infections, auto-immune diseases, etc.
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                                                                                                                                                                                                                                                 Gray PW, Schweickart VL, Raport CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 16; Page 47-48; 65pp; English.
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                                                                                         96WO-US020759
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96US-00661393.
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Best Local Similarity 100.0
Best Local Similarity 200.0
                                                                                                                                                                                                                                                                                             WPI; 1997-341689/31.
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  WO9722698-A2
                                                                                         20-DEC-1996;
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07-JUN-1996;
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                                             26-JUN-1997.
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AAW88232
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                 Novel human mature G-protein chemokine receptor HDGNRIO (AAW07602) is a 7-transmembrane protein involved in signal transduction. Its amino acid sequence was deduced from a cDNA clone (AAT44042) isolated from a human monocyte library. Isolation of the cDNA allows prodn. of recombinant HDGNRIO in host, e.g. E. coli, COS or Sf9, cells. The recombinant sceptor can be used to identify agonists or antagonists of the receptor, such cpds. can be used to treat conditions related to the under- and over-expression of G-protein chemokine receptors
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                                                                                                                                                                                                                                                                                                                      CC chemokine receptor 5; CCR5; G-protein coupled receptor; human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.
                                                                                                                                                  0; Gaps
                                                                                                                                Length 352;
                                                                                                                                                 0; Indels
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277. 300
/label= VII
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                                                                                                                             100.0%; Score 126; DB 2;
100.0%; Pred. No. 2.6e-11;
tive 0; Mismatches 0;
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/label= I
/note= "transmembrane domain"
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109. .120
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                                                                                                                                                                                                                                                                                                     Human CC chemokine receptor 5 (CCR5).
                                                                                                                                                                                OWDFGNTMCQLLTGLYFIGFFS 114
Claim 1; Page 44-46; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
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                                                                                                                                                                                                                                         AAW23835 standard; protein; 352 AA
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/label= III
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/label= VI
                                                                                                                      Query Match
Best Local Similarity 100.0-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'label= IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194. .219
/label= V
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                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . .210
                                                                                                                                                                                                                                                                                                                                                                                                                                                               .171
                                                                                                           Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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This protein sequence comprises of a novel human macrophage-selective CC demonkine receptor that has been designated CRS. The sequence was deduced from an isolated cDNA clone (see AAT76920). An Ala127teu variant (see W238340 of CCRS was also identified. The susceptibility of human macrophages to HTV infection depends on cell surface expression of CD4 and CCRS. CCRS is a member of the 7-transmembrane superfamily of G-protein coupled cell surface molecules. It plays an essential role in the membrane thaion step of infection by some HIV isolates. The establishment of stable, non-human cell lines and transgenic mammals having cells that occapress human CD4 and CCRS provides valuable tools for research of HIV infection. Antibodies that bind to CCRS. CCRS variants, and CCRS-binding agents capable of blocking membrane fusion between HIV and target cells represent potential anti-HIV therapeutics for macrophage tropic strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGT (Cys) in wild-type CCR5, TGA
                                                                                                             CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion between HIV and a target cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 126; DB 2; Length 352; 100.0%; Pred. No. 2.6e-11; ive 0; Mismatches 0; Indels
  Murphy PM;
  Berger EA, Alkhatib G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7. .87
note= "transmembrane domain 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103. .124
/note= "transmembrane domain 3"
142. .167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "transmembrane domain 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "transmembrane domain 6" 275. .301
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(Stop) in CCr5m303"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93 QWDFGNTMCQLLTGLYFIGFFS 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW88232 standard; protein; 352 AA.
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                                                                                                                                                                   Claim 68; Fig 1C; 70pp; English
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Best Local Similarity 100.
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/note= '
Combadiere C, Feng Y,
Broder CC, Kennedy PE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy; human.
                                                    WPI; 1998-032650/03
                                                                        N-PSDB; AAT76920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 352 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, G-protein coupled receptor; G-protein chemokine receptor; HDGNR10; diagnosis; haematopoiesis; wound healing; coagulation; anglogenesis; tumour; infection; leukaemia; psoriasis; allergy; T-cell mediated autoimmune disease; atherogenesis; anaphylaxis; inflammation; allergic reaction; silicosis; sarcoidosis; rarcoidosis; rheumatoid arthritis; hyper-eosinophilia syndrome.
                                                                                                                                                                     New CCR5 variant protein of the HIV-1 co-receptor - useful in developing resistance of CCR5-expressing cells to HIV-1 infection.
                                                                                                                                                                                                                                        This is the amino acid sequence of wild-type human CCR5, which serves as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 126; DB 2; Length 352; 100.0%; Pred. No. 2.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                       Beretta A, Quillent C, Arenzana Siesdedos F, Braun J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human G-protein chemokine receptor HDGNR10 SEQ ID NO:2.
                                                                             (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                              Disclosure; Page 34-35; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY80128 standard; protein; 352 AA.
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                         98WO-EP003437.
                                                     97US-0048057P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                WPI; 1999-059835/05.
                                                                                                                                              N-PSDB; AAV84126,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 352 AA;
                         29-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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 03-DEC-1998
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The present sequence represents a human G-protein chemokine receptor
designated HDGNR10. HDGNR10 polynucleotides are useful in methods of
screening for compounds which bind to and either: (1) activate the
HDGNR10 polypepides caushing stimulation of hematopolesis, wound
compound infections, leukaemia, T-cell mediated autoimmune diseases,
chronic infections, leukaemia, T-cell mediated autoimmune diseases,
parasitic infections, psoriasis, and to stimulate growth factor activity,
or (2) inhibit activation of the HDGNR10 polypeptides which is useful for
preventing and/or treating allargy, atherogenesis, anaphylaxis,
malignancy, chronic and eaute inflammation, histamine and immunoglobulin
E-mediated allergic reactions, prostaglandin-independent fever, bone
(marrow failure, silicosis, sarcoidosis, rheumacoid arthritis shock and
hyper-eosinophilia syndrome. The polynucleotides are also useful for
diagnostic assays for detecting diseases related to mutations in the
nucleic acid sequences encoding the polypeptides are also useful for
polynucleotides are also useful for in vitro purposes related to
constitute tresearch, synthesis of DNA and manufacture of DNA vectors
                                                                                                                                                                                                                                                 Isolated nucleic acid encoding human G-protein chemokine receptor useful for diagnostic assays, scientific research and screening for compounds which bind to and activate or inhibit activation of the receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, receptor, DC-SIGN, dendritic cell, T lymphocyte, HIV, 9p120;
C-type lectin, ICAM3, HIV entry, T cell, macrophage, HIV infection, CCRS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QWDFGNTMCQLLTGLYFIGFFS 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 1; 22pp; English.
(HUMA-) HUMAN GENOME SCI INC.
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Best Local Similarity 100.0
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                                                                                                                                          WPI; 2000-181807/16.
                                                                                                                                                                                  N-PSDB; AAZ91481
                                                                   Li Y, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200164752-A2.
                                                                                                                                                                                                                                                                                                                                                                polypeptides.
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WPI; 2001-602565/68.

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An antibody for the treatment or prevention of HIV-infection comprises a gpl20 portion which binds to DC-SIGN or is exposed upon gpl20 binding of DC-SIGN due to concomitant conformational change.

142. 166 /label= Transmembrane\_domain /note= "Segment 4"

Intracellular\_loop\_2

label=

Domain Domain Domain

196. .223 /label= Transmembrane\_domain /note= "Segment 5"

. 235

Domain Domain

36. .260 |abel= Transmembrane\_domain label= Intracellular\_loop\_3

'note= "Segment 6"

Domain

67. .195 label= Extracellular\_loop\_2

Disclosure; Page 118-119; 131pp; English

The specification describes an antibody which is specific for an antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN or conformational change. DC-SIGN de Concomitant to specification of DC-SIGN de Concomitant of DC-SIGN is a receptor that is specifically expressed on dendritic cells and facilitates infection of T lymphocytes with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin. DC with high affinity. The antibody of the invention inhibits the trans enhancement of HIV entry into a T cell or macrophage facilitated by infection. The present sequence represents a human CCRS protein, which is a translocation promoting agent that interacts with CD4. This receptor functions in HIV-1 entry into cells

Sequence 352 AA;

Gaps 0 Query Match
Best Local Similarity 100.0%; Score 126; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels (

1 OWDFGNIMCOLLIGLYFIGFFS 22 à g

AAE07046 standard; protein; 352 AA. RESULT 16

AAE07046;

(first entry) 16-0CT-2001

Human G-protein chemokine receptor (CCR5) HDGNR10 protein #1.

Human, G-protein chemokine receptor; CCR5; HDGNR10; inflammation; H1V; human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; cytostatic; immunosuppressive; noctrobic; neuroprotective; gene therapy; neurodegenerative disorder; Kaposi's sarcoma, autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia.

Homo sapiens.

. .36 /label= Extracellular\_domain 37. .305 /label= Transmembrane\_domain 37. .58 /label= Transmembrane\_domain 59. .67 /label= Intracellular\_loop\_1 Location/Qualifiers note= "Segment 1" Key Domain Domain Domain Domain Jomain 

58. .88 /label= Transmembrane\_domain /note= "Segment 2" 39. .102
/label= Extracellular\_loop\_1 Domain

/label= Transmembrane\_domain /note= "Segment 3" 125. .141 .124 Domain

287. .305 /label= Transmembrane\_domain /note= "Segment 7" 306. .352 <sup>™</sup> /label≂ Intracellular\_domain Extracellular\_loop\_3 /label= Ex WO200158916-A2 Domain Domain 

16-AUG-2001

09-FEB-2001; 2001WO-US004153

22-SEP-2000; 2000US-0234336P. 09-FEB-2000; 2000US-0181258P. 09-MAR-2000; 2000US-0187999P

(HUMA-) HUMAN GENOME SCI INC.

Li Y, Ruben SM; Rosen CA, Roschke V,

WPI; 2001-488966/53. N-PSDB; AAD13282. Isolated nucleic acid encoding a human G-protein chemokine receptor (CCRS) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders.

Claim 102; Fig 1; 518pp; English.

The invention relates to human G-protein chemokine receptor (CCRE)

HDGNRIO polypeptides and polynucleotides. CCRE HDGNRIO antibodies are
useful for treating, preventing or aneliorating a disease or disorder
associated with inflammation, defective or aberrant chemotaxis of immune
cells. HIV infection (such as Pheumocystis carini pneumonia or Kaposi's
sarcoma) or defective or aberrant T-cell antigen presenting cell
interaction. The disease or disorder may also be an infection a crapped sance or disorder may also be an infection, a
cytomegalovirus infection such as an early stage HIV infection, a
cytomegalovirus infection or a poxvirus infection, an autoimmune
disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The
disease or disorder may be associated with aberrant CCRS expression, lack
of CCRS function, aberrant CCRS ligand expression, or lack of CCRS ligand
function. CCRS HDGNRIO protein is used as a food additive or preservative
con increase or decrease storage capabilities. CCRS HDGNRIO DNA,
cromosome identification and in gene therapy. CCRS HDGNRIO DNA,
con chromosome identification and in gene therapy. CCRS HDGNRIO DNA,
con chromosome identification and in gene therapy. CCRS HDGNRIO DNA,
con chromosome identification and in dense conservative disease,
diagnosis, treatment and prevention of cancer (breast, overy, adrenal
cupgenital); immune disorders (Addison's disease, allergies, autoimmune
chaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
conditional sequence is human CCRS HDGNRIO protein
con present sequence is human CCRS HDGNRIO protein

Sequence 352 AA;

Query Match

DB 4; Length 352; 100.0%; Score 126;

ô Gaps . 0 ; Pred. No. 2.6e-11; 0; Mismatches 0; Indels 100.08; Best Local Similarity 100. Matches 22; Conservative

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RESULT 17 AAE07048

AAE07048 standard; protein; 352 AA

(first entry) 16-OCT-2001 AAE07048;

Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.

Human, G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV; human immunodeficiency virus; antimicrobial; vascdilator; vulnerary; cytosteatic; immunosuppressive; nootropic, neuroprotective; gene therapy; neurodegenerative disorder; Kaposi, s sarcoma; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia.

Homo sapiens.

WO200158916-A2.

16-AUG-2001.

09-FEB-2001; 2001WO-US004153.

09-FEB-2000; 2000US-0181258P. 09-MAR-2000; 2000US-0187999P. 22-SEP-2000; 2000US-0234336P.

HUMA-) HUMAN GENOME SCI INC.

Li Y, Ruben SM; Rosen CA, Roschke V,

WPI; 2001-488966/53. N-PSDB; AAD13299.

Isolated nucleic acid encoding a human G-protein chemokine receptor (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders.

Example 40; Page 504-505; 518pp; English.

The invention relates to human G-protein chemokine receptor (CCRS)
HDGNR10 polypeptides and polynucleotides. CCRS HDGNR10 antibodies are
useful for treating, preventing or ameliorating a disease or disorder
associated with inflammation, defective or aberrant chemotaxis of immune
cells, HIV infection (such as Pheumocystis carini pneumonia or Kaposi's
sarcoma) or defective or aberrant T-cell antigen presenting cell
interaction. The disease or disorder may also be an infectious disease
(e.g. a viral infection such as an early stage HIV infection, a
cytomegalovirus infection, or a poxvirus infection, an autoimmune
disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The
disease or disorder may be associated with aberrant CCRS expression, lack
of CCRS function, aberrant CCRS ligand expression, or lack of CCRS ligand
function. CCRS HOGNR10 protein is used as a food additive or preservative
to increase or decrease storage capabilities. CCRS HDGNR10 DNA are useful
for thomosome identification and in gene therapy. CCRS HDGNR10 DNA,
protein, antibodise, agonists and antagonists are also useful in the
diagnosis, treatment and prevention of cancer (breast, overy, adrenal gland, bone, bone marrow, gastrointestinal tract, liver, lung, urogenital); immune disorders (Addison's disease, allergies, autoimmune 

ö haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rhewmatoid arthritis and ulcerative colitis); cardiovascular disorders (myocardial ischaemias) and wound healing. The present sequence is human CCRS HDGNR10 protein 0; Gaps 100.0%; Score 126; DB 4; Length 352; 100.0%; Pred. No. 2.6e-11; ive 0; Mismatches 0; Indels C 93 OWDFGNTMCOLLTGLYFIGFFS 114 AAG80111 standard; protein; 352 AA. 1 OWDFGNTMCQLLTGLYFIGFFS 22 17-JAN-2002 (first entry) Local Similarity 100. es 22; Conservative Human CCR5 protein. Sequence 352 AA; AAG80111; Query Match Matches RESULT 18 8 x 3 3 3 3 3 ď ઠે

Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection; inflammation; autoimmune disease; metestasis; brondhal asthma; lupus; ofronic bowel inflammation; rheumatoid arthritis; cytostatic; antiinflammatory; antisthmatic; immunosuppressive; dermatological; antirheumatic; antiarthritic. 

Homo sapiens.

WO200172830-A2

02-APR-2001; 2001WO-EP003708.

31-MAR-2000; 2000DE-01016013.

(IPFP-) IPF PHARM GMBH. FORS/) FORSSMANN U. Forssmann W, Adermann K, Heitland A, Spodsberg N;

WPI; 2001-626256/72.

Diagnostic agent containing two or more receptor-specific ligands, useful for detecting tumors, inflammation etc., also therapeutic use of ligand inhibitors.

Disclosure; Page 10; 26pp; German.

This invention describes a novel diagnostic agent (A) comprising at least two different ligands (I) for receptors (II) that are implicated in diseases. (A) are used for the diagnosis of tumors (especially colorectal or prostatic), organ rejection, inflammation and autoimmune diseases. Also inflammation (particularly bronchial asthma or chronic bowel inflammation), or autoimmune diseases (theumatoid arthritis or lupus), where the (cardio) vascular, lymphatic, respiratory, nerrous, digestive, andocrine, motor or urogenital systems or skin are affected, and bone marrow diseases. The products of the invention are chemokine derivatives immunosuppressive, dermatological, antitheumatic, antiarthritic. Chemokines act on specific tumor and inflammatory cells through a consideration of chemokine receptors (CR), which control migration and proliferation of these cells. Aka80128 represent human chemokine fragments used to illustrate the method of the invention

Sequence 352 AA;

93 OWDFGNTMCQLLTGLYFIGFFS 114

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; transformed mammalian cell; CD4; reporter gene; translocation; human immuno deficiency virus; HIV; long terminal repeat; LTR; therapy; chemokine receptor; CKR; cellular dysfunction; HIV infection; cofactor; CC-CKR-5; envelope glycoprotein; anti-HIV.
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Ouery Match
Best Local Similarity 100.0%; Score 126; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human chemokine receptor (CKR), CC-CKR-5 related protein #2.
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(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                           93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                             1 OWDFGNIMCOLLIGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE04321 standard; protein; 352 AA.
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97US-00858660.
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19-JUN-1996;
19-MAY-1997;
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AAE04321
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1 QWDFGNTMCQLLTGLYFIGFFS 22

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Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV; human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; cytostatic; immunosuppressive, notropic; neuroprotective; gene therapy; neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative colitis; Crobin's disease; wound healing; cardiovascular disorder; myocardial ischaemia.
                                                                                    Human G-protein chemokine receptor (CCR5) HDGNR10 protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        287. 305
/label= Transmembrane_domain
/note= "Segment 7"
                                                                                                                                                                                                                                                         37. .305
/label= Transmembrane domain
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'label= Transmembrane_domain
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label= Transmembrane_domain
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|Jabel= Transmembrane_domain
|note= "Segment 4"
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|Jabel= Transmembrane_domain
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label= Intracellular_loop_3
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/label= Transmembrane_domain
/note= "Segment 6"
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| Jabel = Extracellular_loop_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           306. .352
/label= Intracellular_domain
                                                                                                                                                                                                                                                                                                                                             label= Intracellular_loop_1
                                                                                                                                                                                                                                                                                                                                                                                                     label= Extracellular loop 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   label= Extracellular_loop_2
                                                                                                                                                                                                                                             Location/Qualifiers
                   AAE07037 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "Segment 3"
                                                                                                                                                                                                                                                                                                                                                                                note= "Segment 2"
                                                                                                                                                                                                                                                                                                                          "Segment 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "Segment 5"
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42
                                                               (first entry)
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                                                                16-OCT-2001
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                                         AAE07037;
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RESULT 20
            AAE0703.
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HDGNR10; human; G-protein chemokine receptor; antiinflammatory;
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                                                                                                                                                                                                                                                                                                                                                              2001-488965/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 352 AA;
                                              WC200158915-A2.
    Homo sapiens.
                                                                                          16-AUG-2001.
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04-MAY-2001
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AAB46858
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                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10 protein. CCR5 HDGNR10 cDNA is included in ATCC Deposit No: 97183. CCR5 HDGNR10 antibodies are useful for treating, preventing or ameliorating a disease or disorder associated with inflammation, defective or aberrant chemotaxis of immune cells, HIV infection (such as Pheumocystis carinii presenting cell interaction. The disease or disorder may also be an infections disease (e.g. a viral infection such as an early stage HIV infections disease (e.g. a viral infection, or a poxyirus infection, autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The disease or disorder may be associated with aberrant CCR5 ingand expression, or a cxy or CCR5 function, aberrant CCR5 ligand expression, or a care of CCR5 indand function. CCR5 HOGNR10 protein is used as a food additive or preservative to increase or decrease storage capabilities. CCR5 HOGNR10 DNA are useful for chromosome identification and in genee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapy. CCRS HDGNR10 DNA, protein, antibodies, agonists and antagonists are also useful in the diagnosis, treatment and prevention of cancer (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tractliver, lung, urogenital); immune disorders (Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mallitus, Crohn's disease, multiple solerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular disorders (myocardial ischaemias) and wound
                                                                                                                                                                                                                                               Isolated nucleic acid encoding a human G-protein chemokine receptor (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV; human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; cytostatic; immunosuppressive; noctropic, nauroprotective; gene therapy; neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; hosemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 126; DB 4; Length 352; 100.0%; Pred. No. 2.6e-11;
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                                                                                                                                    Li Y, Ruben SM;
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                                                                                                                                                                                                                                                                                                                                                                Claim 102; Fig 1; 495pp; English.
09-FEB-2000; 2000US-0181258P.
09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
                                                                                          (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                    neurodegenerative disorders.
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                                                                                                                                      Rosen CA, Roschke V,
                                                                                                                                                                                WPI; 2001-488965/53.
N-PSDB; AAD13181.
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The present sequence is human G-protein chemokine receptor (CCRS) HDGNR10 protein. CCRS HDGNR10 antibodies are useful for treating, preventing or ameliotating a disease or disorder associated with inflammation, defective or aberrant chemotaxis of immune cells, HIV infection (such as perman) and control or Kapposi, sarcoma) or defective or aberrant antigen presenting cell interaction. The disease or disorder may also be an infection, a cytomegalovirus infection such as mearly stage HIV infection, a cytomegalovirus infection or a neurodegenerative disorder. The disease or disorder may be associated with aberrant CCRS expression, lack of CCRS function, aberrant CRS expression, and of CCRS ligand function. CRS HGNR10 protein is used as a food additive or preservative to increase or decrease storage capabilities. CRS HIGNR10 protein, antibodies, agonists and antagonists are also useful in the diagnosis, antibodies, agonists and antagonists are also useful in the diagnosis, creatment and prevention of cancer (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract, liver, lung, urogenital); immune disorders (Addison's disease, allergies, autoimmune thempolytic anaemia, autoimmune thyroiditis, diabetes mellitus (crohu's disease, multiple sclerosis, rheumatoid arrhritts and ulcerative colitis); cardiovascular disorders (myocardial ischaemias) and wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated nucleic acid encoding a human G-protein chemokine receptor (CCRS) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
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1 Similarity 100.0%; Score 126; DB 4; Length 352;
2 Similarity 100.0%; Pred. No. 2.6e-11;
22; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 40; Page 486-487; 495pp; English.
                                                                                                                                                                                                                                                                                                                                                                            Rosen CA, Roschke V, Li Y, Ruben SM;
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                                                                                       09-FEB-2000; 2000US-0181258P.
09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
09-FEB-2001; 2001WO-US004152.
                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurodegenerative disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
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Human; G protein-coupled receptor; GPCR; non-endogenous; mutant; constitutively activated GPCR; agonist; disease.

Non-endogenous human GPCR protein, SEQ ID NO: 477

18-FEB-2002 (first entry)

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This invention describes a novel receptor polypeptide (I) selected from (i) a fully defined 329 amino acid sequence (II) fully disclosed in the specification; and (ii) a polypeptide encoded by the CDNA concained in a plasmid, and fragments, analogs and derivatives of the polypeptide. The products of the invention have antiinflammatory, immunomodulatory, antiparastic, antiparaptic, immunompressive, vulnerary, cytostatic, antiparastic, antiparatic, inferein chemokine activity and can be used for gene therapy. The G-protein chemokine also be used for stimulating sematopolesis, wound healing, coagulation, also be used for stimulating nematopolesis, parastic infections, psoriasis, and suffered autoimmune diseases, parastic infections, psoriasis, and mundal mundal sematory, antiparatic infertions, prostaglandin-independent fever, bone marrow failure, estimulating syndrome. (N.B. This record was resubmitted to correct errors in the keyword formatting)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
immunomodulatory; anticoagulant; antiallergic; immunosuppressive; cytostatic; antiparasitic; antiparotic; antibarotic; antibarotic; antibarotic; antiparasitic; antiparotic; antiparotic; antiparotic; antiparotic; antiparotic; antialtic; vasctropic; gene therapy; haematopolesis; would tumour; infection; leukemia; growth factor activity; T-cell mediated autoimmune disease; psoriasis; allergy; atterogenesis; anaphylaxts; malignancy; inflammation; histamine; IgE; silicosis; shock; immunosiboluin E-mediated allergic reaction; rheumatoid arthritis; prostaglandin-independent fever; bone marrow failure; sarcoidosis; hyper-eosinophilic syndrome; vulnerary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human G-protein chemokine receptor polypeptides and polynucleotides, useful for identifying (ant)agonists to the G-protein chemokine receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 OWDFGNIMCOLLIGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim la; Page 15; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                             98US-00195662.
99US-00339912.
                                                                                                                                                                                                                                                                                                                                                            29-NOV-2000; 2000US-00725285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-226317/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LIYY/) LI Y. (RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li Y, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAF26390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 352 AA;
                                                                                                                                                                                                                                                                      JS2001000241-A1.
                                                                                                                                                                                                                                                                                                                                                                                                     06-JUN-1995;
18-NOV-1998;
25-JUN-1999;
                                                                                                                                                                                                                                                                                                                 12-APR-2001
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Identifying agonists of G protein-coupled receptors (GPCRs) for use in disease treatment, comprises contacting candidate compounds with versions

Lehmann-Bruinsma K, Liaw CW, Lin I;

WPI; 2001-648759/74. N-PSDB; ABI97978.

05-APR-2001; 2001WO-US011098. 07-APR-2000; 2000US-0195747P.

Homo sapiens. Synthetic. WO200177172-A2.

18-OCT-2001.

(AREN-) ARENA PHARM INC.

Claim 1; Page 277-278; 394pp; English.

of GPCRB.

The invention relates to G protein-coupled receptors (GPCRs) for which the endogenous ligand has been identified. Non-endogenous constitutively activated versions of known GPCRs are used in the invention for the direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists. Such agonists are useful as therapeutic agents for diseases or disorders associated with GPCRs. The present sequence is a non-endogenous version of a known human GPCRs.

93 OWDFGNTMCOLLTGLYFIGFFS 114

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ABB56342 standard; protein; 352 AA

ABB56342;

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Gaps

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100.0%; Score 126; DB 4; Length 352; 100.0%; Pred. No. 2.6e-11; tive 0; Mismatches 0; Indels 0

Local Similarity 100. 1es 22; Conservative

Query Match Best Local S Matches 22

Sequence 352 AA;

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(AARO-) AARON DIAMOND AIDS RES CENT.
                                  Dragic T, Olson WC;
                                                                    WPI; 2001-611273/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ROSC/) ROSCHKE V. (LIYY/) LI Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RUBEN S M.
                                                                                     N-PSDB; AAH26903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 352 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                            humans.
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(LIYY/)
(RUBE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the human CCR5 protein sequence. The invention relates to a method for determining whether an agent is capable of modulating the interaction of chemother receptor 5 (CCR5) with gpl20, comprising incubating the agent with GCR5 and gpl20 and determining whether the agent modulates the interaction, where gpl20 is associated with CDP4, and where the interaction is a low affinity binding. The method is used to identify an agent capable of modulating the method is used to identify an agent capable of modulating the interaction of CCR5 with gpl20. An agent identified by the method is used to operate composition for the treatment of a disease or condition associated with CCR5 and gpl20 interaction, to treat a subject with a disease or condition associated with CCR5 and gpl20 interaction, and for preparing a pharmaceutical for treating human immunodeficiency, virus (HIV). It can also be treat anti-inflammatory diseases. The method is commercially useful, amenable to high throughput screening, and is commercially useful, amenable to high throughput screening, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCR5; chemokine; co-receptor; human immunodeficiency virus type 1; HIV-1; infection; therapy; vaccine; anti-HIV-1.
                                                                                                                                                                      Determining if an agent can modulate CCRS-gpl20 interaction, comprises incubating the agent with CCRS and gpl20 and determining if the agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 126; DB 4; Length 352; 100.0%; Pred. No. 2.6e-11; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2. .18 /note= "binds to HIV-1 gp120"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB82948 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 OWDFGNTMCOLLTGLYFIGFFS 22
                                                                                                                                                                                                                                            Claim 1, Page 110; 113pp; English.
                                                                                     Rickett GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-FEB-2000; 2000US-0185667P.
19-MAY-2000; 2000US-0205839P.
07-FEB-2001; 2001US-0267231P.
12-JAN-2000; 2000GB-00000663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human HIV-1 co-receptor CCR5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2001; 2001WO-US006699.
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                                                                                                                                                                                                          modulates the interaction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 22; Conservative
                                                                                     Perros M,
                                                                                                                     WPI; 2001-477088/52.
N-PSDB; AAF87099.
                                (PFIZ ) PFIZER LTD (PFIZ ) PFIZER INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200164710-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-SEP-2001.
                                                                                     Dobbs S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB82948;
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AAB82948
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The present sequence is that of human HIV-1 co-receptor CCR5. Amino acids 2-18 in the N-terminal region of CCR5 comprise an HIV-1 gpl20-binding 2-18 in the CRF and HIV-1 gpl20. Post-translational sulfation of the tyrosine regidues in the HIV-1 gpl20. Post-translational sulfation of the tyrosine regidues in the CCR5 N-terminus is required for gpl20 binding and may critically modulate the susceptibility of target cells to HIV-1 infection in vivo. The invention provides claimed sulfated peptides (see AABS294) that are invention provides claimed sulfated peptides (see AABS294) that are based on the CCR5 N-terminal region and which are effective for inhibiting HIV-1 binding to CCR5. These peptides are used in claimed methods of inhibiting HIV-1 infection of CD4+ cells, of preventing CD4+ cells are infected with HIV, of treating a subject whose CD4+ cells are infected with HIV, and of identifying an agent which inhibits binding of a CCR5 ligand to a CCR5 receptor. The methods may be carried out in a subject, appecially a human, infected (therapeutic method), not infected with HIV (prophylactic method), or in a subject who is not infected with, but has been exposed to, HIV
Novel compounds comprising specific amino acids within CCR5 (HIV 1 coreceptor) amino terminal domain including negatively charged and two sulfated tyrosine residues is useful for treating HIV infection in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QWDFGNTMCQLLTGLYFIGFFS 22
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                                                                                                                                                                                                                                                Claim 1; Page 30; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-FEB-2000; 2000US-0181258P.
09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
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The present invention relates to the isolation of a novel human G-protein chemokine receptor (CCR5) designated HDGNR10, and polynucleotide sequences encoding it. The invention also describes antibodies that bind human G-protein chemokine receptor (CCR5) HDGNR10 and polynucleotide that bind human G-protein chemokine receptor (CCR5) HDGNR10 and polynucleotide sequences encoding the antibodies. The antibodies are useful for treating or preventing inflammation, defective or aberrant chemotaxis of immune cells and T-cell/antigen-presenting cell interactions, infections and autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral infections (sepecially early-stage human immune deficiency virus (HIV), cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions associated with aberrant or deficient expression of the CCR5 receptor or its ligands. The antibodies are also useful to determine CCR5 expression, e.g. for diagnosis, prognosis and monitoring of cancer and other hyperproliferative diseases. The polynucleotide sequences encoding human G-protein chemokine receptor, (CCR5) HDGNR10 can be used to produce the recombinant receptor, and in the treatment of a wide range of diseases such as infectious diseases (e.g. hDGNR10 at the ceptor (CCR5) HDGNR10 at the ceptor (CCR5) HDGNR10 at the ceptor (CCR5).

HDGNR10 #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 126; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps
                                                                                                           New nucleic acid encoding an antibody specific for the G-protein chemokine receptor CCR5, useful for treatment and diagnosis of e.g. inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, G-prötein chemokine receptor; CCR5; HDGNR10; inflammation;
immune cell chemotaxis; autoimmune disease; rhematoid arthritis;
neurodegeneration; viral infection; Kayosi sarcoma; cancer;
hyperproliferative disease; neurological disease; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human G-protein chemokine receptor (CCRS) HDGNR10 #2.
                    Li Y, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 OWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU97152 standard; protein; 352 AA
                                                                                                                                                                                                         Claim 61; Fig 1; 180pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                    Rosen CA, Roschke V,
                                                            WPI; 2002-434754/46.
                                                                              N-PSDB; ABK51853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 352 AA;
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The present invention relates to the isolation of a novel human G-protein chemokine receptor (CCRS) designated HDGMR10, and polynucleotide chemokine receptor (CCRS) designated HDGMR10 and polynucleotide human G-protein chemokine receptor (CCRS) HDGMR10 and polynucleotide human G-protein chemokine receptor (CCRS) HDGMR10 and polynucleotide sequences encoding the antibodies. The antibodies are useful for treating or preventing inflammation, defective or aberrant chemotaxis of immune cells and T-cell/antigen-presenting cell interactions, infections and autofendmune defeases, rheumathoid architis, meurodegeneration, viral infections (especially early-stage human immune deficiency virus (HIV), cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions associated with aberrant or deficient expression of the CCRS receptor or its ligands. The antibodies are also useful to determine CCRS expression, e.g. for diagnosis, prognosis and monitoring of cancer and other prepreditive and in the treatment of a wide range of diseases. The polynucleotide sequences encoding human G-protein chemokine receptor (CCRS) HDGMR10 can be used to produce the recombinant receptor, and in the treatment of a wide range of diseases cuch present sequence represents human G-protein chemokine receptor (CCRS) HDGMR10 can be used to grades (e.g. influenza), neurological diseases (e.g. present sequence represents human G-protein chemokine receptor (CCRS). The present sequence represents human G-protein chemokine receptor (CCRS) presents control control

New nucleic acid encoding an antibody specific for the G-protein chemokine receptor CCR5, useful for treatment and diagnosis of e.g.

Li Y, Ruben SM;

Rosen CA, Roschke V, WPI; 2002-434754/46. N-PSDB; ABK51870.

(LIYY/) LI Y. (RUBE/) RUBEN S M.

Disclosure, Page 165-166; 180pp, English.

inflammation.

Gaps

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100.0%; Score 126; DB 5; Length 352; 100.0%; Préd. No. 2.6e-11; tive 0; Mismatches 0; Indels (

1 OWDFGNIMCOLLIGLYFIGFFS 22

à

22; Conservative

Best Local Similarity Matches 22; Conserv

Query Match

Sequence 352 AA;

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CCRS; CC chemokine receptor 5; human; HIV infection; human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome; drug screening; identification; variant.
                                                                                                                                                                                                                                             /note= "Glu replaces wild-type Leu; encoded by CTG"
                                                                                                                                                                                                                                                                 /note= "Encoded by AGC"
                                                                                                                                                                                                                     Location/Qualifiers
93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                 AAM52829 standard; protein; 352 AA
                                                                                                                                                                                                                                                                                                                                   21-MAR-2001; 2001WO-US009155.
                                                                                                                                Human CCR5 Gln 55 variant.
                                                                                                             22-FEB-2002 (first entry)
                                                                                                                                                                                                                                Misc-difference 55
                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                        WO200171346-A2
                                                                                                                                                                                                                                                                                                             27-SEP-2001.
                                                                                      AAM52829;
                                           RESULT 28
                                                       AAM52829
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09-FEB-2000; 2000US-0181258P. 09-MAR-2000; 2000US-0187999P. 22-SEP-2000; 2000US-0234336P.

ROSEN C A.

(ROSE/)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method for identifying a binding compound for CC Chemokine receptor 5 (CCR5). The method involves screening a library of test molecules (particularly peptides) with immobilised CCR5, and then identifying those molecules which bind. The invention also relates to CCR5-binding molecules identified using the method of the invention, methods for identifying consensus motifs for CCR5-binding peptides, a transfer vector encoding tagged CCR5, a computer-aided methods for determining the relative binding affinity of a test molecule to CCR5 and a computer aided drug screening assay that utilises the three-dimensional structure of CCR5. Compounds identified using the methods of the invention are useful for treating or preventing HIV (human immunodeficiency virus) infection or AIDS (acquired immunodeficiency syndrome) in a patient. The methods of the invention may also be used to identify agonists or antagonists of the interaction of CCR5. The present squence represents a naturally courting variant of human CCR5 in which there is a glutamine, rather than a leucine, at position 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCR5; CC chemokine receptor 5; human; HIV infection;
human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;
drug screening; identification.
                                                                                                                                                                                 Identifying CC chemokine receptor 5 binding compound for treating AIDS, comprises binding a molecule from library to a molecule having binding property corresponding to CCR5 and identifying bound molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 126; DB 5; Length 352;
100.0%; Pred. No. 2.6e-11;
tive 0; Mismatches 0; Indels 0; Gaps
                                                                                                                        Tan Hehir CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human CC chemokine receptor 5 (CCR5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93 CWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM52828 standard; protein; 352 AA.
                                                                                                                                                                                                                                     Example 3; Fig 4B; 50pp; English.
                                                                                                                        See RH,
                    21.WAR-2000; 2000US-0190996P.
20.WAR-2000; 2000US-0191299P.
20.WAR-2001; 2001US-00813448.
20.WAR-2001; 2001US-00813651.
20.WAR-2001; 2001US-00813653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-2000; 2000US-0190946P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAR-2001; 2001WO-US009155
                                                                                               (CONS-) CONSENSUS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
Les 22; Conservative
                                                                                                                        Nestor JJ, Wilson CJ,
                                                                                                                                               WPI; 2002-010610/01.
                                                                                                                                                           N-PSDB; ABA02318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200171346-A2
            21-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 29
AAM52828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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The invention relates to a method for identifying a binding compound for CC chemokine receptor 5 (CCR5). The method involves screening a library CC chemokine receptor 5 (CCR5). The method involves screening a library of test molecules (particularly peptides) with immobilised CCR5, and then classified those molecules which bind. The invention also relates to CCR5-binding molecules identified using the method of the invention. CC cross-binding molecules identified using the method of the invention. CC cross-binding peptides, a computer aided drug screening assay that utilises the three-dimensional a computer aided drug screening assay that utilises the three-dimensional corputation are useful for treating or preventing HTW (human invention are useful for treating or preventing HTW (human corputation) infection or AIDS (acquired immunodeficiency virus) infection or AIDS (acquired immunodeficiency syndrome) in a patient. The methods of the invention may also be used to alternal ligand, and to determine a binding motif for CCR5. The present acquired represents human CCR5 and became a binding motif for CCR5. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; G-protein chemokine receptor; HDGNR10; CCRS receptor; haematopoiesis; solid tumour; chronic infection; leukaemia; T-cell mediated autoimmune disease; parasitic infection; portassis; growth factor activity; allergy; parasitic infection; psortassis; growth factor activity; allergy; attherogenesis; anaphylaxis; mallignancy; inflammation; histamine; immunoglobulin E; IgE-mediated allergic reaction; sarcoidosis; prostaglandin-independent fever; bone marrow failure; shock; rheumatodia arthitis; hyper-eosinophilic syndrome; cytostatic; antiparastic; antiparastic; antiparastic; antiparastic; antiparastic; antitheumator; antiathritic; antiathritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying CC chemokine receptor 5 binding compound for treating AIDS, comprises binding a molecule from library to a molecule having binding property corresponding to CCR5 and identifying bound molecule.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                  Tan Hehir CA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 OWDFGNTMCQLLTGLYFIGFFS 114
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                                                                                                                                                                                                                                                                                                                                  See RH,
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21-WAR-2000; 2000US-0190996P.
21-WAR-2001; 2000US-0191299P.
20-MAR-2001; 2001US-00813448.
20-MAR-2001; 2001US-00813651.
20-WAR-2001; 2001US-00813653.
                                                                                                                                                                                                                                                   (CONS-) CONSENSUS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-DEC-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                  Nestor JJ, Wilson CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antipyretic, receptor.
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-010610/01.
N-PSDB; ABA02317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2002099176-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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The present invention relates to the isolation of human G-protein chemokine receptor, HDGNR10 (CCRS receptor), and the polynucleotide sequence encoding it. HDGNR10 polypeptide and polynucleotide sequences are or useful for diagnosine of HDGNR10. They are useful for identifying related to underexpression of HDGNR10. They are useful for identifying modulators for stimulating haematopoiesis, wound healing, coagulation, angiogenesis, to treat solid tumours, chronic infections, psoriasis, or for stimulating growth factor activity. The sequences are also useful for preventing and/or treating allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation, histamine and immunoglobulin E (IgE) -mediated allergic reactions, prostaglandin-independent fever, bone marrow failure, sarcoidosis, theumatoid arthritis, shock and hypersessing essents sequence represents human G-protein chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human G-protein chemokine receptor polypeptide useful for identifying modulators for stimulating hematopoiesis, wound healing, leukemia, for treating allergy, rheumatoid arthritis, shock and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Fig 1; 22pp; English.
                                                                                                                                                     95US-00466343
                                                                              99US-00339912
                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-690494/74.
N-PSDB; ABS54272.
                                                                                                                                                                                                                           (LIYY/) LI Y.
(RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor, HDGNR10
                                                                                                                                                                                                                                                                                                                                       Li Y, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  research agents.
                                                                          25-JUN-1999;
                                                                                                                                                     36-JUN-1995;
25-JUL-2002
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Query Match
100.0%; Score 126; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps
                                                                                                                                     93 QWDFGNTWCQLLTGLYFIGFFS 114
                                                                                                          1 OWDFGNIMCOLLTGLYFIGFFS 22
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Immunoglobulin; variable heavy chain; variable light chain; human; G-protein chemokine receptor; CCRS; HDGNR10; cancer; inflammation; immunologic deficiency syndrome; blood protein disorder; nephritis; ataxia telangiectsaia; endotaxin lethality; inflammatory bowel disease; histiocytosis; chemotaxis; infectious disease; autoimmune disease; Addison's disease; dermatitis; rheumatoid arthritis; allorgy; neurodegenerative disorder; viral infection; poxvirus infection; HIV; human immunodeficiency virus; cytomegalovirus; Kaposis sarcoma; Pneumocystis çarnii infection; cardiovascular disorder; atherosclerosis;
                                                                                                                                                                  Human immunoglobulin variable heavy domain #1.
                                      ABG92883 standard; protein; 352 AA
                                                                                                                       19-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                      lymphocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                 ABG92883;
RESULT 31
                    ABG92883
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Immunoglobulin; variable heavy chain; variable light chain; human; G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation;

Human G-protein chemokine receptor (CCR5) HDGNR10 #1.

(first entry)

19-NOV-2002

ABG92880;

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The invention describes an isolated polymucleotide encoding a first antibody at least 95-100% identical to a second antibody consisting of an antibody at least 95-100% identical to a second antibody consisting of a wariable heavy (WH) or variable light (NL) domain of the antibody conversable heavy (WH) or variable light (VL) domain of the antibody conversable heavy (WH) or variable light (VL) domain of the antibody conversable heavy (WH) or variable light (VL) domain of the antibody conversable heavy (WH) or variable light (VL) domain of the antibody conversable heavy (WH) or variable light (VL) domain of the antibody conversable heavily preventing, preventing, proposing of propositions are an attained, prognosing or monitoring concents or other diseases or disorders and ataxia telangiectusia, inflammation associated disorders such as endotoxin lethality, nephritis conditions proceed with an increase in certain heamatopoletic cells such as histocytosis, defective or aberrant chemotaxis of immune cells or T-cell antigen presenting cell interaction, confined disease, an autodimmune disease such as Addison's disease, dermatitis and rheumatoid arthritis, alleadies, a neurodegenerative disorder, a viral infection e.g. HIV infection, cytomegalovirus or cardiovascular disorders such as atherosolerosis, lymphocytopenias, or disease or disorder associated with aberrant expression of novel human Genote of human immunoglobulin sequence associated with the antibodies against HDGNRIO
                                                                                                                                                                                                                                                                                                                                                                                                 New human G-protein Chemokine Receptor gene (HDGNR10) useful for treating, preventing, ameliorating or monitoring diseases or disorders associated with aberrant expression of HDGNR10 e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 126; DB 5; Length 352;
100.0%; Pred. No. 2.6e-11;
Live 0; Mismatches 0; Indels 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 55; Fig 4; 562pp; English.
                                                                                                                                                                                                                                                                                                   Roschke V, Rosen CA, Ruben SM;
                                                                                                                                                       12-JUN-2001; 2001US-0297257P.
08-AUG-2001; 2001US-0310489P.
12-OCT-2001; 2001US-0326447P.
21-DEC-2001; 2001US-0341725P.
                                                                             08-FEB-2002; 2002WO-US003634.
                                                                                                                                        2001WO-US004153.
                                                                                                                                                                                                                                                          HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                          WPI; 2002-643455/69.
                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABS68606.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 352 AA;
WO200264612-A2
                                                                                                                  09-FEB-2001;
                                      22-AUG-2002.
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Human, G-protein chemokine receptor; CCRS, HDGNR10 protein, cancer, inflammation, viral infection; autoimmune disease; neurodegeneration; rheumatical arthritis; Pneumocystis carinii infection; Kaposi's sarcoma; hyperproliferative disease; receptor.

09-FEB-2001; 2001US-00779880. 09-FEB-2000; 2000US-0181258P. 09-MAR-2000; 2000US-0187999P. 22-SEP-2000; 2000US-0234336P.

US2002061834-A1.

23-MAY-2002.

Homo sapiens.

Human G-protein chemokine receptor (CCR5), HDGNR10 #1.

24-FEB-2003 (first entry)

AAE25808 standard; protein; 352 AA.

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The invention describes an isolated polynuclectide encoding a first antibody at least 95-100% identical to a second antibody consisting of antibody at least 95-100% identical to a second antibody consisting of an anino acid sequence comprising at least one, two or three CDR regions of a variable heavy (VH) or variable light (VL) domain of the antibody consisting of XF3-57-57-58-1818.

CC expressed by a hybridoma cell line consisting of XF3-571, XF1.1F6, XF2/28.25G1, XF2/28.36A1, XF2/28.35F1, OFF1.1F6, XF2/28.35G1 or AF2/28.38F1 or XF2/28.38F2. The antibody is useful treating, preventing, ameliorating, prognosing or monitoring cancers or other diseases or disorders e.g. immunologic deficiency syndromes such as blood protein disorders and ataxia telanglectasia, inflammation associated disorders such as endoctoxin lethality, nephritis and inflammatory bowel disease, conditions associated with an increase in certain haematopoietic cells such as histiocytosis, defective or aberrant chemotaxis of immune cells or T-cell antigen presenting cell interaction, an infections disease, an autoimment disease such as Addison's disease, disorder an viral infection, eycomegalovitus or poxvirus infection, a Pneumocystis carnii infection, eycomegalovitus or poxvirus infection, a Pneumocystis carnii infection, kaposi's sarcoma, cardiovascular disorders such as atheroselerosis, lymphocytopenias, or a disorder associated with aberrant expression of novel human G-protein chemokine receptor (CCRS) HDGNRIO #1 and and or disorder receptor (CCRS) HDGNRIO #1 and and or disorder protein chemokine receptor (CCRS) HDGNRIO #1
                                                                                                 neurodegenerative disorder; viral infection; poxvirus infection; HIV;
human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;
Pneumocystis carnii infection; cardiovascular disorder; atherosclerosis;
immunologic deficiency syndrome; blood protein disorder; nephritis; ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease; histicoytosis; chemotaxis; infectious disease; autcimmune disease; Addison's disease; dermatitis; rheumatoid arthritis; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human G-protein Chemokine Receptor gene (HDGNR10) useful for treating, preventing, ameliorating or monitoring diseases or disorders associated with aberrant expression of HDGNR10 e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Fig 1A-B; 562pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roschke V, Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                          09-FEB-2001; 2001WO-US004153.
12-UUN-2001; 2001US-029757P.
08-AUG-2001; 2001US-0310458P.
12-OCT-2001; 2001US-03447P.
21-DEC-2001; 2001US-0341725P.
                                                                                                                                                                                                                                                                                                                                                                        08-FEB-2002; 2002WO-US003634.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
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Best Local Similarity
                                                                                                                                                                             lymphocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 352 AA;
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                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                          09-FEB-2001;
                                                                                                                                                                                                                                                                                                                         22-AUG-2002.
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New nucleic acid encoding antibodies to the human CCRS receptor HDGNR10, useful for treatment, prevention and diagnosis of e.g. cancer, also

Claim 61; Page 163-164; 186pp; English.

related antibodies.

Ruben SM;

Li Y,

Rosen CA, Roschke V, WPI; 2002-499674/53.

N-PSDB; AAD42409.

ROSE/) ROSEN C A. ROSC/) ROSCHKE V. (RUBE/) RUBEN S M.

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The invention relates to human G-protein chemokine receptor (CCR5), HDGNR10 proteins and nucleic acid molecules encoding such proteins. CCR5 antibodies are used for the treatment or prevention of inflammation, defective or aberrant chemotaxis of immune cells or T cell antigenpresenting cell interaction, viral infections (specifically human immune deficiency (including its early stages), cytomegalo or pox viruses), autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis carinii infection, Raposi's sarcoma or any condition associated with aberrant expression of CCR5 or their ligands. They are also used for the detection, diagnosis, prognosis and monitoring of cancers or other hyperproliferative diseases. The present sequence is human G-protein chemokine receptor (CCR5), HDGNR10 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 126; DB 5; Length 352; 100.0%; Pred. No. 2.6e-11;
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Best Local Similarity 100.0
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE25811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 34
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Gaps ; 0

0; Indels

Mismatches

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Conservative

22;

Matches

à g

> RESULT 33 AAE25808

100.0%; Score 126; DB 5; Length 352; 100.0%; Pred. No. 2.6e-11;

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98US-00195662

18-NOV-1998;

20-JUN-2002.

36-JUN-1995;

US2002076745-A1.

Homo sapiens.

Page 19

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The invention relates to human G-protein chemokine receptor (CCRS), this invention relates to human G-protein chemokine receptor (CCRS) antibodies are used for the treatment or prevention of inflammation, defective or aberrant chemotaxis of immune cells or T cell antigenpresenting cell interaction, viral infections (specifically human immune deficiency (including its early stages), cytomegalo or pox viruses), autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis carinii infection, Kaposi's sarcoma or any condition associated with detection, diagnosis, prognosis and monitoring of cancers or other hyperproliferative diseases. The present sequence is human G-protein chemokine receptor (CCRS), HDGNR10 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding antibodies to the human CCRS receptor HDGNR10, useful for treatment, prevention and diagnosis of e.g. cancer, also
                                Human; G-protein chemokine receptor; CCR5; HDGNR10 protein; cancer; inflammation; viral infection; autoimmune disease; neurodegeneration; rheumatoid arthritis; Pheumocystis carinii infection; Kaposi's sarcoma; hyperproliferative disease; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 126; DB 5; Length 352; 100.0%; Pred. No. 2.6e-11; tive 0; Mismatches 0; Indels
 Human G-protein chemokine receptor (CCR5), HDGNR10 #2.
                                                                                                                                                                                                                                                                                                                                                                                                                          Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 170; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 OWDFGNIMCOLLIGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                          Li Y,
                                                                                                                                                                                                                                                            09-FEB-2000; 2000US-0181258P.
                                                                                                                                                                                                                                                                                 09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
                                                                                                                                                                                                                            09-FEB-2001; 2001US-00779880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100..
Best 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        Rosen CA, Roschke V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-499674/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               related antibodies.
                                                                                                                                                                                                                                                                                                                                (ROSE/) ROSEN C A. (ROSC/) ROSCHKE V.
                                                                                                                                                                                                                                                                                                                                                                                    (RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAD42426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 352 AA;
                                                                                                                                                      US2002061834-A1
                                                                                                                       Homo sapiens,
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                                                                                                                                                                                                                                                                                       7-transmembrane receptor; G-protein coupled receptor; GFCR; HDGNR10; G-protein chemokine receptor; haematopoietic; immunosuppressant; antiparasitic; antipsoriatic; antiallergic; antiinflammatory; cytostatic; antirheumatic; antiarthritic; gene therapy; human; receptor.
0; Gaps
                                                                                                                                                                                                                                                           G-protein chemokine receptor, HDGNR10.
                                                                                                                                                    ABB81054 standard; protein; 352 AA
                                                                                                                                                                                                                         05-NOV-2002 (first entry)
                                                                                                                     RESULT 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel human 7-transmembrane receptor, HDGNR10, which has been identified as a G-protein chemokine receptor. The GPCR HDGNR10 polypeptide can be expressed by standard recombinant methodology. Compounds that activate or inhibit the receptor polypeptide, optionally expressed from DNA in gene therapy vectors, are used to treat diseases that require: (a) activation of the receptor (e.g. stimulation of haematcopoises, treatment of solid tumours, T-cell mediated autoimmune diseases, parasitic infections, psoriasis etc.); or (b) inhibition of the receptor (e.g. allergy, inflammation, rheumatoid arthritis, silicosis etc.). The present sequence represents the human HDGNR10 receptor
                                                                                                                                                                                                                                                                                    New polynucleotide encoding a human G protein chemokine receptor HDGNR10, useful e.g. for treating tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human chemokine C-C motif receptor 5, CCR5, haplotype pair; isogene; single nuclectide polymorphism; SNP; human immunddeficiancy virus 1; HIV-1 infection; acquired immunodeficiency syndrome; AIDS; antiviral; genotype; polymorphic variant; transgenic; drug screening; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 126; DB 5; Length 352; 100.0%; Pred. No. 2.6e-11; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human chemokine (C-C motif) receptor 5 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB08343 standard; protein; 352 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 OWDFGNIMCOLLIGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label= Leu, Gln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Phe, Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 223
/label= Arg, Gln
                                                                                                                                                                                                                                                                                                                                Claim 7; Fig 1; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22; Conservative
                                                                                                                                                                                                                                          WPI; 2002-598724/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                              (LIYY/) LI Y.
(RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                       N-PSDB; ABN86542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 352 AA;
                                                                                                                                                                                                             Li Y, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosome 3p21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB08343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB08343
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The present sequence is that of a polypeptide encoded by the human chemokine (C-C motif) receptor 5 (CCR5) gene of the invention (see ABA97119, ABA97119). The specification describes haplotyping the CCR5 gene of an individual by determining if the individual has one of the CCR5 haplotypes or haplotype pairs fully defined in the specification. The specification also describes an isolated polymorlectide comprising a nucleotide sequence which is a polymorphic variant of the reference CCR5 gene sequence and comprises an isogene defined by a haplotype described in the specification and itse encoded polypeptide. The methods of the invention are useful to diagnose and develop treatment for diseases associated with abnormal expression or function of the gene. The CCR5 immunodeficiency virus (HIV)-1 infection and the progression to acquired immunodeficiency virus (HIV)-1 infection and the progression to acquired immunodeficiency virus (HIV)-1 infection and the progression to acquired individual; predicting a haplotype pair for the CCR5 gene of an individual; predicting an association between a trait and a haplotype or haplotype pair of the CCR5 gene. The specification describes a composition comprising a genotyping oligonucleotide for detecting a CCR5 polymorphism, a recombinant non-human organism transformed with CCR5 polymorphism, a recombinant non-human organism transformed with CCR5 polymorphism, a recombinant the CCR5 polypeptide and a method for screening drugs targeting the CCR5 polypeptide and a method for cereening drugs targeting the CCR5 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New haplotypes of the human chemokine (C-C motif) receptor 5 gene, useful to diagnose and treat diseases associated with its abnormal expression or function, including human immunodeficiency virus-1 infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 126; DB 5; Length 352; 100.0%; Pred. No. 2.6e-11; tive 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human G-protein chemokine receptor, HDGNR10, protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG75540 standard; protein; 352 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 29; Fig 3; 61pp; English.
                                                                                                                                                                                                                                                                                                               (GENA-) GENAISSANCE PHARM INC.
                                                                                                                                                                                                                                      05-APR-2000; 2000US-0194361P.
                                                                                                                                                       04-APR-2001; 2001WO-US010708.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABA97318, ABA97319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-APR-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                              Kliem SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-041282/05
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WO200177125-A2.
                                                                         18-OCT-2001,
                                                                                                                                                                                                                                                                                                                                                                                                  Choi JY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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The invention discloses a G-protein chemokine receptor (sometimes referred to as a 7-transmembrane receptor) polypeptide, HDGNR10, and the polymuclectide encoding it. G-protein chemokine receptors are involved in signal transduction pathways. The polymuclectide and polypeptide can be used to identify compounds which activate or inhibit activation of the protein and these compounds are useful for treating a patient having need to activate or inhibit a G-protein chemokine receptor. The compound is administered by providing to the patient DNA encoding the agonist or antagonist and expressing them in vivo (gene therapy). The oplymuclectides and polypeptide are also useful for for disquasing of the protein, for chromosome identification or as immunogens for producing the protein, for chromosome identification or as immunogens for producing national elevations, andiogenesis, to treat solid tumours, chronic infections, leukaemia, T-cell mediated auto-immune diseases, parasitic infections, psoriasis and to stimulate growth factor activity. Antagonists are useful in the prevention and treatment of allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation, histamine and IgS-mediated allergic reactions, prostaglandin-independent fever, bone marrow failure, sillogis, sarcoidosis, rheumatoid arthritis, human uncertices. The sequence presented is the the prevented of the prevented of the beaution and the prevented of the beaution.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human G-protein chemokine receptor polypeptide useful for diagnostic purposes and for identifying modulators of the polypeptide useful for treating leukemia, autoimmune diseases, psoriasis and allergic
sarcoidosis; rheumatoid arthritis; shock; hyper-eosinophilic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, cancer; diagnosis; screening; modulator; leukaemia; ischaemia; heart disease; atherosclerosis; endometriosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 126; DB 6; Length 352; 100.0%; Pred. No. 2.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cancer related protein SEQ ID NO:259.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93 OWDFGNÍMCOLLÍGLÝFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 OWDFGNIMCOLLIGLYFIGFFS 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; Fig 1; 22pp; English.
                                                                                                                                                                              11-FEB-2000; 2000US-00502783.
                                                                                                                                                                                                                            95US-00466343.
                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUL-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human HDGNRIO protein
                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-208944/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ABX10635.
                                                                                         US2002132269-A1.
                                                                                                                                                                                                                                                                                                                 Li Y, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 352 AA;
                                                                                                                                                                                                                          06-JUN-1995;
                                              Homo sapiens.
                                                                                                                                     19-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABR58602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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The present invention describes an isolated nucleic acid molecule, which comprises the sequence of any of the genes that are up-regulated or down-regulated in specific cancers (e.g. about 1031 genes up-regulated in a require lukemia). ACC72641 to ACC72860 represent cancer related gene nucleotide sequences which encode the proteins given in ARR58709. Also described: (1) determining the presence or absence of a pathological cell in a patient; (2) an expression vector comprising a nucleic acid molecule described above; (3) a host cell comprising the vector; (4) an isolated polypeptide, which is encoded by the nucleic acid; (5) an antibody that specifically binds the polypeptide of (4); (6) specifically targeting a compound to a pathological cell in a patient by administering to the patient the antibody above; and (7) a drug screening assay. The nucleic acid is useful for therapeutic targets. In particular, the nucleic acid is useful for charapeutic targets. In particular, the nucleic acid is useful for bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary, pancreas, prostate, skin and uterus, wounds, ischaemia, heart diseases, athonic contracts and endometriosis. The nucleic acid is also useful in a bathology screening, pancrearing the reating these asthonic acid is also useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, urological disorder; stress urinary incontinence; prostate cancer; benign prostatic hyperplasia; overactive bladder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98
                                                                                                                                                                                                                                                                                                                                                                                                                                                              New genes that are up-regulated or down-regulated in cancers, useful a markers for diagnosing e.g. cancer, ischemia or heart diseases, or as therapeutic targets for screening drugs for treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 126; DB 6; Length 352; 100.0%; Pred. No. 2.6e-11; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                         Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human C-C chemokine receptor type 5 (333) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Page 745; 767pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAO29514 standard; protein; 352 AA.
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                                                                                                                                                       17-SEP-2001; 2001US-0323469P.
20-SEP-2001; 2001US-0323897P.
13-NOV-2001; 2001US-035666P.
09-FEB-2002; 2002US-0355145FP.
                                                                                                                                                                                                                                                                                                  (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                          08-FEB-2002; 2002US-0355257P. 12-APR-2002; 2002US-0372246P.
                                                                                                                     17-SEP-2002; 2002WO-US029560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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Best Local Similarity 100.0
Matches 22, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-354600/33.
N-PSDB; ACC72740.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 352 AA;
                                       WO2003025138-A2.
  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-AUG-2003
                                                                              27-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pathologies
                                                                                                                                                                                                                                                                                                                                                             Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA029514;
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SXXXXX
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The invention relates to a method for treating an urological disorder which comprises assaying the ability of the compound to modulate 313, 334, 5464, 188717 or 33524 nucleic acid expression or polypeptide activity. The method is useful for identifying a compound for treating an urological disorder comprising urinary incontinence e.g., overactive/oversensitive bladder, overflow urinary incontinence, stress urinary incontinence ansect by peripheral nervous system, prostatitis, benign prostatic hyperplasia, prostate cancer or kiney disorders. It is also used in gene therapy. The prostate cancer or kiney disorders. It is also used in gene therapy. The prostate the method of the invention protein. This sequence is used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                           Identifying a compound, capable of treating urological disorder e.g., benign prostatic hyperplasia, by assaying the ability of the compound to modulate 313, 333, 5464, 188717 or 33524 nucleic acid expression or polypeptide activity.
overflow urinary incontinence; gene therapy; nephrotropic; prostatitis; kidney disorder; C-C chemokine receptor type 5; CCR5; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 126; DB 6; Length 352; 100.0%; Pred. No. 2.6e-11; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human G-protein chemokine receptor (HDGNR10) polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; G-protein chemokine receptor; receptor; HDGNR10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 81; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABU61654 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 OWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                               07-NOV-2002; 2002WO-US035824.
                                                                                                                                                                               07-NOV-2001; 2001US-0344552P.
                                                                                                                                                                                                             (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-00195662.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-SEP-2002; 2002US-00232686.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-00466343.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7-transmembrane receptor.
                                                                                                                                                                                                                                                                               WPI; 2003-449396/42.
                                                                                                                                                                                                                                               Silos-Santiago I;
                                                                                                                                                                                                                                                                                           N-PSDB; AALS9912.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 352 AA;
                                                                               WO2003039475-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2003023044-A1.
                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUN-1995;
                                                                                                               15-MAY-2003
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99US-00339912.
                              (HUMA-) HUMAN GENOME SCI INC.
                                                               Li Y, Ruben SM;
25-JUN-1999;
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WPI; 2003-456307/43. N-PSDB; ACA61721.

Producing an antibody, involves immunizing an animal with a polypeptide or with a polypeptide encoded by the human G-protein chemokine receptor clone in ATCC 97183, and recovering the antibody: Claim 1; Fig 1; 23pp; English.

The invention relates to a method of producing an antibody, involving immunishing an animal with a human G-protein chemokine receptor (HDGNR10) polypeptide (also referred to as a human 7-transmembrane receptor) and recovering an antibody which binds the polypeptide. The method is useful for producing an antibody which binds specifically to the human G-protein chemokine receptor polypeptide. This sequence represents the HDGNR10 polypeptide of the invention 

Sequence 352 AA;

0; Gaps 100.0%; Score 126; DB 6; Length 352; 100.0%; Pred. No. 2.6e-11; ive 0; Mismatches 0; Indels ( Query Match Best Local Similarity 100.0 Matches 22, Conservative

ò g

Search completed: September 28, 2004, 09:03:37 Job time : 56.525 secs

September 28, 2004, 09:00:23; Search time 19.8 Seconds (without alignments) 57.362 Million cell updates/sec GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM protein - protein search, using sw model Run on:

US-10-084-813-12 Perfect score:

126 1 QMDFGNTMCQLLTGLYFIGFFS 22 BLOSUM62 Scoring table: Sequence:

389414 seqs, 51625971 residues Searched:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/Purus\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/Purus\_COMB.pep:\* Issued\_Patents\_AA:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	Segmence 4, Appli	equence 17,	equence 6,	N	equence 13,	14,	e 2,	equence 52,	ທີ	equence 52,	'n	7	1,	equence 9,	3,	equence 4,	equence 4,	20,	20,	7,	equence 2,	20,		7	7	7	
DI.	US-08-833-752-4	-087-2	-08-833-75	US-08-466-343D-2	US-09-087-232A-13	US-08-861-105-14	9	-09-045-583-	-09-217-605-	4-1	-08-833-75	US-09-502-783A-2	-964-60-	US-08-466-343D-9	US-08-461-244-3	-08-45	-08-446-6	-09-045-58	-09-534-18	US-08-833-752-7	-09-131-	US-09-131-827A-20	PCT-US95-00476-4	US-08-450-393A-2	US-08-446-669-2	r-US95-00476-;	38-307-499-
DB.	4	m	4	m	m	m	m	ო	4	4	4	4	4	m	~1	ч	m	ო	4	4	4	4	Ŋ	н	m	w	н
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Query	100.0		100.0	100.0		00		00	00		00	00	100.0		69.0		0.69								0.69		65.9
Score	126	126	126	126	126	126	126	126	126	126	126	126	126	87	87	87	87	87	87	87	87	87	87	87	87	87	83
esult No.	-1	7	ო	4	D	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

equence		Sequence 56, Appl	•	51,	Sequence 51, Appl	Sequence 2, Appli	13,	o,	~	Ŋ	'n	Sequence 53, Appl	Seguence 1, Appli	53, App	Sequence 14, Appl	Sequence 5, Appli	ď
-09-299	US-08-461-244-2	US-09-045-583-56	US-09-534-185-56	US-09-045-583-51	US-09-534-185-51	US-08-724-984A-2	US-09-886-319A-13	US-09-502-783A-9	US-08-012-988A-2	US-08-450-393A-5	US-08-446-669-5	US-09-045-583-53	US-09-239-938-1	US-09-534-185-53	US-09-886-319A-14	PCT-US95-00476-5	US-08-833-752-9
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269	355	355	355	360	360	354	355	329	355	355	355	355	355	355	355	355	355
	65.1	65.1	65.1	64.3	64.3		60.3			56.3	ġ	ė.	6	Ġ	9	6	4
83	82	82	82	81	81	80	16	74	71	71	71	77	71	71	71	71	
				32	33	34		36	37	38	39	40	41	42	43	44	

```
APPLICANT: SAMSON, MICHEL
APPLICANT: SAMSON, MICHEL
APPLICANT: VASSART GILEER
APPLICANT: VASSART GILEER
APPLICANT: USSART, GILEER
APPLICANT: LIBERY, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEWOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: Of SAME AND SEGRET OF STREET: 620 Newport Center Drive 16th Floor
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STREET: CA
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
APPLICATION DATA: US/08/833,752
FILING DATE: US/08/833,752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 QWDFGNTMCQLLTGLYFIGFFS 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 9-ARR-1997
GLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
FREJESTATION NUBBER: 34,115
REFERENCE/DOCKET NUBBER:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE GRARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-833-752-4
                                                Sequence 4, Application US/08833752
Patent No. 6448375
                                                                                                    GENERAL INFORMATION:
RESULT 1
US-08-833-752-4
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RESULT 2

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,752
FILING DATE: 9-APR-1997
CLASSIFICATION: 536
ATTORNEY/AGATION: 1NFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,343D FILING DATE: 06-UNN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION VINBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEFRIX: (202) 371-2600
TELEFRIX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                    JOLECUTE 215 amino acids
TYPE: amino acid
TOPOLOGY: line
                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGIH: 215 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 352 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                 / MOLECULE TYPE: protein
US-08-833-752-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein US-08-466-343D-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: USA
COUNTRY: USA
20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-08-466-343D-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                 GENERAL INFORMATION:
APPLICANT. Quillent et al.
APPLICANT. Quillent et al.
TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS;
ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
STREET: 30 ROCKefeller Plaza
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: SAMSON, MICHEL
APPLICANT: PARENTIER, MAKE
APPLICANT: PARENTIER, MAKE
APPLICANT: PARENTIER, MAKE
APPLICANT: USERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 126; DB 3; Length 215; Best Local Similarity 100.0%; Pred. No. 1.5e-11; Matches 22; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/087,232A
FILING DATE: 28 MAY 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 28 MAY 1998
CLASSIFICATION: 435
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/048,057
FILING DATE: 30 MAY 1997
ATTORNEY/AGENT INFORMATION:
NAME: KOLE, LISA B.
REGISTRATION NUMBER: 35,225
REGISTRATION NUMBER: 35,225
REFENCE/OCCET NUMBER: AP 31115
TELEPHONE: (212) 408-2628
TELEPHONE: (212) 765-2219
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 ÓWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                         Sequence 17, Application US/09087232A Patent No. 6153431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 OWDFGNIMCOLLIGLYFIGFFS 22
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Patent No. 6448375
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
GY: linear
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                                                                                                                                                                                                                                                                                                        USA
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ZIP: 10112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
  US-09-087-232A-17
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Gaps
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                                                                                                                                                                                                                                                                          Sequence 2, Application US/08466343D

Patent No. 6025154

GENERAL INFORMATION:
APPLICANT: LI, YA:
TITLE OF INVENTION: CHEMOKINE RECEPTOR HOGNRIO (AS AMENDED)
INVERE OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: LIOO NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 126; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels (
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93 QWDFGNTMCQLLTGLYFIGFFS 114

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NESOUR: 232A-13

KENOLIS - 09-087-232A-13

Sequence 13, Application US/09087232A

Sequence 13, Application US/09087232A

PARENT NO. 6153431

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Quillent et al.
TITLE OF INVENTION: HUMAN IMMUNOBERICIENCY VIRUS CO-RECEPTOR
TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
STREET: 30 Rockefeller Plaza

STREET: New York

CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-861-105-14

'Sequence 14, Application US/08861105

Sequence 14, Application US/08861105

Sequence 14, Application

Sequence 14, Application

Sequence 14, Application

Patent No. 6258527

APPLICANT: LITTMAN, DAN R.

APPLICANT: LANDAU, NATHANIEL R.

APPLICANT: LANDAU, NATHANIEL R.

APPLICANT: LANDAU, NATHANIEL R.

APPLICANT: LANDAU, NATHANIEL R.

TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH

TITLE OF INVENTION: USES THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
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Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                     STATE: New YORK
COUNTY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Relase #1.0, Version #1.30 (EPO)
SOFWARE: Patentin Relase #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA: VS/09/087,232A
FILING DATE: 28 MAY 1998
CLASSIFICATION: 435
PRICATION NUMBER: 60/048,057
FILING DATE: 30 MAY 1997
ATTORNEY/AGBNT UNCRMATION:
NAME: KOLE, LISA B.
REGISTRATION NUMBER: 35,25
REFERENCE/DOCKET NUMBER: AP 31115
TELEPHONE: (212) 408-2628
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 408-2628
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 anino acids
TYPE: anino acids
TYPE: anino acids
TYPE: anino acids
TYPE: ANINOSANIALION
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STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 QWDFGNTMCQLLTGLYFIGFFS 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-087-232A-13
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Sequence 2, Application US/08575967A
Patent No. 6265184
GENERAL INFORMATION:
APPLICANT: Gray et al.
TITLE OF INVENTION: Chemokine Receptor Materials and Methods
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS: 16
CORRESPENDENCE ADDRESSE: Marchall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 126; DB 3; Length 352; Best Local Similarity 100.0%; Pred. No. 2.5e-11; Matches 22; Conservative 0; Mismatches 0; Indels (
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/575,967A
                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,105
                                                                                                                                                                                                                                                                                                                 PILING DATE:

CLASSIFICATION: 436
PRIOR APPLICATION: 436
PRIOR APPLICATION: 436
PRIOR APPLICATION: 436
CLASSIFICATION: 436
CLASSIFICATION: 436
PRIOR APPLICATION: 436
PRIOR APPLICATION: 436
PRIOR APPLICATION: 436
PRIOR APPLICATION: DATA:
APPLICATION NUMBER: US 08/227,319
PRIOR APPLICATION: DATA:
APPLICATION NUMBER: US 08/227,319
PRIOR APPLICATION: NUMBER: US 08/227,319
TELECOMMONICATION: NUMBER: 1049-1-004 NI
TELECOMMONICATION INFORMATION:
TELECOMMONICATION FOR SEQ 1D NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: ATRINEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECTLE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                         New Jersey
USA
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                    07601
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US-08-575-967A-2
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MESCULE

Sequence 5, Application US/09517605

Sequence 5, Application US/09517605

Sequence 5, Application US/09517605

Sequence 5, Application US/09517605

GENERAL INFORMATION:

APPLICANT: Littman, Dan R.

APPLICANT: Kwon, Douglas S.

APPLICANT: Wan Kooyk, Yvette

APPLICANT: Van Kooyk, Yvette

APPLICANT: Wan Kooyk, Tueo

TITLE OF INVENTION: CELLS

FILE REFERENCE: 1049-1-017

CURRENT APPLICATION: US/09/517,605

CURRENT FILING DATE: 2000-03-02

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 52, Application US/09534185
Patent No. 6403767
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptahelical Receptor Superfamily and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 126; DB 4; Length 352; 100.0%; Pred. No. 2.5e-11; tive 0; Mismatches 0; Indels (
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COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,185
FILING DATE: 24 Mar-2000
CLASSIFICATION NUMBER: US/09/534,185
FILICATION NUMBER: 09/045,583
APPLICATION NUMBER: 09/045,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESSES
ADDRESSES: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PILING DATE: <Unknown>
ATTORNEY/ACRATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                       93 OWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93 QWDFGNTMCQLLTGLYFIGFFS 114
       1 OWDFGNTMCQLLTGLYFIGFFS 22
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INFORMATION FOR SEQ ID NO: 52:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.0
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens US-09-517-605-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-09-534-185-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                   NAWE/KEY: misc feature; OTHER INFORMATION: /= "88C amino acid sequence" US-08-575-967A-2
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 126; DB 3; Best Local Similarity 100.0%; Pred. No. 2.5e-11; Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICALL..
PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MI-044
TELECOMMUNICATION INFORMATION:
TELEFERIOR: (647)22-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEO ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TYPE: ...
THEAT
NAME: NO. 6265184and, Greta E.
REGISTRATION NUMBER: 35.302
REFERENCE/DOCKET NUMBER: 32918
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-485-1900
TELEFAX: 206-485-1900
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 QWDFGNTWCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 OWDFGNIMCOLLIGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 52, Application US/09045583
Patent No. 6287805
                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                  linear
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APPLICANT: Ruben, Steven M.

TITLE OF INVENTION: Polymuclectides Encoding Human G-Protein Chemokine Receptor (CCR5)
FILE OF INVENTION: PLOSMING
FILE OF INVENTION: HDGNIN
FILE OF INVENTION: 1488.1150006
CURRENT APPLICATION NUMBER: US/09/502,783A
CURRENT FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE; Patentin version 3.0
SEQ ID NO SEQ ID NOS: 9
LENGTH: 352
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Patent No. 6025154
GENERAL INFORMATION:
TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGNRIO (AS AMENDED)
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: 9
CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09796202

Sequence 1, Application US/09796202

Parent No. 6548636

GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048641010/DPW/SHS
CURRENT APPLICATION NUMBER: US/09/796,202

CURRENT FILING DATE: 2001-02-28

NUMBER OF SEQ ID NOS: 17

SEQ ID NO 1

SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 126; DB 4; Length 352; Best Local Similarity 100.0%; Pred. No. 2.5e-11; Matches 22; Conservative 0; Mismatches 0; Indels C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93 QWDFGNTWCQLLTGLYFIGFFS 114
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-09-502-783A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: WASHINGTON STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U
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US-08-466-343D-9
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US-09-796-202-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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| Sequence 5, Application US/08833752
| Patent No. 6448375
| GENERAL INFORMATION:
| APPLICANT: PARMENTIER, WARC
| APPLICANT: PARMENTIER, WARC
| APPLICANT: LIBERT, GILDERT
| APPLICANT: LIBERT, FREDERICK
| TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
| TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
| TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
| TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
| TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
| TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
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| TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
| TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
| TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
| TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR NUCLEIC ACID MOLECULES ENCODING SAID RECE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 126; DB 4; Length 352; Best Local Similarity 100.0%; Pred. No. 2.5e-11; Matches 22; Conservative 0; Mismatches 0; Indels (
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
COMPUTER: IBM FC Compatible
COMPUTER: IBM FC COMPATIBLE
COMPATION: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 33 (S) (8) (833,752
FILING DATE: 9-APR-1997
CLASSIFICATION: NUMBER: 34,115
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: 34,115
REFERENCE/COCKET NUMBER: 34,115
SEQUENCE CHARACTERISTICS:

'LENGTH: 352 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-534-185-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 OWDFGNTMCQLLTGLYFIGFFS 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 352 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-833-752-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Li, Yi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-502-783A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-833-752-5
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                                                 Query Match 69.0%; Score 87; DB 1; Length 347; Best Local Similarity 66.7%; Pred. No. 2e-05; Matches 14; Conservative 3; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08450393A

Patent No. 5707815
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Charc, Israel
APPLICANT: Coughlin, Shaun
ITIES OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
ITIES OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS: 200RBNCES: ADDRESS: ADDRESSEE: ADDRESS
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US-08446-669-4
US-08446-669-4
Sequence 4, Application US/08446669
Sequence 10. 6132987
GENERAL INFORMATION:
APPLICANT: Charc, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: PROTEIN RECEPTORS
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/08/450,393A

FILING DATE: May 25, 1995

CLASSIFICATION: 424

ATTORNEY AGENT INFORMATION:

NAME: LOAD CSETT. LUADN

REGISTRATION NUMBER: 31,822

REFERRINGE/DOCKET WINGHER: UCAL-237/02US

TELECOMMUNICATION INFORMATION:

TELE
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ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                      92 EWVFGNAMCKLFTGLYHIGYF 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Palo Alto
STATE: California
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US-08-450-393A-4
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APPLICANT: Soppet, Daniel R.
APPLICANT: Ruben, Steven M.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HOBER32
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: STRART & OLSTEIN
STREET: 6 Becker Farm Road
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,343D
FILING DATE: 06-JUN 1995
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
TELEORWUNICATION INFORMATION:
TELEPRAK: (202) 371-2600
INFORMATION FOR SEQ ID NO: 9:
SRQUENCE CRARACTERISTICS:
LENGTH: 344 anino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFEMATING SYSTEM: RC-DOS/MS-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 69.0%; Score 87; DB 3; I Local Similarity 66.7%; Pred. No. 1.9e-05; Nes 14; Conservative 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INPORMATION:
NAME: Perraro, Gregory D.
REGISTATION NUMBER: 36,134
REFERENCE/DOCKET WUMBER: 325800-445
TELECOMMUNICATION INPORMATION:
TELEPHONE: 201-994-1700
TELEPHONE: 201-994-1744
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/461,244
FILING DATE: 05-JUN-1995
CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08461244
Patent No. 5776729
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 344 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 347 amino acids amino acids
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MOLECULE TYPE: protein
US-08-461-244-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Roseland
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U
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US-08-461-244-3
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Patent No. 6287805

Patent No. 6287805

GENERAL INFORMATION:

TILLE OF INVENTION:

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 69.0%; Score 87; DB 3; Length 360; Best Local Similarity 66.7%; Pred. No. 2e-05; Matches 14; Conservative 3; Mismatches 4; Indels
                                                                                 COMPLEX: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,669
FILING DATE: May 25, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meeley, Richard
REGISTRATION NUMBER: 30,092
REPERENCE/POCKET NUMBER: 30,092
RELEPAN: 415-843-500
TELEPAN: 415-843-500
TELEFAX: 415-843-500
TELEFAX: 415-843-6063
TELEFAX: 415-843-6063
TELEFAX: 415-817-063
TELEFAX: 415-817-063
TELEFAX: 308816COOleyPA
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 anino acids
TYPE: amino acids
TYPE: amino acids
TYPE: Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONTINUE READABLE FORM:

MEDIUM TYER READABLE FORM:

MEDIUM TYES: Floppy disk
COMPUTER: IBM PC COMPACIBLE
OPERATING SYSTEM:
OPERATING SYSTEM:
OPERATING SYSTEM:
OFFICATION DATA:
APPLICATION NUMBER: US/09/045,583
FLING DATE:
APPLICATION NUMBER:
FLING DATE:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
NAME: MANDARGOUTABLY MAY E.
REGISTRATION NUMBER: 36,207
REGISTRATION NUMBER: 36,207
REGISTRATION NUMBER: 36,207
REGISTRATION NUMBER: MNI-044
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 OWDFGNTMCOLLTGLYFIGFF 21
5 Palo Alto Square
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-669-4
                       CITY: Palo Alto
STATE: California
COUNTRY: USA
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PRODRATION FOR ESC ID NO: 50:

REQUEST: 10 CARACTERISTICS:

LENGTH: 310 caid

TYPE: alio acid

TYPE: alio ac
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ATTORNEY/AGENT INFORMATION:
NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555-291
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-977-1001
                                                                                                                                                                                                                                  US-09-131-827A-20
; Sequence 20, Application US/09131827A
Patent No. 6600030
; GENERAL INFORMATION:
                                                                                                                                        105 EWVFGNAMCKLFTGLYHIGYF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QWDFGNTMCQLLTGLYFIGFF 21
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Best Local Similarity 66.7*
Matches 14; Conservative
Query Match
Best Local Similarity 66.74
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Homo sapiens
US-09-131-827A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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                 Sequence 7, Application US/08833752

Patent No. 6448375

Barent No. 6448375

Barent No. 6448375

Barent No. 6448375

Barent Narchart Samon, MICHEL

APPLICANT: BARNENTIER, MARC

APPLICANT: VASSART, GILBERT

APPLICANT: LIBERT, FREDERICK

TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR

TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: ADDRESS:

ADDRESSEE: Roobe, Martens, Olson & Bear

STRRET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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66.7%; Pred. No. 2e-05;
tive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: FLODDY disk
COMPUTER: 1BM FC compatible
COMPUTER: 1BM FC COMPATIBLE
COMPUTER: 1BM FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
RELIGORATION NUMBER: US/08/833,752
FILING DATE: 9-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: O'Brien, Michael
APPLICANT: O'Brien, Stephen J.
APPLICANT: O'Brien, Stephen J.
APPLICANT: Carrington, Mary
APPLICANT: Carrington, Mary
TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
TITLE OP INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
FILE REFERENCE: 14014 0333
CURRENT APPLICATION NUMBER: US/09/131,827A
CURRENT FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
ENGTH: 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 EWVFGNAMCKLFTGLYHIGYF 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09131827A Patent No. 6600030 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: No. 6448375e
US-08-833-752-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 9-APR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Conservative
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CRGANISM: Homo sapiens
US-09-131-827A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 14; Conserva
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                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U
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  US-08-833-752-7
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69.0%; Score 87; DB 4; Length 360; 66.7%; Pred. No. 2e-05; tive 3; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application PC/TUS9500476
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson
STREET: 201 N. Figueroa Street, 5th Floor
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: O'Brien, Michael
APPLICANT: O'Brien, Stephen J.
APPLICANT: Smith, Michael
APPLICANT: Smith, Michael
APPLICANT: Smith, Michael
APPLICANT: Smith, Michael
APPLICANT: Carrington, Mary
TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
TITLE OF INVENTION: MISSENER ALLELE OF THE CR2 GENE
FILE REFERENCE: 14014.0333
CURRENT APPLICATION NUMBER: US/09/131,827A
CURRENT FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/055,659
PRIOR APPLICATION NUMBER: 60/055,659
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIF: 90012-2628
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00476
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Patent No. 6132987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL IN FORMATION:
APPLICANT: Charo, Israel
APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE 14
CORRESPONDENCE 14
CORRESPONDENCE 14
CORRESPONDENCE 14
COUNTRY: Dalo Alto Square
CITY: Palo Alto
STREET: 5 Palo Alto
STREET: 5 Palo Alto
COUNTRY: USA
ZIP: Palo Alto
STREET: MAY 25, 1995
CLASSIPICATION NUMBER: USAL-237/02US
FILICATION NUMBER: USAL-237/02US
TELECOMMUNICATION INFORMATION:
NAME: CSGTT, LUBAN
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEX: 38816COOLEYPA
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH 374 MAINO acids
TERER MINDORMATION COLOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
69.0%; Score 87; DB 1; Length 374;
Best Local Similarity 66.7%; Pred. No. 2.1e-05;
Matches 14; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                Query Match
69.0%; Score 87; DB 5; Length 360;
Best Local Similarity 66.7%; Pred. No. 2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 EWVFGNAMCKLFTGLYHIGYF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                   105 EWVFGNAMCKLFTGLYHIGYF 125
                                                                                                                                                                                                                                                                                                                                                                                                       1 OWDFGNIMCOLLTGLYFIGFF 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08450393A
Patent No. 5707815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QWDFGNTMCQLLTGLYFIGFF 21
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                                               invormation For SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TYPE: amino acid
MULBCULE TYPE: protein
PCT-US95-00476-4
TELEFAX: 310-977-1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-450-393A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-450-393A-2
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Tue Sep 28 15:49:55 2004

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Query Match 65.9%; Score 83; DB 1; Length 269; Best Local Similarity 54.5%; Pred. No. 6e-05; Matches 12; Conservative 7; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-299-268-30
) Sequence 30, Application US/09299268
) Sequence 30, Application US/09299268
) Patent No. 62178629
) APPLICANT: Moyer, Richard W. APPLICANT: Vi uela, Eladio
APPLICANT: Vi uela, Eladio
APPLICANT: Vi uela, Eladio
TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as:
TITLE OF INVENTION: Live Vaccine Vector
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
APPLICATION NUMBER: US 07/908,241
FILING DATE: 1-UTL-1992
APPLICATION DATA:
APPLICATION NUMBER: US 07/908,630
FILING DATE: 29-JUN-1992
CLASSIFICATION:
                                                                                                                                                                                                                                                                     1 OWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                            20 QWIFGNILCKIMSVLYYVGFFS 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QWDFGNTMCQLLTGLYFIGFFS 22
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APPLICATION NUMBER: 08/901,127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 269 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 54.5<sup>†</sup>
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
   ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-307-499-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U.S.A.
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Florida COUNTRY: U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 30, Application US/08307499; Patent No. 5651972; GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Woyer, Richard W. APPLICANT: Vi uela, Eladio APPLICANT: Vi uela, E.P.J. TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a TITLE OF INVENTION: Live Vaccine Vector NUMBER OF SEQUENCES: 60; CORRESPONDENCE ADDRESSE; David R. Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 CITT. Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69.0%; Score 87; DB 5; I
66.7%; Pred. No. 2.1e-05;
tive 3; Mismatches 4.
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CLASSIFICATION 1435

PRIOR APPLICATION DATA;

APPLICATION NUMBER: US 07/908,241

FILING DATE: 1-JUL-1992

PRIOR APPLICATION NUMBER: US 07/908,630

FILING DATE: 29-JUN-1992

CLASSIFICATION 0ATA;

APPLICATION NUMBER: US 07/342,212

FILING DATE: 21-APR-1992

CLASSIFICATION 1435

ATYONEX/ABRATION: 435

ATYONEX/ABRATION: 435

ATYONEX/ABRATION: 435

REGISTRATION NUMBER: 31,794

REGISTRATION NUMBER: 31,794

REGISTRATION NUMBER: 31,794

REGISTRATION NUMBER: 31,794

TELEPHONE: 904-375-8100

TELEPHONE: 904-375-8100

INFORMATION FOR SEQ ID NO: 30: SEGURNATION FOR SEGURNATION FOR SEQ ID NO: 30: SEGURNATION FOR SEGURNA
                                                                       5555-291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 EWVFGNAMCKLFTGLYHIGYF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QWDFGNTMCQLLTGLYFIGFF 21
NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555
TELECOMMUNICATION INFORMATION:
TELEPHAX: 310-977-1001
TELEFAX: 310-977-1003
                                                                                                                                                                                                 TELEX:
| INFORMATION FOR SEQ ID NO: 2:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 374 amino acids:
| TYPE: amino acid
| TOPOLOGY: linear |
| MOLECULE TYPE: protein |
| PCT-US95-00476-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 269 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 14; Conserva
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STATE: Florida
COUNTRY: U.S.A.
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54.5%; Pred. No. 6e-05;
itive 7; Mismatches 3; Indels
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/342,212
FILING DATE: 21-APR-1992
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF35.1.FWCC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
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COMPUTER:
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Sequence 56, Application US/09045583
Sequence 10. 6287805
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 628780561 Molecules of the G Frotein-Coupled NUMBER OF SEQUENCES: 56
CORRESPONDENCES 56
CORRESPONDENCE ADAPTES.
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STREET: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 65.1%; Score 82; DB 1; Length 355; Best Local Similarity 54.5%; Pred. No. 0.00011; Matches 12; Conservative 6; Mismatches 4; Indels
                                                                                                                                                                                                                   APPLICANT: Supper, Daniel R.
APPLICANT: Yi, Li
APPLICANT: Ruben, Steven M.
APPLICANT: Ruben, Craig A.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBER32
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESSEE: STUBRT & OLSTEIN
STREET: Roseland
CITY: Roseland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: usa

ZIP: 0706

COMPUTER: READABLE FORM: ...
MEDIUM TYPE: Floppy disk

COMPUTER: The PC compatible

COMPUTER: THE PC compatible

COMPUTER: THE PC COMPUTER: COMPUTER: COMPUTER: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: ...
APPLICATION NUMBER: Us/08/461,244

FILING DATE: OS-JUN-1995

CLASSIFFACTION: 33 6

ATTORNEY/AGENT INVERMATION: ...
NAME: Ferraro, Gregory D. REGISTRATION NUMBER: 32500-445

TELEFONE: 201-994-1700
TELEFONE: 201-994-1700
TELEFONE: 201-994-1704
TELEFONE: 201-994-1704
TELEFONE: 31-994-1704
TELEFONE: SEQ ID NO: 2: SEQUENCE CHARACTER.ESTICS: ...
LENGTH: 355 emino acide ...
TYPE: amino acid
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20 QWIFGNILCKIMSVLYYVGFFS 41
                                                                                                                                           Sequence 2, Application US/08461244
Patent No. 5776729
GENERAL INFORMATION:
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ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-045-583-56
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Sequence 56, Application US/09534185
Patent No. 6403767
GENERAL INFORMATION: Gerard J. et al.
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled Heptahelical Receptor Superfamily and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDLINI TYPER: FlopRy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PATA:

APPLICATION NUMBER: US/09/534,185

FILING DATE: 24-MARIOWN>

PRIOR APPLICATION NUMBER: 09/045,583

FILING DATE: CONKNOWN>

APPLICATION NUMBER: 09/045,583

FILING DATE: CONKNOWN>

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, AMY E

REFERENCE/DOCKET NUMBER: MNI-044

TELEFONE: (6.17) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 65.1%; Score 82; DB 3; Length 355; Best Local Similarity 54.5%; Pred. No. 0.00011; Matches 12; Conservative 6; Mismatches 4; Indels
              OCHARATING STSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                     PILING DATE:
PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MAIGHAGOURAE, AMW E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECHONIS: (617)227-7400
TELEPAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98 QWVFGTVMCKVVSGFYYIGFYS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 OWDFGNTMCOLLTGLYFIGFFS 22
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IBM PC compatible
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COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: peptide; FRAGMENT TYPE: internal US-09-045-583-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
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GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptanelical Receptor Superfamily and Uses
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Patent No. 638055
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: No. 6388055el Mouse Genomic Clone of the CC-
TITLE OF INVENTION: CKFS Receptor
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: SMICHKline Beecham Corporation
STREET: 709 Swedeland Road, P.O. Box 1539
CITY: King of Prussia
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MEDIUM TYPE: FLOSPY disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,185
FILING DATE: 24-Mar-2000
CLASSIFICATION: UNKNOWN>
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 09/045,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 64.3%; Score 81; DB 4; Length 360; Best Local Similarity 65.0%; Pred. No. 0.00016; Matches 13; Conservative 3; Mismatches 4; Indels
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COUNTRY: USA
COUNTRY: USA
COUPTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MD STORAGE
                                                                                                                                                                               ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: CURNOWN:
ATTORNEY/ABENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REPERENCE/DOCKET NUMBER: MI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECTLE TYPE: peptide
FRAGNENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 360 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617) 742-4214 INFORMATION FOR SEQ ID NO: 51:
                                                                                                                                                                                                                                                       STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHARACTERISTICS
                                                                                                                                   NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                Boston
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US-08-724-984A-2
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TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                      y Match 65.1%; Score 82; DB 4; Length 355; Local Similarity 54.5%; Pred. No. 0.00011; nes 12; Conservative 6; Mismatches 4; Indels
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65.0%; Pred. No. 0.00016;
ive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FLING DATE: 20-MAR-98
CLASSIFICATION: 435
PROR APPLICATION NUMBER:
FILING DATE:
FILING DATE:
                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
                                                                                                                                                                                                                                                                                                                                 98 QWVFGTVMCKVVSGFYYIGFYS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                     1 QWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 51, Application US/09045583
Patent No. 6287805
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 33
US-09-534-185-51
Sequence 51, Application US/09534185
Patent No. 6403767
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                    LENGTH: 355 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (617)227-7400
TELEPAX: (617)242-4214
INFORMATION FOR SEQ ID NO: 51
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 360 amino acids amino acids
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Best Local Similarity 65.09
Matches 13; Conservative
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MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boston
                                                                                                                                                             US-09-534-185-56
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                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                       Matches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/012,988A
FILING DATE: 19930128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 WVFGDAMCKILSGFYYTGLYS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 19930128
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 1528
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEPHAX: 415-543-9601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 355 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 355 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 54.5'
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 47.6 tes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 37
US-08-012-988A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-502-783A-9
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APPLICANT: Werner, Sabine
APPLICANT: Werner, Sabine
APPLICANT: Halle, John-Peter
APPLICANT: Halle, John-Peter
APPLICANT: Regembogen, Johannes
APPLICANTENT: Regembogen, Johannes
APPLICANTENT: Regembogen, Johannes
APPLICANTENT

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APPLICATION NUMBER: US/08/724,984A
                                                                                                                                                                                                                                                                                                        ATG50023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13, Application US/09886319A Patent No. 6586185 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 WIFGDAMCKLLSGFYYLGLYS 119
                     FILING DATE: October 3, 1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTCANEY/AGENT INFORWATION:
NAME: William T. Han
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATGSON
TELECHONE: 610 270 5024
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 OWDFGNIMCQLLTGLYFIGFF 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 WDFGNTMCQLLTGLYFIGFFS 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 354
TYPE: Amino Acid
TOPOLOGY: Linear
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APPLICANT: Ruben, Steven M.

IITLE OF INVENTION: Polymucleotides Encoding Human G-Protein Chemokine Receptor (CCR5) TITLE OF INVENTION: PLOSMENTO POLYMUCLEO FILE OF INVENTION: PLOSMENTO PRICE PREPERINCE: 1488-1150006 CURRENT APPLICATION NUMBER: US/09/502,783A CURRENT FILING DATE: 2001-08-23 PRIOR FILING DATE: 1995-06-06 NUMBER OF SEQ ID NOS: 9

NUMBER OF SEQ ID NOS: 9
SEQ ID NO 9
SEQ ID NO 9
LENGTH: 329
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| Sequence 2, Application US/0801298BA
| Patent No. 565133
| GENERAL INFORMATION:
| TITLE OF INVENTION: Cloning and Expression of Human
| TITLE OF INVENTION: alpha]/RANTES Receptor
| TITLE OF INVENTION: alpha]/RANTES Receptor
| TITLE OF INVENTION: alpha]/RANTES Receptor
| NUMBER OF SEQUENCES: 2
| CORRESPONDENCES: 2
| ADDRESSEE: Townsend and Townsend Khourie and Crew
| STREET: One Market Plaza, Steuart Tower, Suite 2000
| CITY: San Francisco
| STATE: California
| COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Matches
                           Sequence 5. Application US/08450393A;
Patent No. 5707815;
GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Cooghlin, Shaun
ITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5' Fallo Alto
GITY: Palo Alto
CONTRESS COLIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.3%; Score 71; DB 1; Length 355; 47.6%; Pred. No. 0.0053; tive 6; Mismatches 5; Indels
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APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
UNDBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UCAL-237/02US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/450,393A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/450, FILING DATE: MAY 25, 1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CBETT. LUANN
REGISTRATION NUMBER: 31,822
REFRENCY/DOCKET NUMBER: UCAL-
TELECHONE: 415-843-5165
TELECHONE: 415-843-5165
TELEX: 38.0916Coleypa
INFORMATION FOR SEQ ID NO: 5: SEQUENCE GHARACTERISTICS:
LENGTH: 355 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08446669 Patent No. 6132987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ICPOLOGY: linear MOLECULE TYPE: protein HYPOTHEICAL: NO ANTI CHILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94306-2155
COMPUTER READABLE FORM:
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CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                    US-08-450-393A-5
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RESULT 38
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                                                                                     Query Match 56.3%; Score 71; DB 3; Length 355; Best Local Similarity 47.6%; Pred. No. 0.0053; Matches 10; Conservative 6; Mismatches 5; Indels
                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-045-583-53
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Search completed: September 28, 2004, 09:21:31 Job time : 20.8 secs

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us-10-084-813-12.rapb

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September 28, 2004, 09:06:23; Search time 72.875 Seconds (without alignments) 97.074 Million cell updates/sec
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"GGNZ_6/ptodata1/pubpaa/USO6_NEW_PUB.pep:*

"GGNZ_6/ptodata1/pubpaa/USO6_NEW_PUB.pep:*

"GGNZ_6/ptodata1/pubpaa/USO7_NEW_PUB.pep:*

"GGNZ_6/ptodata1/pubpaa/USO8_PUBCOMB.pep:*

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"GGNZ_6/ptodata1/pubpaa/USO8_PUBCOMB.pep:*

"GGNZ_6/ptodata1/pubpaa/USO8_PUBCOMB.pep:*

"GGNZ_6/ptodata1/pubpaa/USO8_PUBCOMB.pep:*

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"GGNZ_6/ptodata1/pubpaa/USO8_PUBCOMB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1349238 seqs, 321558718 residues
                                                                                                                  OM protein - protein search, using sw model
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Maximum Match 1008
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                     US-10-084-813-12
126
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                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	בייין פטופונהפט	Semience 4 Appli	Semience 4 Appli	Semience 4 Appli	- 4	Semience 4. Appli	A	Semience 6 Appli	Semience 6. Appli	Segmence 6 Appli	Semience 18 Appl	Semience A some	·	٩,	Sequence 2, Appli
SUMMARIES	ID	. US-10-084-813-12	US-09-938-719-4	US-09-939-226-4	US-09-938-703-4	US-10-661-798-4	US-10-612-791-4	US-09-938-719-6	US-09-939-226-6	US-09-938-703-6	US-10-661-798-6	US-10-661-798-18	US-10-612-791-6	US-10-612-791-18	US-10-095-876A-2	US-09-725-285-2
	DB	14	σ	σ	σ	16	16	თ	Q	σ	16	16	16	16	14	σ
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	Score	126	126	126	126	126	126	126	126	126	126	126	126	126	126	126
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Sequence 2, Appli	equence 22	equence 2.	22	equence 15	equence 17	equence 1.	equence 2.	equence 2,	equence 5.	equence 5.	equence 5,	2	Secuence 1	4	equence 5	equence 2	equence 2	equence 2	equence 1	equence 2	equence 2	equence 6	equence 3	egience 1	-	equence 5	equence 1	2e 2
US-09-759-841-2 IIS-09-779-8792-2	09-779-879A-	-09-779-88	-09-779-880A-	09-813-653-1	-09-813-6	-09-796-2	09-195-662A	-09 - 33	09-938-719-	-09-939-226-	09-938-7	09-502-78	-09-734-221A	-09-826-509-4	-10-151-274-	-10-106-62	0-106-623-	-10-232-686-	10-086-814-	0-067-8	US-10-067-800-22	US-10-290-058A-6	10-225-56	-10-323-314-1	10-072-301-	-10-164-64	71-866-1	US-10-135-839-2
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16	18	19	20	21	22	23	. 24	25	56	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	

# ALIGNMENTS

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Sequence 12, Application US/10084813

Publication No. US20030068615A1

GENERAL INFORMATION:

TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC

TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE

TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE

CURRENT APPLICATION NUMBER: US/10/084,813

CURRENT APPLICATION NUMBER: DO2-27

PRIOR PILING DATE: 2000-08-25

PRIOR FILING DATE: 1999-08-27

PRIOR FILING DATE: 1999-08-27

NUMBER OF SEQ ID NOS: 1242

SEQ ID NO 12

LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
PEATURE:
OTHER UNEXATION: Description of Artificial Sequence: binding peptide
US-10-084-813-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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100.0%; Score 126; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 4e-11;
Matches 22; Conservative 0; Mismatches 0; Indels
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OWDFGNTMCQLLTGLYFIGFFS 22 1 OWDFGNIMCOLLIGLYFIGFFS 22 RESULT 2 US-09-318-719-4 ; Sequence 4, Application US/09938719 ; Patent No. US20020106742A1 ઠે

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US-09-938-703-4
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Sequence 4, Application US/09939226
Patent No. US20020110805A1
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                            TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 126; DB 9; Length 184; Best Local Similarity 100.0%; Pred. No. 3.3e-10; Matches 22; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 24-Aug-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 09/626,939
PILING DATE: 27-UTLY-2000
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 QWDFGNTWCQLLTGLYFIGFFS 114
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MEDIUM TYPE: Floppy disk
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
                                                                                                                                                                                                                                                                                                             CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
                                                                                                                                                                                                    NUMBER OF SEOUENCES:
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Sequence 4, Application US/09938703

Patent No. US20020110870A1

GENERAL INFORMATION:

APPLICANT: SAMENOW, MICHEL

PARMENTIER, WARC

VASSART, GILBERT

LIBERT, FREDERICK

TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOXINES RECEPTOR

AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 126; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 3.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/626,939
FILING BATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <UNKnown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION: <university control of the control of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; IENGTH: 184 amino acids; TYPE: amino acid acid TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-09-939-226-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 QWDFGNTWCQLLTGLYFIGFFS 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 184 amino acids
TYPE: amino acid
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CORRESPONDENCE ADDRESS:
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ZIP: 92660
COMPUTER READABLE FORM:
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PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     Length 184;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Parentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,719
FILING DATE: 24-Aug-2001
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
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ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 126; DB 16;
Best Local Similarity 100.0%; Pred. No. 3.3e-10;
Matches 22; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 3.9e-10;
ive 0; Mismatches 0;
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REGISTRATION NUMBER: 34,115
REPREBNCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
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FILING DATE: 27-JULY-2000
ATTORNEY/AGENT INFORMATION:
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MOLECTLE TYPE: protein | SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-09-938-719-6
                                                             96870102.9
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Patent No. US2002016742A1
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
              PRIOR FILING DATE: 1996-03-01
PRIOR APPLICATION NUMBER: EP 968
PRIOR FILING DATE: 1996-08-06
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 184
TYPE: PRT
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STATE: CA
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Best Local Similarity 100.
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-10-612-791-4
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US-09-938-719-6
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i) Sequence 4, Application US/10661798

i) Sequence 4. Application NO. US20040110127A1

i) SPAPLICANT: Samon, Michael

APPLICANT: Parmentier, Marc

APPLICANT: PAPLICANTON WIMBER: US/10/661,798

CURRENT APPLICANTON NUMBER: 09/938,703

PRIOR APPLICANTON NUMBER: 09/824

PRIOR APPLICANTON NUMBER: 08/833,752

PRIOR APPLICANTON NUMBER: 08/833,752

PRIOR APPLICANTON NUMBER: 08/833,752

PRIOR APPLICANTON NUMBER: EP 96870012.1

PRIOR APPLICANTON NUMBER: EP 96870012.1

PRIOR APPLICANTON NUMBER: EP 96870012.9

PRIOR APPLICANTON NUMBER: EP 96870102.9

PRIOR APPLICANTON NUMBER: EP 96870102.9

PRIOR APPLICANTON NUMBER: EP 96870102.9

PRIOR FILING DATE: 1996-03-03

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              Length 184;
                                                                               Indels
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Query Match
100.0%; Score 126; DB 9;
Best Local Similarity 100.0%; Pred. No. 3.3e-10;
Matches 22; Conservative 0; Mismatches 0;
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100.0%; Score 126; DB 16;
Best Local Similarity 100.0%; Pred. No. 3.3e-10;
Matches 22; Conservative 0; Mismatches 0;
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Publication No. US2004016173941

Publication No. US2004016173941

GENERAL INFORMATION:
APPLICANT: Samson, Michael
APPLICANT: Parmentier, Maxc
APPLICANT: Parmentier, Maxc
TITLE OF INVENTION: HIV Diagnostic Methods.
FILE REFERENCE: 9409/20238
CURRENT APPLICATION NUMBER: US/10/612,791
CURRENT APPLICATION NUMBER: 09/938,703
PRIOR PILING DATE: 2001-08-24
PRIOR FILING DATE: 2000-07-27
PRIOR FILING DATE: 1997-04-09
PRIOR PILING DATE: 1997-04-09
PRIOR PILING DATE: 1997-04-09
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APPLICATION NUMBER: EP 96870021.1
                                                                                                                                            1 QWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-10-661-798-4
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                                                                                                                    APPLICANT: SAMSON, MICHEL
PARMENTIER, NARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/09938703
Sequence 6, Application US/09938703
Sequence 6, Application US/09938703
Sequence 6, Application US/09938703
GENERAL INFORMATION:
APPLICANT: SANSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, REDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOXINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION: CURKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 215;
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STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 126; DB 9;
100.0%; Pred. No. 3.9e-10;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: 40nknown>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE; protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-939-226-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 OWDFGNTMCOLLTGLYFIGFFS 114
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                                            Sequence 6, Application US/09939226 Patent No. US20020110805Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 215 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                     Newport Beach
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CORRESPONDENCE ADDRESS:
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ZIP: 92660
COMPUTER READABLE FORM:
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Best Local Similarity 100.8
Matches 22; Conservative
                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 92660
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US-09-938-703-6
RESULT 8
US-09-939-226-6
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 215;
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100.0%; Pred. No. 3.9e-10;
ive 0; Mismatches 0;
                                                                                                                                                                                      NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                          APPLICATION NUMBER: US/09/938,703
FILING DATE: 24-Aug-2001
CLASSIFICATION: «Unknown».
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 OWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QWDFGNTMCQLLTGLYFIGFFS 22
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Publication No. US20040110127A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                    LENGTH: 215 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Partches 22; Conservative 0;
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US-10-661-798-6
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1 OWDFGNTMCQLLTGLYFIGFFS 22

LENGTH: 215

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Gaps

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Query Match 100.0%; Score 126; DB 16; Length 215; Best Local Similarity 100.0%; Pred. No. 3.9e-10; Matches 22; Conservative 0; Mismatches 0; Indels 0;
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100.0%; Score 126; DB 16; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.9e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0;
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| Sequence 2, Application US/10095876A
| Publication No. US20030148294A1
| GENERAL INFORMATION:
| APPLICANT: AL'YOUNG; Janice; Bandman, Olga
| APPLICANT: Coleman, Roger; Wilde, Craig G
| TILE OF INVENTION: DNA ENCODING NOVEL CHEMOKINE RECEPTORS
| FILE ERFERENCE: PF-0066-1 CON
| CURRENT APPLICATION NUMBER: US/10/095,876A
| CURRENT FILING DATE: 1996-04-26
| PRIOR APPLICATION NUMBER: US 08/638,081
| PRIOR PILING DATE: 1996-04-26
| SOFTWARE: PERL PROGram
| CONTWENT: SEQ ID NOS: 6
| SOFTWARE: PERL PROGram
| TYPE: PRI
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GENERAL INVOKAMILONI

APPLICANT: Samson, Michael

APPLICANT: Parmentier, Marc

APPLICANT: Vassart, Gilbert

GILCANT: Passart, Gilbert

FILE REFERENCE: 9409/2021

CURRENT APPLICATION NUMBER: US/10/612,791

CURRENT APPLICATION NUMBER: 09/938,703

PRIOR FILING DATE: 2000-07-02

PRIOR FILING DATE: 2000-07-27

PRIOR FILING DATE: 1997-04-09

PRIOR PRILING DATE: 1997-04-09

PRIOR FILING DATE: 1997-03-01

PRIOR FILING DATE: 1997-03-01

PRIOR FILING DATE: 1996-03-01

SEQ ID NO 18

LENGARRE: PatentIn version 3.1

SEQ ID NO 18
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US-10-612-791-18
US-10-612-791-18
Sequence 18, Application US/10612791;
Publication No. US20040161739A1
GENERAL INFORMATION:
TYPE: PRT
CORGANISM: Homo sapiens
US-10-612-791-6
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JS-10-612-791-18
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US-10-095-876A-2
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APPLICANT: Parmentier, Marc
APPLICANT: Parmentier, Marc
APPLICANT: Parmentier, Marc
APPLICANT: Vassart, Gilbert
APPLICANT: Vassart, Gilbert
APPLICANT: Vassart, Gilbert
TITLE OF INVENTION: Screening Methods for Identifying Compounds which Decrease HIV En
TITLE OF INVENTION: a cell
TITLE OF INVENTION: a cell
FILE SPERENCE: 9409/2023F
CURRENT APPLICATION NUMBER: US/10/661,798
CURRENT APPLICATION NUMBER: 09/938,703
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-06-27
PRIOR FILING DATE: 1997-04-09
PRIOR FILING DATE: 1997-03-03
PRIOR FILING DATE: 1997-03-03
PRIOR FILING DATE: 1997-03-03
PRIOR FILING DATE: 1996-03-01
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Best Local Similarity 100.0%; Pred. No. 3.9e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0;
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APPLICANT: Parmentier, Marchael
TITLE OF INVENTION: HIV Disgnostic Methods
FITLE REFERENCE: 9409/2021
CURRENT APPLICATION NUMBER: US/10/612,791
CURRENT FILING DATE: 2003-07-02
PRIOR APPLICATION NUMBER: 09/938,703
PRIOR APPLICATION NUMBER: 09/626,939
PRIOR FILING DATE: 1997-04-09
PRIOR FILING DATE: 1997-04-03
PRIOR FILING DATE: 1997-04-03
PRIOR APPLICATION NUMBER: EP 96870021.1
PRIOR APPLICATION NUMBER: EP 96870021.1
PRIOR FILING DATE: 1996-03-01
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 6
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                                                                                       US-10-661-798-18

'Sequence 18, Application US/10661798
'Publication No', US20040110127A1
'GENERAL INFORMATION:
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Publication No. US20040161739A1
GENERAL INFORMATION:
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US-10-661-798-18
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US-10-612-791-6
                                                           RESULT 11
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100.0%; Score 126; DB 9; Length 352; 100.0%; Pred. No. 6.3e-10; ative 0; Mismatches 0; Indels 0
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Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0
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SOFTWARE: PatentIn version 3.0
                                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 22; Conservative
  ) LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-841-2
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US-09-779-879A-22
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US-09-779-879A-2
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LENGTH: 352
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APPLICANT: Li, Yi
APPLICANT: Ruben, Steven, M. Antibodies to Human G-Protein Chemokine Receptor HDGNR10
TITLE OF INVENTION: (CRS Receptor)
FILE PERENNCE: 1488,1150003
CURRENT APPLICATION NUMBER: (2/09/725,285
CURRENT APPLICATION NUMBER: 09/339,912
PRIOR APPLICATION NUMBER: 09/339,912
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1998-11-18
PRIOR FILING DATE: 1998-11-18
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
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Best Local Similarity 100.0%; Pred. No. 6e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0;
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                                                  ; NAME/KEY: misc feature
?; OTHER INFORMATION: Incyte ID No. US20030148294A1 478861
US-10-095-876A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: Deduced Amino Acid Sequence US-09-725-285-2
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Sequence 2, Application US/09759841

Sequence 2, Application US/09759841

Sequence 2, Application US/09759841

Septicant: Rickett, Graham A

APPLICANT: Rickett, Graham A

APPLICANT: Dobbs, Susan

APPLICANT: Perros, Manoussos

TITLE OF INVENTION: Assay Method

FILE REFERENCE: PC10348APWE

CURRENT APPLICATION NUMBER: US 000/01-12

PRIOR APPLICATION NUMBER: GB 0000661.9

PRIOR APPLICATION NUMBER: GB 0000661.9

PRIOR PLIING DATE: 2000-01-12

PRIOR RELIGH DATE: 2000-01-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence: Genomic
                                                                                                                                                                                                                                                                                             84 QWDFGNTMCQLLTGLYFIGFFS 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 2, Application US/09725285; Patent No. US20010000241A1; GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.1
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Matches 22; Conservative
ORGANISM: Homo sapiens FEATURE:
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LENGTH: 352
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APPLICANT: Roschke, Viktor
APPLICANT: Roschke, Viktor
APPLICANT: Roschke, Viktor
APPLICANT: Ruben, Steven, M.
ITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
FILE REFERENCE: 1488.11500049779,879A
CURRENT APPLICATION NUMBER: US/09/779,879A
FRIOR APPLICATION NUMBER: US 60/181,258
PRIOR PILING DATE: 2000-02-09
PRIOR PILING DATE: 2000-02-09
PRIOR PILING DATE: 2000-03-09
PRIOR PILING DATE: 2000-03-20
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APPLICANT: Rosen, Craig A.

APPLICANT: Rosen, Craig A.

APPLICANT: Rosen, Steven, M.

TILE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNRIO

FILE REPERENCE: 1480.1150004.

CURRENT APPLICATION NUMBER: US (09/779, 879A.

CURRENT APPLICATION NUMBER: US 60/181, 258

PRIOR APPLICATION NUMBER: US 60/181, 258

PRIOR PILING DATE: 2000-02-09

PRIOR PILING DATE: 2000-03-09

PRIOR FILING DATE: 2000-03-09

PRIOR FILING DATE: 2000-03-09

PRIOR FILING DATE: 2000-03-09

PRIOR FILING DATE: 2000-03-09

PRIOR PILING DATE: 2000-03-09
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Query Match
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels C
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     , ORGANISM: Homo sapiens
US-09-779-880A-22
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US-09-813-653-15
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Sequence 2. Application US/09779880A
Fatent No. US20020061834A1
GENERAL INFORMATION:
APPLICANT: Roschke, Viktor
APPLICANT: Roschke, Viktor
APPLICANT: Roschke, Viktor
APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGNR10
FILE REPERENCE: 1488.115000C
CURRENT APPLICATION NUMBER: US 60/181,258
FRICH FILING DATE: 2000-02-09
FRICH FILING DATE: 2000-02-09
FRICH FILING DATE: 2000-03-09
FRICH APPLICATION NUMBER: US 60/187,999
FRICH FILING DATE: 2000-03-09
FRICH RELING DATE: 2000-03-09
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Sequence 22, Application US/09779880A

Patent No. US200006834A1

GENERAL INFORMATION:

APPLICANT: Rosen, Craig A.

APPLICANT: Rosen, Craig A.

APPLICANT: Rosen, Wktor

APPLICANT: Ruben, Steven, M.

TILL OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10

FILE REFERENCE: 1488.115000C

CURRENT APPLICATION NUMBER: US/09/779,880A

CURRENT APPLICATION NUMBER: US 60/181,258

PRIOR PRILING DATE: 2000-02-09

PRIOR FILING DATE: 2000-03-09

PRIOR PRIOR FILING DATE: 2000-03-09

PRIOR FILING DATE: 2000-03-09
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Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                            Query Match 100.0%; Score 126; DB 9; Length 352; Best Local Similarity 100.0%; Pred. No. 6.3e-10; Matches 22; Conservative 0; Mismatches 0; Indels
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-879A-22
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US-09-779-880A-2
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US-09-779-880A-2
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LENGTH: 352
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APPLICANT: Neetor, John
APPLICANT: Neetor, John
APPLICANT: Wilson, Carol
APPLICANT: Wilson, Carol
APPLICANT: Wilson, Carol
APPLICANT: Tan Hehir, Christina
TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
FILE REFERENCE: CNS-005
CURRENT APPLICATION NUMBER: US 60/190,946
PRIOR PELING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/190,996
PRIOR APPLICATION NUMBER: US 60/190,996
PRIOR APPLICATION NUMBER: US 60/190,996
PRIOR APPLICATION NUMBER: US 60/191,299
PRIOR PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
SPRIOR FILING DATE: 2000-03-21
FRIOR FILING DATE: 2000-03-21
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Batent No. US200064770A1

GENERAL INFORMATION:

APPLICANT: Nestor, John
APPLICANT: Mestor, John
APPLICANT: Tan Hehir, Christina
APPLICANT: Tan Hehir, Christina
APPLICANT: Tan Hehir, Christina
APPLICANT: Tan Hehir, Christina
APPLICANT: See, Raymond
APPLICANT: See, Raymond
APPLICANT: Tan Hehir, Christina
APPLICANT: Tan Hehir, Christina
APPLICANT: Tan Hehir, Christina
APPLICANT: See, Raymond
APPLICANT: See, Raymond
APPLICANTON NUMBER: US/09/813,653
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/190,996
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
ANTHER OF SEQ ID NOS: 44
SOSTWARE: Patentin version 3.0
SEQ ID NO 17
LENGTH: 352
TYPE: PRT
CREANISM: Homo sapiens
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Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels C
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Sequence 15, Application US/09813653
Patent No. US20020064770A1
GENERAL INFORMATION:
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1 QWDFGNTMCQLLTGLYFIGFFS 22
Sequence 2, Application US/09339912A Patent No. US20020099176A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
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APPLICANT: Ruben, Steven, M.
APPLICANT: Ruben, Steven, M.
APPLICANT: Ruben, Steven, M.
APPLICANT: Ruben, Steven, M.
FILIE OF INVENTION: Human G-Protein Chemokine Receptor HDGNRIO (CCRS Receptor)
FILE REPRENCE: 1488.115002
CURRENT APPLICATION NUMBER: US/09/195,662A
PRIOR APPLICATION NUMBER: 08/466,343
PRIOR APPLICATION NUMBER: 08/466,343
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
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                                                                                                         0; Gaps
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                                                Query Match
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Dragic, Tarjana
APPLICANT: Olson, William
ITTLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/61010/JFW/SHS
CURRENT APPLICATION NUMBER: US/09/796, 202
CURRENT FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 126; DB 9; Length 352; Best Local Similarity 100.0%; Pred. No. 6.3e-10; Matches 22; Conservative 0; Mismatches 0; Indels 0
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Best Local Similarity 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0
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OTHER THORMATION: Deduced Amino Acid Sequence
US-09-195-662A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence: Genomic
                                                                                                                                                                                        93 QWDFGNTMCQLLTGLYFIGFFS 114
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                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09796202 Patent No. US20020068813A1
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APPLICANT: Li, Yi
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ORGANISM: human
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  US-09-813-653-17
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LENGTH: 352
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LENGTH: 352
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RESULT 25 US-09-339-912A-2

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Sequence 2, Application US/0333912A
Application US/033912A
Application US/033912A
Application US/033912A
Application US/033912A
Application US/0393912A
Application US/0393912A
Application US/0393912A
Application US/0393812A
Application US/0393812A
Application US/0393813A
Application US/03813A
Appl
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GILBERT

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LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:

MEDIUM TYPE: Ploppy disk
COMPUTER: PLOPPY disk
COMPUTER: PLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Release #1.0, Version #1.25 (EPO)
SOFTWARE: PATCHIN NUMBER: US/09/938,703
FILING DATE: 24-Aug-2001
CLASSIFICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altern. Deniel E
REGISTRATION NUMBER: 34,115
REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSES: KNobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 126; DB 9; Best Local Similarity 100.0%; Pred. No. 6.3e-10; Matches 22; Conservative 0; Mismatches 0;
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-703-5
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TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
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Sequence 5, Application US/09939226
Sequence 5, Application US/09939226
Sequence 5, Application US/09939226
Sequence 5, Application US/0993926
Sequence 5, Application US/0993926
Sequence 5, Application US/0993926
Sequence 5, Application US/0993926
Sequence 6, Application US/0993926
Sequence 6, Application US/0993926
Sequence 7, Application US/099
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                                                                                                                                                                            Length 352,
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CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: NewPort Beach
COUNTRY: 0.S.A.

ZIP: 92660

COUNTRY: U.S.A.
ZIP: 92660

CONFUTE: Thoppy disk
MEDIUM TPEE: Floppy disk
COMPUTER: TBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/939,226
FLING DAFE: 24-Aug-2001
CLASSIFICATION NUMBER: 09/626,939
FLING DAFE: 24-Aug-2001
PRIOR APPLICATION NUMBER: 09/626,939
FLING DAFE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: ALEMAN, Daniel B
REGISTRATION NUMBER: 34,115
REGISTRATION NUMBER: 34,115
REGISTRATION NUMBER: 34,115
REGISTRATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acide
TYPE: amino acide
TYPE: amino acide
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100.0%; Score 126; DB 9;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0;
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100.0%; Score 126; DB 9;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0;
MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 5: US-09-938-719-5
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-939-226-5
                                                                                                                                                                                                                                                                                                                                                                                              93 OWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                       1 QWDFGNTMCQLLTGLYFIGFFS 22
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Sequence 2, Application US/09502783A

Patent No. US20020132269A1

Patent No. US20020132269A1

GENERAL INFORMATION:

APPLICANT: Li, Yi

APPLICANT: Li, Yi

APPLICANT: Li, Yi

APPLICANT: Li, Yi

APPLICANT: Ruben, Steven M.

TITLE OF INVENTION: PRORNICH

TITLE OF INVENTION: HABS.1150006

CURRENT APPLICATION NUMBER: US/09/502,783A

CURRENT APPLICATION NUMBER: 08/466,343

PRIOR APPLICATION NUMBER: 08/466,343

PRIOR FILING DATE: 1995-06-06

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin version 3.0

SEQ ID NO 2

LENGTH: 352
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100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels (
93 QWDFGNTMCQLLTGLYFIGFFS 114
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US-09-502-783A-2
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JS-02-30-10-30 Sequence 5, Application US/09938703 Sequence 5, Application US/09938703 Patent No. US20020110870A1 GENERAL INFORMATION: APPLICANT: SAMSON, MICHEL PARMENTIER, MARC

RESULT 28 US-09-938-703-5

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Gaps

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Length 352; Indels

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APPLICANT: Lehmann-Bruinsma, Karin
APPLICANT: Liaw, Chen W.
APPLICANTON: No. US20030204073A1-Endogenous, Constitutively Activated Known G.
TITLE OF INVENTION: Precein-Coupled Receptors
TITLE OF INVENTION: Precein-Coupled Receptors
CURRENT APPLICATION NUMBER: US/09/826,509
CURRENT APPLICATION NUMBER: 2001-04-05
PRIOR APPLICATION NUMBER: 60/195,747
PRIOR APPLICATION NUMBER: 09/170,496
RIOR APPLICATION NUMBER: 09/170,496
RIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 589
SOFTWARE: Patentin Version 2.1
ENGTH: 352
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APPLICANT: Kwon, Douglas S.
APPLICANT: Kwon, Douglas S.
APPLICANT: Kwon, Douglas S.
APPLICANT: Would S.
APPLICANT: Geijtenbeck, Tnee
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY
TITLE OF INVENTION: GELLS
TITLE OF INVENTION: MUMBER: US/10/151,274
CURRENT PILING DATE: 2002-05-20
FRIOR FILING DATE: 2000-03-02
FRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATCHIN VET: 2.0
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| Sequence 2, Application US/10106623
| Sequence 2, Application No. US20020150888A1
| GENERAL INFORMATION:
| APPLICANT: Gray, Patrick W. Schweickert, Vicky L. Raport, Carol J. Raport, Carol J. Raport, Carol J. TITLE OF INVENTION: Chemokine Receptor Materials and Methods
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Best Local Similarity 100.0
Matches 22; Conservative
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| LENGTH: 352
| TYPE: PRT
| OKGANIEM: Homo sapiens
US-10-151-274-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-826-509-477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 32
US-10-151-274-5
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 33
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                                                                                                                                                                                            PELICANT: LITTAN, DATE DENG HONGKUI
BELGHER, HONGKUI
BELGHER, WILFRIED
LANDAU, NATHANIEL R.
LIU, RONG
TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
WACROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 126; DB 10; Length 352; 100.0%; Pred. No. 6.3e-10; Live 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/734,221A

FILING DATE: 11.Dec-2000

CLASSIFICATION ATA:

APPLICATION NUMBER: US 08/666,020

FILING DATE: 19-JUN-1996

APPLICATION NUMBER: US 08/227,319

FILING DATE: 13-APR-1994

ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-004 N2
TELECONMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPHONE: 201-487-5801
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
;
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-734-221A-14
93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 OWDFGNTMCOLLTGLYFIGFFS 114
                                                                                                                                                  Sequence 14, Application US/09734221A
Publication No. US20030096221A1
GENERAL INFORMATION:
APPLICANT: LITTMAN, DAN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QWDFGNTMCQLLTGLYFIGFFS 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 352 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 22; Conservative
                                                                                                  RESULT 30
US-09-734-221A-14
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Sequence 2, Application US/10232686;
Publication No. US20030023044A1
GENERAL INFORMATION:
APPLICANT: Li, Yi,
APPLICANT: Li, Yi,
TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGNRIO
FILE REFERENCE: 1488.11500N
CURRENT APPLICATION NUMBER: US/10/232,686
CURRENT FILING DATE: 2002-09-03
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1998-11-18
PRIOR FILING DATE: 1998-11-18
PRIOR FILING DATE: 1998-10-66
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LEAST AND 10 2
LEAST AND 10 2
SEQ ID NO 2
LEAST AND 10 2
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CLASSIFICATION: «Unknow...

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/771,276
FILING DATE: «Unknown»
TORNEY AGENT INFORMATION:
NAME: No. US20020150888Aland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 37,866/33670
TELECOMMUNICATION INFORMATION:
TELETAN: 312-474-6300
TELETAN: 312-474-6300
TELETAN: 312-474-6300
TELETAN: 312-474-6300
TELETAN: 312-474-6300
TYPE: AMANTION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGHH: 352 amino acids
TYPE: amino acids

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100.0%; Score 126; DB 13;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 20: US-10-106-623-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 QWDFGNTWCQLLTGLYFIGFFS 114
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                                                                                       NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago.
                                                                                                                                                                                                                                                                                                                                                         STATE: Lilinois
COUNTRY: USA
ZIP: 6066
COUNTRY: USA
ZIP: 6066
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
CURRENT APPLICATION NUMBER: US/10/106,623
FILING DATE: 26-Mar-2002
CLASSIFICATION NUMBER: US/11/276
FILING DATE: CURROWN>
PRIOR APPLICATION NUMBER: 08/771,276
FILING DATE: CURROWN>
APPLICATION NUMBER: 35,302
REGISTRATION NUMBER: 35,302
REFERENT INFORMATION:
TELECOMMUNICATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33670
TELECOMMUNICATION NUMBER: 32,474-6300
TELEPHONE: 312-474-6300
TELEPHONE: 312-474-6300
TELEPHONE: 312-474-6300
TELEPHONE: 312-474-6300
TELEPHONE: 21 PANCEL COURTERIESTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) NAME/KEY: misc_feature
OTHER INFORMATION: /= "88C amino acid sequence"
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-106-623-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 352 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein FEATURE:
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.; 0 Length 352; RESULT 36
US-10-086-814-1
S-20-086-814
Publication No. US20030092632A1
GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Dragic, William C.
TITLE OF INVENTION SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 61010-AB-1
CURRENT APPLICATION NUMBER: US/10/086,814 Indels Query Match
100.0%; Score 126; DB 14;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; 93 QWDFGNTMCQLLTGLYFIGFFS 114 1 OWDFGNTMCQLLTGLYFIGFFS 22 à 

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Gaps

TYPE: PRT ORGANISM: Homo sapiens

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Indels

Length 352;

Query Match
100.0%; Score 126; DB 13;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0;

à d RESULT 34 US-10-106-623-20

The state of the s

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/106,623
FILING DATE: 26-Mar-2002

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Sequence 6, Application US/10290058A
Publication No. US20030104455A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Urological Disorders Using 313, 333, 5464, 18817 or 33524
FILE REFERENCE: MPIO1-289PIRM
CURRENT APPLICATION NUMBER: US/10/290,058A
CURRENT FILING DATE: 2002-11-07
FRIOR PRILING DATE: 2001-11-07
FRIOR PILING SEQ 1001-11-07
NUMBER OF SEQ 1D NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: 09/779,880
PRIOR FILING DATE: 2001-02-09
PRIOR PELLON NUMBER: 60/297,257
PRIOR PILING DATE: 2001-06-12
PRIOR PLING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: 60/310,458
PRIOR APPLICATION NUMBER: 60/328,447
PRIOR PILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-12-11
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PATENTIN VERSION 3.1
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 ÓWDFGNTMCOLLTGLYFIGFFS 114
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                                                                                                                                                                                                                                                                                                                      LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                              US-10-067-800-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-290-058A-6
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LENGTH: 352
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Sequence 2, Application US/10067800

Sequence 2, Application US/10067800

Publication No. US203010005841

GENERAL INFORMATION:
APPLICANT: Rosenke, Viktor
APPLICANTON NUMBER: US/10/67,800
CURRENT APPLICANTON NUMBER: PCT/US01/64153
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-06-02
PRIOR FILING DATE: 2001-06-03
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-10-12
PRIOR SEQ ID NOS: 70
SOFTWARE: Patentin Version 3.1
SEQ ID NO S
                                                                                                                                                                                                                                                                            Gaps
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Sequence 22, Application US/10067800

Publication No. US20030100058A1

Publication No. US20030100058A1

APPLICANT: Roschke, Viktor

APPLICANT: Roschke, Viktor

APPLICANT: Roschke, M.

TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNRIO

TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNRIO

CURRENT APPLICATION NUMBER: US/10/067,800

CURRENT FILE OF SECONDALIA STREET SOUR-02-08

PRIOR FILING DATE: 2002-02-08

PRIOR FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 126; DB 14; Length 352; 100.0%; Pred. No. 6.3e-10; Live 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                         100.0%; Score 126; DB 14; Length 352; 100.0%; Pred. No. 6.3e-10;
                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                  93 QWDFGNTWCQLLTGLYFIGFFS 114
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       CURRENT FILING DATE: 2002-02-28
                         NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 352
                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 22, Conservative
                                                                                                                            TYPE: PRT
CORGANISM: Homo sapiens
US-10-086-814-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CORGANISM: Homo sapiens
US-10-067-800-2
                                                                                                                                                                                                                           Query Match
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; SOFTWARE: Patentin version 3.1 ; SBQ ID NO 352 ; LENGTH: 352 ; TYBE: PRT ; ORGANISM: Homo sapiens US-10-225-567A-352

Query Match
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0;

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Search completed: September 28, 2004, 09:44:41 Job time: 74.875 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Copyright

- protein search, using sw model OM protein

September 28, 2004, 08:57:36; Search time 11.825 Seconds (without alignments) 178.961 Million cell updates/sec Run on:

US-10-084-813-12 126 1 QWDFGNTMCQLLTGLYFIGFFS 22

Title: Perfect score: Seguence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Minimum Match 0% Maximum Match 100% Listing first 45 summaries Post-processing:

PIR\_78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

-	Description	et (C-C) eniverse	500	(C)	Ū	ī,	MIP-1 alpha recept		rece	kine (C	(0-0)	recepto		G profe	G protein-coupled	orphan G protein-c	G protein-compled	G protein-compled	G protein-coupled	melanin-concentrat	G protein-coupled	lymphocyte-specifi	complement Csa ana	G protein-coupled	interleukin-8 rece	probable INK-activ	hypothetical prote	andiotensin II rec	G protein-coupled	interferon-inducib
SUMMARIES	ID	A43113	44	45	C50	933	I49340	A45177	I49341	G02436	A57160	JC5942	JC4587	158186	JC5068	JC4304	S55594	138973	A55735	JC7080	A45680	B55735	S27357	JN0621	A48921	732	T16256	137	573	334
	DB	7	~	N	7	~	7	N	~	~	~	~	7	7	~	~	~	7	7	~	0	~	Н	N	7	~	7	~	7	0
	Length				355																									
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	Score	126	87	87	82	16	74	71	70	29	99	65	65	9	59	56	ц	53.5	53	53	25	52	51	20	50	20	20	49.5	4. Q	49
	Result No.	ч	(7)	m	4	Ŋ	9	7	ω .	σ.	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	52	26	27	28	53

mu opioid receptor thrombin receptor	hypothetical prote probable TonB-depe fusin (TECTRA)		probable transport probable transport thrombin receptor	G protein-coupled olfactory channel protein 80212 5 [i	feptahelical P2Y5- bradykinin B1 rece
A57510 A37912 S17148	AG1086 A81848 G00048	A45747 F65067	A85937 IS1667	S65766 T37241 D88651	JC5549 JC4681
0 0 0	1000	000	700	000	00
398 425 427	186 706 352	352 409	4 4 4 0 0 0 0 0 0	482 937 957	370
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	38.5.5	38.1	38.1	38.1 38.1	37.7
44 44 00 00 00	4.4 8.8 7.7.4	4 4 4 8 8 6	1, 4, 4, 4 0 00 00 6	4. 4. 4. 80 80 80	47.5
33 33 35	. ധ ക വ . ധ എ വ	34	0 W 4 .	4 4 4 1 2 6	44 5

## ALIGNMENTS

chemokine (C-C) receptor 5 - human
NyAlternate names: C-C CKR-5; CCR5
(Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 12-Jul-1996 #sequence\_revision 12-Jul-1996 #text\_change 20-Jun-2000
C; Accession: A43113; S71808; Ā58834; A58832; G02653; A58833
R; Samson, M; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
Biochemistry 35, 336-3367, 1996
A; Title: Molecular cloning and functional expression of a new human CC-chemokine recepto
A; Reference number: A43113; MUID:96241590; PMID:8639485
A; Accession: A43113
A; Residues: 1-352 cSAM1>
A; Residues: 1-352 cSAM

Appleaule type: DNA
A;Residues: 182-206;207-230 <SAM2>
A;Residues: 182-206;207-230 <SAM2>
A;Residues: 182-206;207-230 <SAM2>
A;Residues: 182-206;207-230 <SAM2>
A;Residues: 182-206;207-230 <SAM3>
A;Residues: 192-184, TKDSHLGAGPAACHGHLLIGNPKNSASVSK, <SAM3>
A;Residues: 1-184, TKDSHLGAGPAACHGHLLIGNPKNSASVSK, <SAM3>
A;Rosidues: 1-184, TKDSHLGAGPAACHGHLIGNPKNSASVSK, 
A;Rosidues: 1-184, TKDSHLGAGPAACHGHLIGNPAACHGHLIGNPKNSANASVSK, 
A;Rosidues: 1-184, TKDSHLGAGPAACHGHLIGN

A,Accession: A58832
A;Molecule type: mRNA
A;Residues: 1-352 <COM1>
A;COM1>
A;COSS-references: GB:U57840; NID:g1502408; PIDN:AAB17071.1; PID:g1502409
A;Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes

A,Rocesbus: translated from GB/EMBL/DDBJ
A,Status: translated from GB/EMBL/DDBJ
A,Status: translated from GB/EMBL/DDBJ
A,Rolecule type: mRNA
A,Rosidues: 1-89,'1', 91-352 <CCM2>
A,Rosidues: 1-89,'1', 91-352 <CCM2>
B,Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
A,Ritle: Molecular cloning and functional characterization of a novel human CC chemokine
A,Reference number: A58833; MUID:96291862; PMID:8663314 R;Combadiere, C. submitted to the EMBL Data Library, May 1996 A;Reference number: H01541 A;Accession: G02653

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138450 chemokine (C-C) receptor 2, splice form A - human Cispecial Homostine (C-C) receptor 2, splice form A - human Cispecial Homosapiens (T-C CGR-2; monocyte chemoattractant protein 1 receptor; monocyte chemosises (Special Homosapiens) (T-C CGR-2; monocyte chemoattractant procession: 138450 (T-C CGR-2) 
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O protein-coupled receptor CKR-L1 - human

NiAlternate names: chemokine receptor-like protein TER1; GPR-CY6

C;Species: Homo sapiens (man)

C;Date: 31-Jan-1997 #sequence revision 31-Jan-1997 #text_change 21-Jul-2000

C;Accession: JC5067; G02776; G02387

R;Zaballos, A.; Varona, R.; Guterrez, J.; Lind, P.; Marquez, G.

Biochem. Blophys. Res. Commun. 227, 846-853, 1996

A;Title: Molecular cloning and RNA expression of two new human chemokine receptor-like g

A;Accession: JC5067, MUID:97040707; PMID:8886020

A;Accession: JC5067

A;Molecule type: DNA

A;Rolecule type: DNA
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F;114/Binding site: carbohydrate (Asn) (covalent) #status predicted F;113-190/Disulfide bonds: #status predicted
                                                                                                                                                                                      Length 360;
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                                                                                                                                                                        69.0%; Score 87; DB 2; I
66.7%; Pred. No. 1.4e-05;
Live 3; Mismatches 4;
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Pred. No. 1.5e-05;
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Local Similarity 66.7%;
es 14; Conservative
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                                                                                                                                                                                                                                     Local Similarity
les 14; Conserv
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Matches
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A; Description: G protein-coupled receptor for chemokines MIP-lalpha, MIP-lbeta and RANTE
A; Description: G protein-coupled receptor for chemokines MIP-lalpha, MIP-lbeta and RANTE
A; Description: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane fistatus predicted <TM1>
C; Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane fistatus predicted <TM2>
F; 67-87/Domain: transmembrane fistatus predicted <TM3>
F; 67-87/Domain: transmembrane fistatus predicted <TM3>
F; 142-166 foundain: transmembrane fistatus predicted <TM5>
F; 256-257/Domain: transmembrane fistatus predicted <TM5>
F; 256-269 foundain: transmembrane fistatus predicted <TM5>
F; 256-269 foundain: transmembrane fistatus predicted <TM5>
F; 256-300 foundain: transmembrane fistatus predicted <TM5>
F; 256-300 foundain: transmembrane fistatus predicted <TM5>
F; 256-300 foundain: transmembrane fistatus predicted <TM7>
F; 259-269 foundain: transmembrane fistatus predicted <TM7>
F; 269-301 foundaing site: carbohydrate (Asn) (covalent) fistatus predicted
F; 340,343/Binding site: phosphate (Thr) (covalent) fistatus predicted
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NiAlternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chem
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
C; Accession: JC2443; Tokuda, X: Ishii, K.; Tanaka, H.; Endo, N.
Biochem: Biophys. Res. Commun. 202, 1156-1152, 1994
A; Title: cDNA cloning and functional expression of a human monocyte chemoattractant prot
A; Reference number: JC2443; MUID:94324942; PMID:8048929
A; Residues: 1-360 expx-
A; Redard A; Residues: DBB:D29984; NID:9531246; PIDN:BAA06253.1; PID:9531247
A; Couphin, A; Franci, C; Connolly, A.J; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 275-2756, 1994
A; Title: Molecular cloning and functional expression of two monocyte chemoattractant prop
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S. Superfamily: vertebrate rhodopsin

C; Superfamily: vertebrate rhodopsin

C; Superfamily: vertebrate rhodopsin

C; Superfamily: vertebrate splicing; G protein-coupled receptor; glycoprotein; transmembrane #status predicted <TM1>
F; 19-100/Domain: transmembrane #status predicted <TM2>
F; 11-100/Domain: transmembrane #status predicted <TM4>
F; 115-136/Domain: transmembrane #status predicted <TM4>
F; 107-2-26/Domain: transmembrane #status predicted <TM4>
F; 207-226/Domain: transmembrane #status predicted <TM6>
F; 244-268/Domain: transmembrane #status predicted <TM7>
F; 245-309/Domain: transmembrane #status predicted <TM7>
                                                      A;Molecule type: mRNA
A;Residues: 1-352 <RAP>
A;Cross-references: GBU54994; NID:g1457945; PIDN:AAC50598.1; PID:g1457946
C;Comment: This is a receptor for chemckines MIP-lalpha (see PIR.A30574), MIP-lbeta (see
C;Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemckine (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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C, Ge
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A Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-360 «RES>
A; Cross-references: EMBL: U03905; NID: 9472557
C; Genetics:
A; Genetics:
A; Genetics: GDB: GMKBR2
A; Cross-references: GDB: 337364; OMIM: 601267
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Best Local Similarity
      A, Accession: A58833
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C.Keywords: disulfiede bond, G.protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane #status predicted TM1>
F.36-60/Domain: transmembrane #status predicted TM1>
F.71-91/Domain: transmembrane #status predicted TM3>
F.10-91/Domain: transmembrane #status predicted TM3>
F.108-129/Domain: transmembrane #status predicted TM4>
F.108-120/Domain: transmembrane #status predicted TM4>
F.208-220/Domain: transmembrane #status predicted TM5>
F.208-210/Domain: transmembrane #status predicted TM6>
F.208-310/Domain: transmembrane #status predicted TM7>
F.208-315/Domain: transmembrane #status predicted TM5>
F.208-315/Domain: transmembrane #status predicted TM7>
F.208-315/Domain: transmembrane #status predicted TM5>
F.208-315/Domain: transmembrane (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999 C; Accession: A45177; I55671 R: Neote, K.; Didregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J. A15-455, 1993 A; Title: Molecular cloning, functional expression, and signaling characteristics of a C-A; Reference number: A45177; MUID:93161416; PMID:7679328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.525. Med. 177, 1421-1427, 1993
Affile: Structure and functional expression of the human macrophage inflammatory 1 alp.
A,Reference number: I55671; MUD:93240122; PMID:7683036
A,Rocession: I55671
A,Rotatus: preliminary; translated from GB/EMBL/DDBJ
A,Moledule type: mRNA
A,Residues: 1-355 <RES>
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NyAlternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
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MIP-1 alpha receptor like-2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1998
C;Accession: 149341
            A;Residues: 1-356 <RES>
A;Cross-references: EMBL:U28405; NID:g881549; PIDN:AAA89154.1; PID:g881550
C;Superfamily: vertebrate rhodopsin
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A;Residues: 15355 <NEO>
A;Cross-references: GB1.110918; NID:g292416; PIDN:AAA36543.1; PID:g292417
A;Experimental source: HL60 cells
A;Experimental source: AL60 cells
A;Note: sequence extracted from NCBI backbone (NCBIP:124876)
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                                                                                                                                                                      Query Match 58.7%; Score 74; DB 2; Length 356; Best Local Similarity 47.6%; Pred. No. 0.0013; Matches 10; Conservative 6; Mismatches 5; Indels
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Best Local Similarity 47.6%; Pred. No. 0.0038;
Matches 10; Conservative 6; Mismatches 5; Indels
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A;Cross-references: GDB:138446; OMIM:601159
A;Map position: 3p21-3p21
G;Superfamily: vertebrate rhodopsin.
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A; Molecule type: DNA
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C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: 149940
C;Accession: 149940
B;Gao, J.L.; Murphy, P.M.
J; Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemoki A;Reference number: 149339; MJD:95340546; PMID:7542241
A;Accession: 149340
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Molecule type: DNA
A;Residues: 1-352 <RES.
A;Cross-references: EMBL:U28404; NID:g881547; PIDN:AAA89153.1; PID:g881548
C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                        A)Residues: 1755 <BON>
A)Cross-references: EMBL:U45983; NID:g1245056; PID:g1245057
C;Comment: This protein belongs to the family of beta chemokine receptors.
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A, Gene: GDB: CMKBRL2; TER1; CKR-L1
A, Cross-references: GDB: 6033733; OMIN: 601834
A, Map position: 3921-3921
C, Superfamily: vertebrate rhodopsin
C, Superfamily: vertebrate a rhodopsin
C, Keywords: G protein-coupled receptor; transmembrane protein
C, Keywords: G protein-coupled receptor; predicted <TM1>
F, 73-94/Domain: transmembrane #status predicted <TM2>
F, 108-129/Domain: transmembrane #status predicted <TM3>
F, 147-171/Domain: transmembrane #status predicted <TM4>
F, 200-222/Domain: transmembrane #status predicted <TM5>
F, 201-222/Domain: transmembrane #status predicted <TM5>
F, 201-204/Domain: transmembrane #status predicted <TM5>
F, 201-304/Domain: transmembrane #status predicted <TM5>
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                    A;Reaidues: 1-355 <NAP>
A;Reaidues: 1-355 <NAP>
A;Cross-references: EMBL:U62556; NID:g1468978; PID:g1468979
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54.5%; Pred. No. 7.9e-05;
tive 6; Mismatches 4;
                                                                                                 R'Bonner, T.I.
submitted to the EMBL Data Library, January 1996
A'Reference number: H01154
A'Accession: G02387
A'Status: preliminary; translated from GB/EMBL/DDBJ
A'Molecule type: DNA.
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Best Local Similarity
Matches 12; Conserv
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N;Alternate names: C-C CKR-4
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C;Accession: A57160
R;Power, C. CA: Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; W. J; Biol. Chem. 270, 1945-19500, 1995
A;Title: Nolecular Cloning and functional expression of a novel CC chemokine receptor CD A;Retaus: preliminary not compared with conceptual translation
A;Retaus: preliminary not compared with conceptual translation
A;Retaus: preliminary not compared with conceptual translation
A;Residues: 1.360 expo.
A;Residues: 1.360 expo.
A;Coss.references: GB:R85740; NID:g1370103; PIDN:CAA59743.1; PID:g971452
A;Note: source clone K5-5
C;Ganetica: GD:CKRB4
A;Coss.references: GD:CYRB4
A;Coss.references: GD:CKRB4
A;Coss.references: GD:CKRB4
A;Coss.references: GD:CYRB4
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Cipates: Homo sapiens (man)
Cipates: Howo sapiens (man)
Cipates: Cipates: Cipates (man)
A; Reference number: UC5942; MUID:98139902; PMID:9473515
A; Recession: UC5942; MUID:98139902; PMID:9473515
A; Cocession: UC5942; MUID:98139902; PMID:9473515
Cipates: Dreliminary
A; Molecule type: DNA
A; Residues: L344 ergNA>
A; Cocessions: Cipates: Cipat
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les 9; Conservative
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Matches 10; Conservative
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A;Gross-references: GDB:579624; OMIM:601268
A;Map position: 3p21-3p21
C;Superfamily: vertebrate indopsin
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane #status predicted <TM1>
F;36-60/Domain: transmembrane #status predicted <TM2>
F;108-129/Domain: transmembrane #status predicted <TM3>
F;108-129/Domain: transmembrane #status predicted <TM5>
F;240-221/Domain: transmembrane #status predicted <TM5>
F;240-261/Domain: transmembrane #status predicted <TM5>
F;240-261/Domain: transmembrane #status predicted <TM7>
F;240-271/Onmain: transmembrane #status predicted <TM7>
F;240-271/Onmain
                                            R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemoki
A;Reference number: 149339; MUID:95340546; PMID:7542241
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R;Combadiere, C.; Ahuja, S.K.; Murphy, P.M.
J. Biol. Chem. 270, 16491-16494, 1995
A;Title: Cloning and functional expression of a human eosinophil CC chemokine receptor. A;Ference number: A57237; MUID:95348056; PMID:7622448
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A;Residues: 1-106,'N', 108-275,'S',277-280,'R',282-355 <COM>
A;Coss-references: GB:U28694; NID:g1199579; PIDN:AAC50469.1; FID:g1199580
A;Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC50469.
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Systems: Sapiens (man)
C;Bate: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 04-Mar-2000
C;Accession: G02436; A57237
Syponath, P.D.
Submitted to the EVBL Data Library, February 1996
A;Reference number: H01272
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53.2%; Score 67; DB 2; Length 355;
Best Local Similarity 52.4%; Pred. No. 0.015;
Matches 11; Conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                         A, Accession: 149341
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
A, Residues: 1-359 «EREs»
A, Cross-references: EMBL:U28406; NID:9881551; PID:9881552
C, Superfamily: vertebrate rhodopsin
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A;Molecule type: DNA
A;Residues: 1-355 <PON>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chemokine (C-C) receptor 3 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 40.>>
Best Local Similarity
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: G02436
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ò

Gaps

3; Indels

C;Species: Mus musculus (house mouse) C;Species: Mar-1996 #sequence\_revision 19-Apr-1996 #text\_change 20-Jun-2000

chemokine (C-C) receptor 4 - mouse

chemokine (C-C) receptor 4 - human

RESULT 10

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A,Accession: JC4304
A;Molecule type: mRNA
A;Residues: 1-552 RARP>
A;Residues: 1-552 RARP>
A;Cross-treferences: GB:UZ0350; NID:g665580; PIDN:AAA91783.1; PID:g665581
A;Experimental source: peripheral blood mononuclear cell
C;Comment: This protein is a cell-surface receptor which recognizes extracellular signal
C;Comment: This protein is a key regulator of many immune and homeostatic responses, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claccession: JC4304
Rikaport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Rikaport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Aprille: The orphan G-protein-coupled receptor-encoding gene V28 is closely related
Aprille: Mikeference number: JC4304; MUID:96011651; PMID:7590284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transmembrane protein
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                               transmembrane protein
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A,Map position: 6q27-6q27
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane pr
F;42-68/Domain: transmembrane #status predicted <TM1>
F;79-99/Domain: transmembrane #status predicted <TM2>
F;115-136/Domain: transmembrane #status predicted <TM2>
F;160-180/Domain: transmembrane #status predicted <TM3>
F;212-233/Domain: transmembrane #status predicted <TM5>
F;250-271/Domain: transmembrane #status predicted <TM5>
F;250-271/Domain: transmembrane #status predicted <TM5>
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C,Species: equine herpesvirus 2
                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; lymphokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.26;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 52.6%; Pred. No. 0.26
Matches 10; Conservative 2; Mismatches
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2; Mismatches
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NAMCKFTTAFFFIGFF 114
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nes 9; Conserv
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C,Superfamily: vertebrate rhodopsin
C,Superfamily: vertebrate rations in receptor; thymus
C,Reyworks: glycoprotein, phosphoprotein; receptor; thymus
F;2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;2,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pred
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: IS8886
R;Harrison, J.K.; Barber, C.M.; Lynch, K.R.
Reurosci. Lect. 169, 85-89, 1994
A;Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and A;Reference number: 158186; MUID:94323113; PMID:8047298
A;Accession: IS8186
A;Accession: IS8186
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Accession: JG5068
R;Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A;Reference number: JG5067, MUID:97040707; PMID:8886020
A;Reference number: JG5067, MUID:97040707; PMID:8886020
A;Accession: JG5068
A;Accession: JG5068
A;Accession: JG5068
A;Accession: JG5068
A;Cross-references: EMB:Z79784; NID:91668737; PIDN:CAB02144.1; PID:91668738
C;Gomment: This protein belongs to the family of alpha chemokine receptors.
';Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A. diochem. Biophys. Res. Commun. 218, 337-343, 1996
';Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines ';Reference number: JC4587; MUID:96136324; PMID:8573157
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0
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A;Cross-references: EMBL:X90862; NID:gll67851; PIDN:CAA62372.1; PID:gll67852
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Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-354 <RES>
A;Cross-references: EMEL:U04808; NID:g2558635; PIDN:AAB87093.1; PID:g439861
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
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Pred. No. 0.18;
2; Mismatches
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100 NAMCKLTTAFFFIGFF 115
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ilarity 62.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                           Experimental source: thymus
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Best Local Similarity
-hea 9; Conserv?
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les 10; Conserv
                                                                                                                                                                                  A; Accession: JC4587
A; Molecule type: mRNA
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RESULT 13

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Gaps

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Gaps

RESULT 17

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melanin-concentrating hormone receptor [validated] - human
NyAlternate names: MCHR; orphan somatostatin-like receptor 1 (SLC-1)
(Species: Homo sapiens (man)

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N;Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1
S;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: B55735; S52443
C;Accession: B55735; S52443
Genomics 23, 643-650, 1995
A;Echweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
A;Title: Cloning of human and mouse EBI1, a lymphoid-specific G-protein-coupled receptor
A;Reference number: A55735; MUID:95154835; PMID:7851893
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A;Note: sequence extracted from NCBI backbone (NCBIN:127094, NCBIP:127095)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Best Local Similarity 42.9%; Pred. No. 3.1;
Matches 9; Conservative 4; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 WVFGVHFCKLIFAIYKMSFFS 142
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Matches 8; Conservative
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-378 <SCH>
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Gspecies: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 24-Amy-1996 #sequence_revision 24-May-1996 #text_change 21-Jul-2000
C;Accession: 138973
R;O'Dowd, B.F.; Scheideler, M.A.; Nguyen, T.; Cheng, R.; Rasmussen, J.S.; Zastawny, R.;
Genomics 28, 84-91, 1955
A;Title: The cloning and chromosomal mapping of two novel human opioid-somatostatin-like
A;Reference number: A57647; MUID:96070436; PMID:7590751
A;Reference number: A57647; MUID:96070436; PMID:A60197.1; PID:G953233
A;Status: 1-328 <-RES>
A;Generics:
A;Generics
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G protein-coupled receptor EBI1 - mouse
C;Species. Mus musculus (house mouse)
C;Species. Mus musculus (house mouse)
C;Species. Mus musculus (house mouse)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999
C;Accession: A55735
C;Accession: A55735
A;Reference number: A55735; MulD:95154835; PMID:7851893
A;Accession: A55735
A;Accession: A55735
A;Accession: A55735
A;Reference number: A55735
A;Reference number: A55735
A;Reference CB:L31580; NID:9468340; PIDN:AAA74232.1; PID:9468341
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor
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                                             A;Cross-references: GB:U20824; NID:9695172; PIDN:AAC13788.1; PID:9695173
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor
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ative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                    DB 2; Length 383;
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                                                                                                                                                                                                                                                                                             43.7%; Score 55; DB 2
38.1%; Pred. No. 1.1;
tive 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 QWPFGELMCKLIVAIDQYNTFSSLYFLTVMS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QWDFGNTMCQLL -----TGLYFIGFFS 22
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Best Local Similarity 38.1%
Matches 8; Conservative
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Matches 9; Conservative
A; Residues: 1-383 <TEL>
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RESULT 19

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C'Accession: JN0621
A'Matsudoka, I:, Mori, T.; Aoki, J.; Sato, T.; Kurihara, K.
Biochem. Biophys. Res. Commun. 194, 504-511, 1993
A,Title: Identification of novel members of G-protein coupled receptor superfamily expr
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;Mosidues: 1.359 <CER>

;Crossidues: 1.359 <CER>

;Crossidues: 1.359 <CER>

;Suzuki, H.; Prado, G.N.; Wilkinson, N.; Navarro, J.

. Biol. Chem. 269, 18263-18266, 1994

:Title: The N terminus of interleukin-8 (IL-8) receptor confers high affinity binding the researce number: A53677; MUID:94308043; PMID:7518426
                                                                                                                                                                                                                                                                                                                                                                          A; Mocedia type: mRNA
A; Residues: 1-350 < MAT>
A; Cross-references: Gs:63848; NID:g399710; PIDN:AAB27547.1; PID:g399711
A; Experimental source: tongue taste papillae
C; Comment: This protein is involved in modulating taste sensitivity or regeneration of to comment: This protein is involved in modulating taste sensitivity or regeneration of to; Roywords: G protein-coupled receptor; glycoprotein; reansmembrane #status predicted < TM2>
F; 140-99/Domain: transmembrane #status predicted < TM3>
F; 154-175/Domain: transmembrane #status predicted < TM5>
F; 154-175/Domain: transmembrane #status predicted < TM5>
F; 200-222/Domain: transmembrane #status predicted < TM5>
F; 201-225/Domain: transmembrane #status predicted < TM5>
F; 201-22
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C;Specias: Mus musculus (house mouse)
C;Dpcies: 20-Feb-1995 #sequence revision 20-Feb-1995 #text change 05-Nov-1999
C;Accession: A48921; A55677; T49348; I55421; H48909; I53774
R;Cerretti, D.P.; Nelson, N.; Kozlosky, C.J.; Morrissey, P.J.; Copeland, N.G.; Gilbert, Genomics 18, 410-413, 1993
A;Title: The murine homologue of the human interleukin-8 receptor type B maps near the A;Reference number: A48921; MUID:94117014; PMID:8288247
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A;Cross-references: GB:L26549
A;Orces sequence extracted from NCBI backbone (NCBIP:149812)
A;Note sequence extracted from NCBI backbone (NCBIP:149812)
B;Nec, J.; Gacalano, G.; Camerato, T.; Toy, K.; Moore, M.W.; Wood, W.I.
J. Immunol. 155, 2158-2164, 1995
A;Title: Chemokine binding and activities mediated by the mouse IL-8 receptor.
A;Reference number: 149348; MUID:95363183; PMID:7636264
                                     24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 19-May-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 50; DB 2
Pred. No. 5.8;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 WVLGKIMCKVTSALYTVNFVS 125
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Best Local Similarity 38.1
Matches 8; Conservative
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C; Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; inflammation; polymorp
F; 13-8 f Domain: extracellular #status predicted <TM1>
F; 39-62/Domain: transmembrane #status predicted <TM1>
F; 39-52/Domain: intracellular #status predicted <TM2>
F; 39-52/Domain: transmembrane #status predicted <TM2>
F; 73-95/Domain: transmembrane #status predicted <TM2>
F; 112-133/Domain: transmembrane #status predicted <TM3>
F; 112-133/Domain: transmembrane #status predicted <TM4>
F; 134-150/Domain: transmembrane #status predicted <TM5>
F; 130-229/Domain: transmembrane #status predicted <TM5>
F; 209-229/Domain: transmembrane #status predicted <TM5>
F; 209-229/Domain: transmembrane #status predicted <TM5>
F; 266-208/Domain: extracellular #status predicted <TM6>
F; 267-208/Domain: extracellular #status predicted <TM6>
F; 267-208/Domain: transmembrane #status predicted <TM7>
F; 267-208/Domain: transmembrane #status predic
                the chemokine receptor BLR2/EBI1 is specifically transa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anaphylatoxin C5a receptor. Evi
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C;Function:
A;Description: mediates the inflammatory and chemotactic responses of polymorphonuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement CSa anaphylatoxin receptor - dog
C/Species: Canis lupus familiaris (dog)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: S27357
R/Perret, J.J.; Raspe, E.; Vassart, G.; Parmentier, M.
Biochem. J. 288, 911-917, 1992
A/Itlle: Cloning and functional expression of the canine anaphylatoxin CSa r
A/Reference number: S27357; MUID:93111969; PMID:1472004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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:Cross.references: EMBL:X65860; NID:g878; PIDN:CAA46690.1; PID:g879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 378;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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40.5%; Score 51; DB 1
Best Local Similarity 33.3%; Pred. No. 4.1;
Matches 7; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
A; Description: The expression of the chemokine A; Reference number: $52443
A; Accession: $52443
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 21.378 < BUR>
A; Cross-references: EMBL: X84702
C; Genetics:
A; Genetics:
A; Genetics: A; Genetics: A; Genetics: A; CR7
A; Cross-references: GDB: 342065; CMIM: 600242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 42.9%; Pred. No.
Matches 9; Conservative 4; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 17q12-17q21.2
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 WDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 WPFGNAACRILPSLILLNMYA 123
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A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA

G protein-coupled receptor type B - bovine
C,Species: Bos primigenius taurus (cattle)

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Gaps

Length 350; Indels

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A; Residues: 1-359 < RE2>

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A,Accession: IS1372
A,Stetus: preliminary; translated from GB/EMBL/DDBJ
A,Accession: IS1372
A,Stetus: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: maxA
A,Molecule type: maxA
A,Molecule type: maxA
A,Residues: 1-59 eMUR
A,Residues: 1-59 eMUR
A,Residues: 1-59 eMUR
A,Residues: 1-59 eMUR
A,Reference number: PN0449; MUD:93221469; PND:1993
A,Accession: NN0449
A,Molecule type: maxA
A,Reference number: PN0449; MUD:93221469; PMD:7916599
A,Accession: NN0449
A,Molecule type: maxA
A,Reference number: PN0449; MUD:93221469; PMD:7916599
A,Accession: NN0449
A,Reference number: PN0449; MUD:93221469; PMD:7916599
A,Accession: Sold turkey adrenocortical call angiotensin II (AII) receptor partial C,Reference number: PN0449; MUD:93221469; PMD:7916599
A,Accession: Sold turkey adrenocortical call angiotensin II (AII) receptor partial C,Reference number: PN0449; MUD:93221469; PMD:7916599
A,Accession: Sold turkey adrenocortical call angiotensin I (AII) receptor partial C,Reference number: Hataus predicted A,IN1>
A,Residues: 33-91,CV,CV, 39-162, ASETULY D,MOSDNOPTOTEN; Transmembrane #status predicted A,IN1>
F,GS-64/Domain: intracellular #status predicted A,IN1>
F,GS-102/Domain: extracellular #status predicted A,IN1>
F,GS-102/Domain: transmembrane #status predicted A,IN1>
F,GS-102/Domain: extracellular #status predicted A,IN1>
F,GS-102/Domain: transmembrane #status predicted A,IN1>
F,GS-104/Domain: transmembrane #status p
                                                                                                                                                                                                                                                                                                                           angiotensin II receptor - turkey
Cispecies: Meleagris gallopavo (common turkey)
Cjate: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 24-Nov-1999
CjAccession: 151372; PNO449
R;Murphy, T.J.; Nakamura, Y.; Takeuchi, K.; Alexander, R.W.
Mol. Pharmacol. 44, 1-7, 1993
A;Title: A cloned angiotensin receptor isoform from the turkey adrenal gland is pharmacol.
A;Reference number: 151372; MUID:93341466; PMID:8341266
                                                                                                                                                                     hypothetical protein F35C8.3 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Jan-2000
C.Accession: T16256
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320 WSLGITVYQLVTGLY 334
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Best Local Similarity 60.0
Matches 9; Conservative
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A;Cross-references: GB:L13239; NID:g293665; PIDN:AAA62109.1; PID:g293666
R;Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.G Genomics 18, 175-184, 1993
A;Title: Identification, chromosomal location, and genome organization of mammalian G-pr A;Reference number: A48909; MUID:94116980; PMID:8288218
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R;Kawasaki, M.; Hisamoto, N.; Iino, Y.; Yamamoto, M.; Ninomiya-Tsuji, J.; Matsumoto, K.
R;Kawasaki, M.; Hisamoto, N.; Iino, Y.; Yamamoto, M.; Ninomiya-Tsuji, J.; Matsumoto, K.
A;Tile: A Caenorhabditis elegans JNK signal transduction pathway regurates coordinated
A;Reference number: Z21688; MUID:99321749; PMID:10393177
A;Accession: T37324
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-435 <KAW>
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rosidues: 145-258 < WIL.
A;Cross-references: GB:L20337; NID:9438800; PIDN:AAA16853.1; PID:9438801
R;Harada, A.; Kuno, K.; Nomura, H.; Mukaida, N.; Murakami, S.; Matsushima, K.
Gene 142, 297-300, 1994
A;Title: Cloning of a cDNA encoding a mouse homolog of the interleukin-8 receptor.
A;Reference number: I53774; MUID:94252584; PMID:8194768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable JNK-activating protein kinase (EC 2.7.1.-) JKK-1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 03-Dec-1999 #text_change 21-Jul-2000
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Cs.Superfamily: vertebate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
F;49-74/Domain:/transmembrane #status predicted <TM1>
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Best Local Similarity 60.0%; Pred. No. 7.3;
Matches 9; Conservative 2; Mismatches 4; Indels
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*Molecule type: maRNA
A;Residues: 1-359 «RE3»
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         307 WSLGITVYÖLVTGLY 321
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Matches

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A)Cross-references: BMBL:U10561; NID:9555696; PIDN:AAB60673.1; PID:9565069
R;Rossi, G.C.; Pan, Y.X.; Brown, G.P.; Pasternak, G.W.
R;BSL bett. 369, 192-196, 1935
A;Title: Antisense mapping the MOR-1 opioid receptor: evidence for alternative splicing A;Reference number: 149300; MUID:95377399; PMID:7649256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Introns: 95/2; 213/1; 386/3
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteolytic
                                                                                                                                                                                                                                                                                                                    of a mouse mu opioid receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: nucleic acid sequence not shown; translation not shown A; Molecule type: mRNA A; Residues: 1-998 < ROS-A; Residues: 1-998 < ROS-A; Coss-references: EMBL:U26915; NID:g1055230; PIDN:AAA81170.1; PID:g1055231 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995
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AjCross-references: GDB:127737; OMIN:187930
AjMap position: 5q13-5q13
C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-425/Product: thrombin receptor #status predicted <MAT>
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A;Residues: 1-425 <VUA>
A;Cross.references: GB:M62424; NID:g339676; PIDN:AAA36743.1; PID:g339677
            J. Biol. Chem. 270, 15877-15883, 1995
A;Title: Characterization of the murine mu opioid receptor gene.
A;Reference number: A57510; MUID:95318184; PMID:7797593
A;Accession: A57510
A;Status: nucleic acid sequence not shown
A;Rolecule rype: mRNA
A;Residues: 1-398 «KNA
A;Residues: 1-398 «KNA
A;Residues: 1-398 «KNA
A;Residues: 1-398 «KNA
A;Title: Augustin, L.B.; Felsheim, R.F.; Fuchs, J.A.; Loh, H.H.
Broc. Natl. Acad. Sci. U.S.A. 91, 9081-9085, 1994
A;Title: Genomic structure analysis of promoter sequence of a mouse
A;Reference number: 148665; MUID:94377496; PMID:8090773
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C;Species: Homo saptens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change (C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change (E;Accession: A37912
R;Vu, T.K.H.; Hung, D.T.; Wheaton, V.I.; Coughlin, S.R.
Cell 64, 1057-1068, 1991
A;Title: Molecular cloning of a functional thrombin receptor revision A;Reference number: A37912; MUID:91168254; PMID:1672265
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Pred. No. 10;
8; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Pred. No. 9.5;
7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                              A;Accession: I48665
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-398 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 18.9%;
Local Similarity 28.6%;
les 6; Conservative
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ilarity 23.8%;
Conservative
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Best Local Similarity
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C,Species: Mus musculus (house mouse)
C,Species: Mus musculus (house mouse)
C,Accession: 05-Reb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
C,Accession: JE0349
Biochem. Biophys. Res. Commun. 251, 41-48, 1998
Biochem. Biophys. Res. Commun. 251, 41-48, 1998
A;Title: Cloning of the murine interferon-inducible protein 10 (IP-10) receptor and its A;Reference number: JE0349; MUID:99009219; PMID:9790904
A;Accession: JE0349
A;Residues: 1-367 < TAM>A;Residues: 1-367 < TAM>A;Residues: 1-367 < TAM>A;Comment: This protein is important for lymphocyte trafficking to lymphoid organs.
C;Comment: This protein is important for lymphocyte trafficking to lymphoid organs.
                                                                                                                                                                                                                                                                                                        G protein-coupled receptor GPR2 - human (fragment)
C; Species: Home sapiens (man)
C; Species: Home sapiens (man)
C; Species: Home sapiens (man)
C; Accession: B55733
R; Marchese, A.; Docherty, J.M.; Nguyen, T.; Heiber, M.; Cheng, R.; Heng, H.H.Q.; Tsui, A; Title: Cloning of human genes encoding novel G protein-coupled receptors.
A; Title: Cloning of human genes encoding novel G protein-coupled receptors.
A; Accession: B55733
A; Accession: B55733
A; A; Accession: B55733
A; Status: preliminary
A; Moliciale type: DNA
A; Residues: 1-354 < MAR>
A; Residues: 1-354 < MAR>
A; Cross-references: GB: U13667
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A57510
mu opioid receptor - mouse
c;Species: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Date: 08-Dec-1995 #sequence revision 08-Dec-1995 #text_change 24-Nov-1999
C;Accession: A57510; 148665; $66513; I49300
C;Accession: A57510; I48665, $Anton, B.; Tian, J.; Magendzo, K.; Newman, D.;
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                                                                     Indels
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         Score 49.5; DB 2;
Pred. No. 7.1;
i; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.9%; Score 49; DB 36.8%; Pred. No. 8.4; iive 4; Mismatches
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C,Superfamily: vertebrate rhodopsin
C,Keywords: G protein-coupled receptor
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                                                               4,
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                                                                                                                     OWDFGNIMCOLLT-GLYF 17
         39.3%;
Query Match . 39.3
Best Local Similarity 50.0
Matches 9; Conservative
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Best Local Similarity 36.8'
Matches 7; Conservative
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Query Match
38.5%; Score 48.5; D
Best Local Similarity 54.5%; Pred. No. 20;
Matches 12; Conservative 1; Mismatches
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                                                                                                                                                                                                                                                                     41 WOFGGESNT----LTGLYFRGY 58
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A; Residues: 1-352 < HER>
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A; Residues: 1-352 <LOE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Figures, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.D.; Jones, L.M.; Kartet, U. Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluderer, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; P.; A; Lile: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: AG1086
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-186 < GLAA>
A;Cross-references: GB:NC_003210; PIDN:CAC98309.1; PID:g16409453; GSPDB:GN00177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein lmo0094 [imported] - Listeria monocytogenes (strain EGD-e) C;Species: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
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45.5%; Pred. No. 5.1;
tive 4; Mismatches 3; Indels 9
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Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Indels
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38.9%; Score 49; DB 2
Best Local Similarity 28.6%; Pred. No. 10;
Matchies 6; Conservative 6; Mismatches
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A;Gene: lmo0094
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Matches 10; Conservative
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A;Molecule type: mRNA
A;Residues: 1-427 <RAS>
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A; Residues: 1-706 < PAR>
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A;Cross-references: GB:AL162756; GB:AL157959; NID:g7380091; PIDN:CAB84785.1; PID:g738019
A;Experimental source: serogroup A, strain 22491
C;Genetics:
A;Gene: NWA1558
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N;Alternate names: fusin; HM89; leukocyte-derived seven-transmembrane receptor LESTR; re
C;Species; Homo sapiens (man)
C;Species; Homo sapiens (man)
C;Species; Homo sapiens (man)
C;Accession: A45747; A53103; I53006; I59444; I69203; S32761
G;Accession: A45747; A53103; I53006; I59444; I69203; S32761
G;Accession: A45747; A53103; I500c; I59444; I69203; S32761
A;Refereptie: Nolecular cloning of the cDNA and chromosomal localization of the gene for a pu
A;Reference number: A45747; MUID:93315164; PMID:8325644
A;Reference number: A45747; MUID:93315164; PMID:8325644
A;Residues: I-552 cFED>
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R;Jazin, B.E.; Yoo, H.; Blomgvist, A.G.; Yee, F.; Weng, G.; Walker, M.W.; Salon, J.; Lax
Regul. Pept. 47, 247-258, 1993
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R;Loetscher, M.; Geiser, T.; O'Reilly, T.; Zwahlen, R.; Baggiolini, M.; Moser, B.;
J. Biol. Chem. 269, 232-237, 1994
A;Title: Cloning of a human seven-transmembrane domain receptor, LESTR, that is highly A;Reference number: A53103; MUID:94103215; PMID:8276799
A;Accession: A33103
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: EMBL:X71635; NID:9297099; PIDN:CAA50641.1; PID:9297100
R;Herzog, H.; Hort, Y.J.; Shine, J.; Selbie, L.A.
DNA Cell Biol. 12, 465-471, 1993
A;Title: Molecular cloning, characterization, and localization of the human homolog to A;Reference number: 153006; MUID:93319629; PMID:8329116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fugin (LESTRA) - crab-eating macaque
Cispecies: Macaca fascicularis (crab-eating macaque)
Cispecies: Macaca fascicularis (crab-eating macaque)
Cibaces: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 26-Aug-1999
CiAccession: G00048
R.Tatsumi, M.
A.Reference number: H00048
A.Reference number: H00048
A.Reference number: H00048
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary;
A.Status: 1-352 CATAP
A.Residues: 1-352 CATAP
A.Residues: 1-352 CATAP
CiSuperfamily: vertebrate rhodopsin
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Gaps

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probable transporter protein Z4165 [imported] - Escherichia coli (strain O157:H7, subst. C.) Species Escherichia coli (5.) Species Escherichia coli (5.) Species Escherichia coli (5.) Secession: A85937 [1.] Secession: A85937 [1.] Secession: A85937 [1.] Secession: A85937 [1.] Secossion: A.) Detamousis, E.) Potamousis, E.) Mayhew Nature 409, 529-533, 2001 [1.] Secossion: A.) Detamousis, E.) Apodaca, A.) Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7. Apodaca, A.) Accession: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A)Status: preliminary
A)Andecule type: DNA
A)Andecule type: DNA
A)Residues: 1-409 <-2770>
A)Cross-references: GB:AE005174; NID:g12517337; PIDN:AAG57957.1; GSPDB:GN00145; UMGP:Z41
A)Experimental source: strain O157:H7, substrain EDL933
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Cispecies: Xenopus laevis (African clawed frog)
Cispecies: Xenopus laevis (African clawed frog)
Cibate: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
CiAccession: 151667
Rigerszten, R.E.; Chen, J.; Ishii, M.; Ishii, K.; Nanevicz, T.; Turck, C.W.; Vu, T.H.; C Rigerszten, R.E.; Thrombin receptor's specificity for agonist peptide is determined by its extract A; Reference number: 151667; WUID:94195429; PMID:8145852
A; Accession: 151667
                     A;Molecule type: DNA
A;Residues: 1-409 <HAY>
A;Ressidues: 1-409 <HAY>
A;Crossreferences: GB:BA000007; PIDN:BAB37125.1; PID:g13363174; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: BC83702
C;Superfamily: threonine-serine permease
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Pred. No. 14;
3; Mismatches
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A;Residues: 1-420 <GER>
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38.1%; Score 48; DB 2;
Best Local Similarity 30.0%; Pred. No. 14;
Matches 6; Conservative 7; Mismatches
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14;
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C;Superfamily: threonine-serine permease
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A/Crose-references: GB:L01639; NID:g189313; PIDN:AAA16594.1; PID:g189314
A/Crose-references: GB:L01639; NID:g189313; PIDN:AAA16594.1; PID:g189314
B/Nomura, H.; Nielsen, B.W.; Matsushima, K.
Int. Immunol. 5, 1239-1249, 1993
A/Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte chem
A/Reference number: 154751; MUID:94092629; PMID:7505609
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Roteule type: mRNA
A/Roteule type: mRNA
A/Roteule type: mRNA
A/Roteule type: mRNA
A/Genetics:
A/Genetics
'Title: A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its human homold
Reference number: 159444; MUID:94052833; PMID:8234909
Accession: 159444
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Search completed: September 28, 2004, 09:07:07

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GenCore version 5.1.6

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OM protein - protein search, using sw model

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(without alignments)

166.624 Million cell updates/sec

Perfect score: 126
Sequence: 126
Sequence: 1 QWDFGNTMCQLLTGLYFIGFFS 22
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
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Total number of hits satisfying chosen parameters: 14168

141681 seqs, 52070155 residues

Searched:

Minimum DB seq lëngth: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0%

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

PRT; 352 AA.	<pre>.ed) sequence update) annotation update) : 5 (C-C CKR-5) (CCR-5) (CCR5).</pre>	monkey) (Grivet). Craniata; Vertebrata; Buteleostomi; Catarrhini; Cercopithecidae;	11) TISSUE-Kidney, TISSUE-Kidney, TISSUE-Kidney, MEDLINE-980001387; PubMed-9343222; MEDLINE-98001387; PubMed-9343222; "Polymorphisms in the CCR5 genes of African green monkeys and mice implicate specific amino acids in infections by simian and human immunodeficiency viruses."; J. Virol. 71:8642-8656(1997).	12) SEGUENCE FROM N.A. Mizayama Y., Matsunaga S., Inoue-Murayama M.; "CDNA sequence of African green monkey CCR-5 chemokine receptor	gene."; Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or	GIALTELLALOR LOCATION: Integral membrane protein. SUBCELLULAR LOCATION: Integral membrane protein. SIMILARIY: Belongs to family 1 of G-protein coupled receptors.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	EMBL; U83324; AACS1795.1; - EMBL; U83325; AACS1796.1; - EMBL; U83325; AACS1796.1; - EMBL; AB015244; EAAA1328.1; - INTEXPRO, IRRO00276; GPCR.Rhodpsn. Pfam; PF00001; 7tm_1; 1. PROSITE; PS00237; GPRRHODOPSN. PROSITE; PS00237; GPROTEIN RECEP F1 1; 1. PROSITE; PS00262; GPROTEIN RECEP F1 2; 1. Prositein coupled receptor; Transmembrane; Glycoprotein; Sulfation;	EXTRACELLULAR (POTENTIAL).
STANDARD;	793; TUL-1998 (Rel. 36, Created) TUL-1998 (Rel. 36, Last sec CT-2001 (Rel. 40, Last and Chemokine receptor type 5	CCKS OK CMXERS.  Gercopithecus aethiops (Green m Eukaryota, Metazoa, Chordata, C Mammalia, Eutheria, Primates, C Gercopithecinae, Cercopithecus,	NCM N.A. Iney, 0.01387; PubMed=9343 0.01387; PubMed=9343 E., Platt E.J., Kozz isms in the CCRS ge specific amino acid ciency viruses."; 71:8642-8656(1997).	1 N.A. Matsunaga S. se of African	JL-1998) to the Receptor for a and RANTES of the intraction of grainstants.	AR LOCATION: Y: Belongs to	This SWISS-PROT entry is copyright.  between the Swiss Institute of Biol the European Bioinformatics Institut use by non-profit institutions as modified and this statement is not r entities requires a license agreement or send an email to license@isb-sib.	U83324; AAC51795.1; U83325; AAC51796.1; ABD15944; BAA3128.28 PF00001; 7tm 1; 1. PF00001; 7tm 1; 1. PF00027; GPRCHPOD FB; PS00227; GPRCTER FB; PS50262; GPRCTER FB; PS50262; GPRCTER FB; PS50262; GPRCTER FB; PS50262; GPRCTER	1 30
LT 1 CERAE CKRS CERAE	15-JUL-1998 15-JUL-1998 15-JUL-1998 16-OCT-2001	CCKS OR CMXBRS. Cercopithecus ae Eukaryota, Metaz Mammalia, Euther Cercopithecinae,	11) TISSUE=Kidney, TISSUE=Kidney, MEDLINE=98001387, Widhmann S.E., Plail "Polymorphisms in implicate specific immunodeficiency virol. 71:86422	12] SEQUENCE FROM N.A. Murayama Y., Matsu "cDNA sequence of	gene."; Submitted (JUL-1998) -1- FUNCTION: Recept. MIP-1-beta and R. increasing the 1: in the control of differentiation	-!- SUBCELLUI -!- SIMILARIT	This SWISS-PROT entry is copyright. It is between the Swiss Institute of Bioinforn the European Bioinformatics Institute. Were by non-profit institutions as lon modified and this statement is not removentiles requires a license agreement (Swors end an email to license@isb-sib.ch).	EMBL; U83324; EMBL; U83325; EMBL; AB01594 InterPro; IPR Pfam; PF00001 PRINTS; PR00 PROSITE; PS00 PROSITE; PS00 Cuprotein cou	DOMAIN
CKRS CI	Series (	800008	RRRRRRRR RRTRRRRRRRRRRRRRRRRRRRRRRRRRR	r r r r	##88888	3888	388888888		FI

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDINE-99335215; PubMed=10408730; Multiple-99335215; PubMed=10408730; Multiple-Truthwin M.C., Corbet S., Hansen J., Georges-Courbot M.-C., Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.; Stoulet J., Barre-Sinoussi F., Fomsgaard A.; Mutations in CCR5-coding sequences are not associated with SIV carries featus in African nonhuman prinates."; ALS Res. Hum. Retroviruses 15:911-939(1999).
-1. FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-bet and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCRS OR CMKBR5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              differentiation.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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                                                                                                                                                                                                                                                                                                                                             Score 126; DB 1; Length 352;
Pred. No. 1e-11;
Mismatches 0; Indels (
                                                                                                                                                        6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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SULPATION (BY SIMILARITY).
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SULFATION (BY SIMILARITY).
                                     Z (FOIENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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                                                                     CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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0; Mismatches
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(POTENTIAL)
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                                2 (POTENTIAL)
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                CYTOPLASMIC
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NCBI_TaxID=60710;
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ID CKRS CERPY
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EMBL, AF035222; AAD44015.1; -. InterPro, IPR000276; GPCR\_Rhodpsn. Pfam; PF00001; 7tm\_1; 1.

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"Primary SIVsm isolates use the CCR5 coreceptor from sooty mangabeys naturally infected in west Africa: a comparison of coreceptor usage of primary SIVsm. HV.2, and SIVmac.";
virology 246:113-124(1998).
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RAVIES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or
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ID CKRS_CERTO

ID CKRS_CERTO

ID CKRS_CERTO

STANDARD;

AC 062743; 062746;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCRS).

GN CKRS ON CKRSRS.

GN CKRSRS.

GN CKRSRS.

CRS ON CKRSRS.
               PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

SOSSITE; PSS0262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

DOMAIN

EXTRACELLIDAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLUTAR LOCATION: Integral membrane protein.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; 
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; 
Cercopithecinae; Cercocebus.
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EXTRACELLULAR (POTENTIAL).
                                                                                      1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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SULFATION (BY SIMILARITY)
SULFATION (BY SIMILARITY)
EF17D67CRCCC3DB0 CRC64;
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CYTOPLASMIC (POTENTIAL).
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STRAIN=Isolate 079, 085, 087, and 089;
MEDLINE=98321155; PubMed=9656999;
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352 C7
178 BN
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10 ST
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PRINTS; PR00237; GPCRRHODOPSN
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1es 22; Conservative
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CKRS CERTO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CKRS HUMAN STANDARD; PRT; 352 AA.

ID CKRS HUMAN STANDARD; PRT; 352 AA.

AC P51681; 014692; 014693; 014695; 014699; 014699;

AC 014700; 014701; 014702; 014703; 014705; 014705; 014706; 014707;

AC 014709; 018701; 014702; 014703; 014705; 014706; 014707;

AC 014709; 015781; 034, Created)

DT 01-0CT-1996 (Rel. 34, Last sequence update)

DT 10-MAR-2004 (Rel. 34, Last sequence update)

DF C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR-5)

DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR-5)

CR (HIV-1 fusion co-receptor) (CHEMR13) (CD195 antigen).

CR CKRS.

CS HOMO sapiens (Human).

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NED TAXID=9606;
             increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                EMBL, AF005659, AAB62553.1;
InterPro; IPR00276, GPCR_Rhodpsn.
Prom; PR000217; Trm 1, 1.
PROSITE; PS00237; GPCRHFDODEN.
PROSITE; PS00237; G PROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; GPROTEIN RECEP_F1_2; 1.
DOMAIN COUPLED RECEP_F1_2; 1.
30 EXTRACELLULAR (POTENTAL).
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MEDLINE-96241590; PubMed-8639485;
Samson M., Labbe O., Mollereau C., Vassart G., Parmentier M.;
"Molecular cloning and functional expression of a new human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 126; DB 1; Length 352; Pred. No. 1e-11; 0; Mismatches 0; Indels (
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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MEDLINE-97268687; PubMed=9108095;
Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
Paiper S.C., Parmentier M., Broder C.C., Doms R.W.;
Inifferential utilization of CCR5 by macrophage and T cell tropic
simian immunodeficiency virus strains.",
Proc. Natl. Acad. Sci. U.S.A. 9414005-4010(1997).
Proc. Natl. Acad. Sci. U.S.A. 9414005-4010(1997).
Proc. Natl. Acad. Sci. U.S.A. 9414005-4010(1997).
MIP-1-beta and RANTES and subsequently transduces a signal by
EMBL; AF051902; AAC39830.1; --
EMBL; AF051904; AAC39831.1; --
EMBL; AF051904; AAC3983.1; --
EMBL; EP051904; AAC3983.1; --
InterPro; IFR000276; GPCR_Rhodpsn.
Pfam; PR00031; 7tm 1, 1, 1, 1
PRINTS; PR00031; 7cm 7cm 1, 1, 1
PR001TE; PS00237; GPROTEIN RECEP_F1 1; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
DOMAIN 1 30 EXTRACELLULAR (POTENTIAL)
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15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
6-CC obsenokine receptor type 5 (C-C CRR-5) (CC-CKR-5) (CC-CKR)
CCRS OR CMKRRS.
GORILla gorilla (Lowland gorilla)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
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Y -> D (IN ISOLATE 087).
W -> G (IN ISOLATE 087).
L -> V (IN ISOLATE 089).
V -> G (IN ISOLATE 079).
V -> G (IN ISOLATE 079).
Y -> G (IN ISOLATE 079).
T -> I (IN ISOLATE 079).
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W; 20A196E2D47E49CA CRC64;
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4 (POTENTIAL).

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7 (POTENTIAL).

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8 SIMILARITY.

8 SULFATION (BY SIMILARITY).

9 -> 5 (IN ISOLATE 087).

10 -> 6 (IN ISOLATE 087).
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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MEDLINE=96291862; PubMed=8663314; Raport C.J., Gray P.W., Charo I.F.; Raport C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F.; "Molecular cloning and functional characterization of a novel human CC chemokine receptor (CCES) for RANTES, MIP-lbeta, and MIP-lalpha.", J. Biol. Chem. 271:17161-17166(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND POLYMORPHISMS.
MEDLINE=98022612; PubMed=9359654;
Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98049523; PubMed=9388201; Mummidi S., Ahuja S.K.; Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.; Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.; The human CC chemokine receptor S (CCRS) gene. Multiple transcripts with 5'-end heterogeneity, dual promoter usage, and evidence for polymorphisms within the regulatory regions and noncoding exons."; J. Biol. Chem. 272:30662-30671(1997).
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MEDLINE=58001387; PubMed=9343222;
Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.;
"Polymorphisms in the CCR5 genes of African green monkeys and micimplicate specific amino acids in infections by simian and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                  McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K., Gnoj L., la Bastide M., Raplan N., Greco T., Touchman J., Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D., Sagripanti J.L., Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism."; AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
                                                                                                                                                                                                                                                                                     Combadiere C., Ahuja S.K., Tiffany H.L., Murphy P.M.; "Cloning and functional expression of CC CKR5, a human monocyte chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and
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"cDNA clones of human proteins involved in signal transduction
sequenced by the Guthrie cDNA resource center (www.cdna.org).";
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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MEDLINE-96260017; PubMed-8649511;
Deng H., Liu R., Ellmeier W., Choe S., Unutmaz D., Burkhart M., di Marzio P., Marmon S., Sutton R.E., Hill C.M., Davis C.B., Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;
"Identification of a major co-receptor for primary isolates of
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Magierowska M., Barre-Sinoussi F., Issafras H., Theodorou I.,
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SEQUENCE FROM N.A.
MEDLINE=96295970; PubMed=8699119;
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CC-chemokine receptor gene.";
Biochemistry 35:3362-3367(1996),
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the TNBL outstation the Buropean Bicinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license alcense.
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-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-bet and rantes and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation. Acts as co-receptor with CD4 for primary nonsyncytium-inducing strains (NSI) (macrophage-tropic) of HIV-1 virus. It promotes Env-mediated fusion of the virus.
-:- SUBCELIULAR LOCATION: Integral membrane protein.
-:- TISSUE SPECIFICITY: Found in promptleocytic cells.
-:- PTM: SULfation contributes to the efficiency of HIV-1 entry.
-:- PTM: Modified by O-linked glycosylation, but not by N-linked
                                                                                                                                                                                                                                                                                                                                                                                         Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,
Gerard N.P., Gerard C., Sodroski J., Choe H.;
"Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                Paxton W.A., "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor
Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,
Nagashima K.A., Cayanan C., Maddon P.J., Koup R.A., Moore J.P.,
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AF011503, AA865703.11,
AF011504, AA865707.11,
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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                       Score 126; DB 1; Length 352;
Pred. No. 1e-11;
0; Mismatches 0; Indels 0
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DR EMBL; AF011536; AAB65737.1; -...

DR EMBL; AF011536; AAB65737.1; -...

DR EMBL; AF021237; AAB94735.1; -...

DR EMBL; AF025239; AAD18131.1; -...

DR GO: GO:0005763; C:integral to plasma membrane; TAS.

DR GO: GO:0016493; F:C-C chemokine receptor activity; TAS.

DR GO: GO:0016493; F:C-C chemokine receptor activity; TAS.

DR GO: GO:0015686; C:integral to plasma membrane; TAS.

DR GO: GO:0015687; F:coreceptor activity; TAS.

DR GO: GO:0015687; P:cell-cell signaling; TAS.

DR GO: GO:0015698 P:cell-cell signaling; TAS.

DR GO: GO:0005767; P:cell-cell signaling; TAS.

DR GO: GO:0007267; P:cell-cell calcium ion concentration elevation; TAS.

DR GO: GO:0007267; P:integral calcium ion concentration elevation; TAS.

DR GO: GO:0007267; P:integral calcium; ion concentration elevation; TAS.

DR GO: GO:0007204; P:integral calcium; ion concentration elevation; TAS.

DR GO: GO:0007204; P:integral calcium; ion concentration elevation; TAS.

DR GO: GO:0007204; P:integral calcium; ion concentration elevation; TAS.

DR GO: GO:0007204; P:integral calcium; ion concentration elevation; TAS.

DR GO: GO:0007203; P:integral calcium; ion concentration elevation; TAS.

DR PRINTS: PRO0227; GPERREMEDOPSN.

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AR Zhang Y.-W., Ryder O.A., Zhang Y.-P.;

RT Sequence evolution of the CCR5 chemokine receptor gene in primates.";

RT Sequence evolution of the CCR5 chemokine. Binds to MIP-1-alpha, and Biol. Evol. 16:1145-1154(1999).

CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, and PANTES and Subsequently transduces a signal by cc increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKS).
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Wararyota, Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
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ö Gaps 095NCO; 15-MAR-2004 (Rel. 43, Created) 15-MAR-2004 (Rel. 43, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) Hylobates moloch (Silvery gibbon).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hylobatidae, Hylobates. ö

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differentiation.
-!-SUBCELULAR LOCATION: Integral membrane protein.
-!-SUBCELULAR LOCATION: Integral membrane protein coupled receptors.
-!-SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-99416438; PubMed=10486970;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Sequence evolution of the CCR5 chemokine receptor gene in primates.";
Mol. Biol. Evol. 16:1145-1154(1999).
-! FUNCTION: Receptor for a C.C type, chemokine. Binds to MIP-1-alpha,
-! FUNCTION: Receptor for and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
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                                                                                                EMBL, AF177899, AAK43382.1; -.

InterPro; PR00276; GPCR_Rhodpsn.

PRIMTS; PR00237; GPCRHOOPSN.

PROSITE; PS00237; GPCREIN RECEP F1 1; 1.

PROSITE; PS50262; G_PROTEIN TRECEP F1 2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

DOMAIN

EXTRACELLULAR (POTENTIAL).
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15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
C-C chemoxine receptor type 5 (C-C CRR-5) (CC-CKR-5) (CC-CKR-5)
CCRS OR CMKBRS.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
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SULFATION (BY SIMILARITY).
9623CA98340CF274 CRC64;
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                             EMBL; AF177884; AAK43367.1; -.

InterPro; IPR000276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRHODDPSN.

PROSITE; PS00237; GPROTEIN RECEP_F1_2; 1.

PROSITE; PS50262; GPROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
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P79436; 002746;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CRR-5) (CC-CKR-5) (CCRS).
CCRS OR CMKRES.
Macaca mulatta (Rhesus macaque),
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
Macaca emestrina (Pig-tailed macaque)
Bukaryota; Metazoa; Chordata; Czaniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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MEDLINE-97184592; PubMed-9032394;
Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,
Newman W., Gerard N., Gerard C., Sodroski J.;
"Utilization of C-C chemokine receptor 5 by the envelope
glycoproteins of a pathogenic simian immunodeficiency virus,
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F4F64B3AD5AF658A CRC64;
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J. Virol. 71:2522-2527(1997).
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NCBI_TaxID=9544, 9541, 9545;
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R Pfam; PR0001; 7tm 1; 1.

R PASSITE; PR00237; GFCRHODOPSN.

DR PROSITE; PS020237; G PROTEIN RECEP F1 1; 1.

DR PROSITE; PS02022; G PROTEIN RECEP F1 2; 1.

KW G-Protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

FT DOMAIN 13 SHOTELUIAR (POTENTIAL).

FT DOMAIN 59 89 2 (POTENTIAL).

FT DOMAIN 69 89 2 (POTENTIAL).

FT COMBINAL 102 EXTRACELLUIAR (POTENTIAL).

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MEDLINE=97268687; PubMed=9108095;
MEDLINE=97268687; PubMed=9108095;
Bedinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
"Differential utilization of CCR5 by mearcophage and T cell tropic
simian immunodeficiency virus strains.";
Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
- FUNCTION: Receptor for a C.C. type chemokine. Binds to MIP-1-alpha,
Increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
"Genetically divergent strains of simian immunodeficiency virus use CCRS as a coreceptor for entry."; J. Virol. 71:2705-2714(1997).
                                                                                                                                                                                                                                                                                                                                                                                                         differentiation.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                SPECIES=M.mulatta;
MEDLINE=21354176; PubMed=11461684;
Margulies B.J., Hauer D.A., Clements J.E.;
"Identification and comparison of eleven rhesus macaque chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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RY SIMILARITY.
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N'LINKED (GLCNAC...) (POTENTIAL).
M' -> M (IN REF. 3).
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I -> M (IN REF. 3).
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EMBL; U73739; AAC51158.1; -.
EMBL; U96762; AAC34132.1; -.
EMBL; AF005660; AAB62554.1; -.
EMBL; AF005661; AAB62555.1; -.
EMBL; AF005661; AAB62556.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
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--- SUBCELLULAR LOCATION: Integral membrane protein.
--- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phylogeny.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCITON: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
                                                 Gaps
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Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
Ho D.D.;
                                                                                                                                                                                                             P56440, 002778;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-JUL-1998 (Rel. 36, Last sequence update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCRS OR CMKBRS.
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MEDLINE=97426118; PubMed=92822;
Zacharova V., Zachar V., Goustin A.S.;
"Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=97268687; PubMed=9108095;
Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
Sharzon M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
Pelper S.C., Parmentier M., Broder C.C., Doms R.W.;
"Differential utilization of CCRS by macrophage and T cell tropic
simian immunodeficiency virus strains.";
Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
                                                                                                                                                                                                                                                                                                                      Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism."; AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
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MEDILINE=98090115; PubMed=9430250;
Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.;
"Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1.";
AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
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Pred. No. 1e-11;
Mismatches 0; Indels
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Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                    352 AA.
                                                                                                 93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                22
100.0%; Sco
100.0%; Pre
                                                                         1 QWDFGNTMCQLLTGLYFIGFFS
       Query Match
Best Local Similarity 100.
Matches 22, Conservative
                                                                                                                                                                                                    STANDARD;
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                                                                                   EMBL, 194319; AAAS 1840.1, ...

EMBL, AF011542; AAB5542.1; ...

EMBL, 197666; AAC51670.1; ...

EMBL, AF01740; AAB5540.1; ...

EMBL, AF017694; AAK43377.1; ...

EMBL, AF177894; AAK43377.1; ...

EMBL, AF177894; CFCR.Rhodpsn.

PERNITS; PR000237; GFCRRHODDSN.

PERNITS; PR000237; GFCRRHODDSN.

PROSTITE; PS00237; GRRTEIN RECEP F1_1; 1.

PROSTITE; PS50262; G PROTEIN RECEP F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

ACREAGELULAR (POTENTAL).
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15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCRS).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                            . .) (POTENTIAL)
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MEDLINE=97268687; PubMed=9108095;
Bdinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
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Pred. No. 1e-11;
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SULPATION (BY SIMILABITY).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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4A33E698B80FE34C CRC64;
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                     EMBL; AF005663; AAB62557.1; -.
EMBL; U94329; AAB58446.1; -.
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NCBI_TaxID=9557, 9555;
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102
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352 AA;
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es 22; Conserv
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P56441;
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SPECIES=P. anubis;
Benton P.A., Thmanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;
Benton P.A., Thmanus D.K. Shearer M.H., Lee D.R., Kennedy R.C.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RAWIES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
                                                             SPECIES=P.hamadryas;
MEDIJNE=99210133; PubMed=10195758;
Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.;
"Species-specific changes in the CCR5 gene from African and Asian nonhuman primates.";
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EMBL; AF105289; AAD20556.1; --
EMBL; AF105289; AAD20558.1; --
EMBL; AF105289; AAD20558.1; --
EMBL; AF105289; AAD20558.1; --
EMBL; AF003452; AAC63830.1; --
EMBL; AF003452; AAC63830.1; --
EMBL; AF00317; GPCR_Rhodpsn.
PRANTS; PRO0137; GPCR_PODPSN.
PROSITE; PS00237; GPROTEIN RECEP_F1_1; 1.
PROSITE; PS0237; GPROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; TextmanmanDrane; Glycoprotein; Sulfation.
DOMAIN
"Differential utilization of CCR5 by macrophage and T cell tropic
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100.0%; Pred. No. 1e-11;
tive 0; Mismatches 0; Indels
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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             simian immunodeficiency virus strains.";
Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
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1 QWDFGNTMCQLLTGLYFIGFFS 22

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Colobinae;

MEDLINE=99416438; PubMed=10486970;

SEQUENCE FROM N.A. NCBI\_TaxID=61621;

Pygathrix.

352 AA

STANDARD;

PYGBI

93 QWDFGNTMCQLLTGLYFIGFFS 114

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097680;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
38-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR5)
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                                                                                                                                                                                                    The District of the CCR5 chemokine receptor gene in primates.",
"Sequence evolution of the CCR5 chemokine receptor gene in primates.",
"Sequence evolution of the CCR5 chemokine receptor gene in primates.",
MOI. Biol. Evol. 16:1145-11146 (1999).

-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
INTP-1-beta and RANTES and subsequently transduces a signal by
Increasing the intracellular calcium ions level. May play a role
in the control of gramulocytic lineage proliferation or
differentiation.
-!- SUBCELULIAR LOCATION: Integral membrane protein.
-!- SUBCELULIAR LOCATION: Integral membrane protein.
                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
38-FBB-2003 (Rel. 41, Last annotation update)
C-C chemokiñe receptor type 5 (C-C CKR-5) (CCRCR-5) (CCR5)
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PROSITE; PS50262; G_PROTEIN RECEP_F1_2; 1.
DOMAIN 130 LYTRAGELIULAR (POTENTIAL).
TRANSNEM 31 58 LYTRAGELLULAR (POTENTIAL).
TRANSNEM 59 68 CYTOPLASMIC (POTENTIAL).
TRANSNEM 69 89 2 (POTENTIAL).
DOWAIN 90 102 EXTRACELLULAR (POTENTIAL).
                                                                                                                             Eukāryotā, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pongo.
NOBI_TaxID=9600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Score 126; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels (
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SULFATION (BY SIMILARITY).
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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                             352 AA.
                          PRT;
                                                                                                                                                                   [1] SEQUENCE FROM N.A. MEDLINE=99416438; PubMed=10486970;
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INCAFZPO; DR000275; GECR_Rhodpsn.
Pfam; PP00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
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                                                                                                                 Pongo pygmaeus (Orangutan)
                           STANDARD;
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                          CKR5 PONPY
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             CKR5 PONPY
RESULT 12
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DR RHIPS, PRO0276; GPCRRHODOSN.

PROSITE; PS00237; GPCRRHODOSN.

DR PROSITE; PS00237; GPCRIN RECEP F1 1; 1.

DR PROSITE; PS00237; GPCRIN RECEP F1 2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

FT TRANSMEM 31 30 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 59 68 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 103 124 3 (POTENTIAL).

FT TRANSMEM 125 141 GYTOPLASMIC (POTENTIAL).

FT TRANSMEM 125 141 GYTOPLASMIC (POTENTIAL).

FT TRANSMEM 127 188 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 128 166 (POTENTIAL).

FT TRANSMEM 129 218 S (POTENTIAL).

TRANSMEM 129 218 S (POTENTIAL).
Annuary Structures of the CCR5 chemokine receptor gene in primates.";
"Sequence evolution of the CCR5 chemokine receptor gene in primates.";
"Sequence evolution of the CCR5 chemokine in primates.";
MOI. Biol. Bvol. 16:1145-1154(1999).

"Increasing the intracellular chemokine. Binds to MIP-1-alpha, increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.

-I SUBCELULIAR LOCATION: Integral membrane protein.

-I SINILARITY: Belongs to family 1 of Grenctein coupled receptors.
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4366F142730F938F CRC64;
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40585 MW;
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Best Local Similarity 100.
Matches 22; Conservative
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1 QWDFGNTMCQLLTGLYFIGFFS 22

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1 QWDFGNTMCQLLTGLYFIGFFS 22

1 OWDFGNTMCOLLTGLYFIGFFS 22

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2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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                                                                                               PRT; 352 AA
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93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                     differentiation.
                                                                                               PYGNE
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DOMAIN
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                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its web by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                        MEDIINE=99416438; PubMed=10486970; Zhang Y.-W.; Ryder O.A., Zhang Y.-W.; Ryder O.A., Zhang Y.-P.; Sequence evolution of the CCRS chemokine receptor gene in primates."; Mol. Biol. Evol. 16:1145-1154(1999).

-!-FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-bet and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or
                                                                                                                                           Pygathrix nemaeus (Dove langur).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae, Colobinae,
                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
38-FBB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCRS).
CCRS OR CMKBRS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dieerpro; IPRUUL...;
PEAR, PROGOOJ; THI 1: 1.
PRINTS; PROGOJ; GERRUDOPSN.
PROSITE; PSOC237; G PROTEIN RECEP_F1_1; 1.
PROSITE; PSOC245; G PROTEIN RECEP_F1_2; 1.
PROSITE; PSOC452; G PROTEIN RECEP_F1_2; 1.
PROSITE; PSOC452; G PROTEIN RECEP_F1_2; 1.
PROSITE; PSOC452; G PROTEIN RECEP_F1_2; 1.
PROSITE; PSOC451; G PROTEIN RECEP_F1_2; 1.
PROSITE: 1. (POTENTIAL).

1 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                      -: SUBSELLUTAR LOCATION: Integral membrane protein.
-: SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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EXTRACELLULAR (POTENTIAL)
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100.0%; Score 126; DB 1.
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 22; Conservative 0; Mismatches (
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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NCBI_TaxID=54133;
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RESULT 14
CKR5 PYGNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99416438; PubMed=10486970;
MEDLINE=99416438; PubMed=10486970;
MEDLINE=99416438; PubMed=10486970;
Mang Y.-W., Ryder O.A., Zhang Y.-P.;
Sequence evolution of the CCRS chemokine receptor gene in primates.";
Mol. Biol. Evol. 16:1145-1154(1999).
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
-!- FUNCTION: Receptor for a G-C type chemokine. Binds to MIP-1-lapta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Veriebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae, Colobinae, Trachypithecus,
                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
38-FBB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCFS OR CMKBRE)
Trachypithecus francoisi (François' langur) (Indochinese langur)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SUBCELLULAR LOCATION: Integral membrane protein.
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PRINTS; PR00337; GPCRREDDOPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Transmem5rane; Glycoprotein; Sulfation.

DOMAIN

EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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93 QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF075442; AAD19854.1; -. Interpro; IPR000276; GPCR_Rhodpsn.
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-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
-1- SIMILARITY: Belongs to family 1 is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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modified ...

or send an email to llu.

or send an email to llu.

REMBL, APOTS43; AAD19855.1; -..

DR InterPro; IPR000276; GPCR_Rhodpsn.

Pfam, PF00001; TTL 1; 1.

DR PROSITE; PS00237; GPCRRHODDSN.

DR PROSITE; PS00237; GPCRRHODDSN.

DR PROSITE; PS00237; GPCRRHODDSN.

DR PROSITE; PS00237; GPCRRHODDSN.

PROSITE; PS00237; GPCRRHODDSN.

TRANSMEM 31 58 1 (POTENTIAL).

FT DOMAIN 31 58 1 (POTENTIAL).

FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 103 124 3 (POTENTIAL).

FT TRANSMEM 142 166 4 (POTENTIAL).

PT TRANSMEM 142 166 GPCRENTIAL).

TRANSMEM 142 166 GPCRENTIAL).

OUTH 199 218 CYTOPLASMIC (POTENTIAL).

TRANSMEM 142 166 (POTENTIAL).

OUTH 199 218 CYTOPLASMIC (POTENTIAL).

TRANSMEM 199 218 EXTRACELLULAR (POTENTIAL).

OUTH 199 218 CYTOPLASMIC (POTENTIAL).

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Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
"Sequence evolution of the CRES chemokine receptor gene in primates.";
Mol. Biol. Evol. 16:1154-1154 (1999).
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-abha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
                                                                                                                                                                                                                                                                                                                                          Trachypithecus phayrei (Phayre's leaf monkey).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
Trachypithecus.
                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
38-FBB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CRR-5) (CC-CRR-5) (CCRS).
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Pred. No. 1e-11;
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CYTOPLASMIC (POTENTIAL).
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SULFATION (BY SIMILARITY).
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              40509 MW;
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MEDLINE-20501139; PubMed=11046064;
Preobrazhensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. NubMed=8995400; Gosling J., Arai H., Charo I.F.; MEDIATE=97150864; MONDIATE=97150864; MONDIATE—97150864; J., Tsou C.-i., Gosling J., Arai H., Charo I.F.; "Organization and differential expression of the human monocyte chemoattractant procein I receptor gene. Evidence for the role of the carboxyl-terminal tail in receptor trafficking."; J. Siol. Chem. 272:1038-1045(1997).
                                                                                                                     Gaps.
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94195821; PubMed=8146186; Chanci C., Connolly A.J., Charci I.F., Myers S.J., Herman A., Franci C., Connolly A.J., Charci I.F., Myers S.J., Herman A., Franci C., Connolly A.J., Molecular cloning and functional expression of two monocyte chemoatractant protein I receptors reveals alternative splicing of the carboxyl-terminal tails.", Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756 (1994).
                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOO(3) (Rel. 42, Last annotation update)
C-C chemokine receptor type 2 (C-C CRR-2) (CC-CRR-2) (CCR2)
(Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ozuna M., Kuldanek S.A.,
                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,

Mnan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,

Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J.,

Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,

Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,

Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,

Watanabe M., Doggett N., Garcia D., Sagripanti J.L.,

Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                   N-LINKED (GLCNAC. . .) (POTENTIAL)
31EC48642CDB9AE5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-94324942; PubMed=8048929; Tamaka H., Endo N.;
Yamagami S., Tokuda Y., Ishii K., Tamaka H., Endo N.;
Yamagami S., Tokuda Y., Ishii K., Tamaka H., Endo N.;
CDNA cloning and functional propession of a human monocyte
chemoattractant protein 1 receptor.";
Biochem. Biophys. Res. Commun. 202:1156-1162(1994).
                                                                                            70.6%; Score 89; DB 1; Length 353; 63.6%; Pred. No. 4e-06;
                                                                                                                      3; Indels
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Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kulc
Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
  EXTRACELLULAR (POTENTIAL)
                7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                           374 AA.
                                           SIMILARITY.
                                                                                                          Pred. No. 4e-0
5; Mismatches
                                                                                                                                                                || || || || ::::|||:||||||
QWVFGTAMCKVVSGLYYIGFFS 117
                                                                                                                                                1 QWDFGNTMCQLLTGLYFIGFFS 22
                                                                    353 AA; 40045 MW;
                                                                                                           Local Similarity 63.6
nes 14; Conservative
                                                                                                                                                                                                                                           STANDARD;
     278
302
353
181
                                                                                                                                                                                                                                                                                                                                    CCR2 OR CMKBR2.
Homo sapiens (Human)
                                                                                                                                                                                                                                         CKR2_HUMAN
P41597;
                                         DISULFID
CARBOHYD
SEQUENCE
     DOMAIN
TRANSMEM
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                                                                                                                                                                                                                   RESULT 18
CKR2 HUMAN
                                                                                                                        Matches
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MIN; 601267; —.

R GO; GO:0005628; C:integral to plasma membrane; TAS.

R GO; GO:0005628; C:soluble fraction; TAS.

R GO; GO:0006529; C:soluble fraction; TAS.

R GO; GO:0006960; P:chemoxine receptor activity; TAS.

R GO; GO:0006960; P:chemoxine response (sensu Inver. . .; TAS.)

R GO; GO:0006918; P:chemocaxis; TAS.

R GO; GO:0006918; P:chemocaxis; TAS.

R GO; GO:0006918; P:chemocaxis; TAS.

R GO; GO:0007125; P:intlammatory response; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
Chakravarty L., Kolattukudy P.E.;
"Monocyte chemotactic protein-1 receptor CCR2B is a glycoprotein that
has tyrosine sulfation in a conserved extracellular N-terminal
                                                                                                                                                                            region.";

J. Immunol. 165:5295-5303(2000).

-!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.

-!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.

Transduces a signal by increasing the intracellular calcium ions

Transduces a signal by increasing the intracellular calcium.

Invel. Alternative correceptor with CD4 for HIV-1 infection.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS, PRO0237; GPCRRHODOPSN.
PROSITE; PS00237; GPROPEIN RECEP_F1_1; 1.
PROSITE; PS50262; GPROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- PTM: N-glycosylated.
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2 (POTENTIAL).
EXTRACELLUIGR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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DOMAIN
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=P41597-1; Seguence=Displayed;
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EMBL; U03805; AAA19120.1; --
EMBL; U03904; BAC6253.1; --
EMBL; U80924; AAC51637.1; --
EMBL; U80624; AAC51636.1; --
EMBL; U95626; AAB57791.1; --
EMBL; U95626; AAB57792.1; --
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EMBL; U95626; AAB57792.1; -.
EMBL; AF545480; AAN16400.1;
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PIR, JC2443, JC2443.
PDB, IKAD, 14-ANG-02.
PDB, IKPI, 23-JAN-02.
Genew, HGNC.1603, CCR2.
MIM, 601267, -
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us-10-084-813-12.rsp

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                           SLFHIALGGRIAPLOKPVCGGPGVRPGKNVKVTTQGLLDGR
GKGKSIGRAPEASLQDKEGA -> RYLSVFFRKHITKRFCK
QCPVFYRETVDGVTSTNTPSTGEQEVSAGL (in
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Bukaryota, Metaroa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus,
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                   16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR2 OR CMKBR2.

    macrophages.
    INDUCTION: In animals in which experimental allergic encephalomyelitis (EAE) has been induced.
    SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

 . .) (POTENTIAL)
                                                                                                                                                   ö
                                                                                                                              Query Match
69.0%; Score 87; DB 1; Length 374;
Best Local Similarity 66.7%; Pred. No. 8.4e-06;
Matches 14; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U77349; AAC03242.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm; 1.
PRINTS; PR00237; GPRTHODOPSN.
PROSITE; PS00237; GPROTEIN RECEP F1.1; 1.
G-protein coupled receptor; Transmembrane.
1 60 PROTENTIAL.
DOMAIN 1 60 POTENTIAL.
DOMAIN 82 91 CYTOPLASMIC (POTENTIAL).
                                                      isoform B).
/FIId=VSP_001893.
V -> I (in_dbSNP:1799864).
/FIId=VAR_014339.
                                                                                            G -> E. ______/FIIG=VAR_014340.
F865E0D39E74CF0F_CRC64;
(GLCNAC.
          SULFATION.
BY SIMILARITY.
                                                                                                                                                                              1 OWDFGNTMCOLLTGLYFIGFF 21
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-Sprague-Dawley;
MEDLINE-98318173; PubMed-9655467;
                                                                                                              374 AA; 41914 MW;
                                                                                                                                                                                                                                    STANDARD;
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 14
26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-SHIRGH-Dawley,
MEDLINE-98318173; PubMed=9655467;
MEDLINE-98318173; PubMed=9655467;
MEDLINE-98318173; PubMed=9655467;
MEDLINE-98318173; PubMed=9655467;
Defiebre C.M., Pennell N.N., Adhikari S., Xia Y., Feng L., Sonntag M.K., Defiebre C.M., Pennell N.N., Streat W.J., Harrison J.K.;
"Chemokine receptor expression in cultured glia and rat experimental allergic encephalomyslitis.";
"Chemokine receptor expression in cultured glia and rat experimental allergic enceptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-bera and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level.
-: SUBCELLULAR LOCATION: Integral membrane protein.
-: SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus,
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-WAY-2000 (Rel. 39, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (MIP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAINSWIGHERA: TISSUE=Brain;
MEDLINE=98334064; PubMed=9670989;
Spleise O., Gournala N., Boddeke H.W.G.M., Sauter A., Fiebich B.L.,
Berger M., Gebicke-Haerter P.J.;
"Cloning of rat HIV-1-chemokine coreceptor CKR5 from microglia and
upregulation of its mRNA in ischemic and endotoxinemic rat brain.";
J. Neurosci. Res. 53:16-28(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.3%; Score 86; DB 1; Length 373; 66.7%; Pred. No. 1.2e-05; ative 3; Mismatches 4; Indels
                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXTRACELLULAR (POTENTIAL)
                          EXTRACELLULAR (POTENTIAL)
                                                                                                                     POTENTIAL.
EXTRACELLULAR (POTENTIAL)
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                       2E7BB012F5D6FD09 CRC64;
                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                             POTENTIAL. CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :| ||| ||:| ||:| ||:| 118 EWVFGNIMCKLFTGLYHIGYF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QWDFGNTMCQLLTGLYFIGFF 21
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                                                                                                                                                                                                                                                                                                                                                                                                              42763 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Y12009; CAA72737.1; -. EMBL; U77350; AAC03243.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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es 14; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                           373 AA;
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alpha receptor)
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CE1A192CCAB999A3 CRC64;

31509 MW;

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Query Match
Best Local Similarity
269 AA;
                                                                                                                                                                                                                                          Suipoxvirus.
NCBI_TaxID=10277;
                                                                                                                                        VK02 SPVKA
Q08520;
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TRANSMEM
DOMAIN
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CARBOHYD
SEQUENCE
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Swinepox virus (strain Kasza) (SPV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Virology 197:511-528(1993).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Massung R.F., Jayarama V., Moyer R.W.;
"DNA sequence analysis of conserved and unique regions of swine;
virus: identification of genetic elements supporting phenotypic
observations including a novel G protein-coupled receptor
                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL) 77EDB368A4C868D CRC64;
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0
                                                                                                                                                                                                                                                                 66.7%; Score 84; DB 1; Length 354
 Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GFCRRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.

G-DOTCHEIN COUPLE TEASMGENDRAB; Glycoprotein.

DOMAIN

32 EXTRACELLULAR (POTENTIAL).
                                                                   1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                   CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
                                                                                                                                                             (POTENTIAL).
                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                           2.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
01-0CT-1995 (Rel. 23, Last annotation update)
G-protein coupled receptor homolog C3.
                                                                                                                                                                                                                                                                                                                                                                                         269 AA.
                                                                                                                                                                                                                                                                             Pred. No. 2.36
4; Mismatches
                                                                                                                                                                                                                        SIMILARITY
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PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane.
                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                   CYTOPLASMIC (: 6 (POTENTIAL)
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CYTOPLASMIC (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L22013; AAC37868.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                              1 OWDFGNIMCOLLTGLYFIGFF 21
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                                                                                                                                                                                                                                             41030 MW;
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                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                              354 AA;
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                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suipoxvirus.
NCBI_TaxID=10277;
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P32229;
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TRANSMEM
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TRANSMEM
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TRANSMEM
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DOMAIN
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                                                                                                                                                                    DOMAIN
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                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Virology 197:511-528(1993).
- FUNCTION: Putative chemokine receptor.
- SHOGELLULAR LOCATION: Integral membrane protein.
- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Swinepox virus (strain Kasza) (SPV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
76D08613277B0CC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE=94669924; PubMed=8249275; Massung R.F., Jayarama V., Moyer R.W.; massung R.F., Jayarama V., Moyer R.W.; inDNA sequence analysis of conserved and unique regions of swiner virus: identification of genetic elements supporting phenotypic observations including a novel G protein-coupled receptor
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                     Length 269
                     Score 83; DB 1; Length 269
Pred. No. 2.4e-05;
7; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00237; G PROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G_protein coupled receptor; Transmembrane; Glycoprotein.
DOWALN 1 61 EXTRACELLULAR (POTENTIAL).
TRANSMEM 63 94 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
G-protein coupled receptor homolog K2.
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InterPro; IPR000275; GPCR_Rhodpsn.
PF00001, 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                           OWDFGNTMCOLLTGLYFIGFFS 22
                                                                                                                                                                            20 QWIFGNILCKIMSVLYYVGFFS 41
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                              65.9%;
54.5%;
Query Match

Query Match

Best Local Similarity 54.55,

Best Local 12; Conservative
                                                                                                                                                                                                                                                                                                                                                STANDARD;
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370 AA;
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Matches

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RESULT 23

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MEDLINE=97351133; PubMed=9207005; Tiffany H.L., Lautens L.L., Gao J.-L., Pease J., Locati M., Combadiere C., Modi W., Bonner T.I., Murphy P.M.; "Identification of CR8: a human monocyte and thymus receptor for the CC chemokine I-309.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goya I., Gutierrez J., Varona R., Kremer L., Zaballos A., Marquez G., "Identification of CCR8 as the specific receptor for the human beta-chemokine I-309: Cloning and molecular characterization of murine CCR8 as the receptor for TCA-3.";
J. Immunol. 160:1975-1981(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=97040707; PubMed=8886020;
Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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A -> G (IN REF. 1).
V -> G (IN REF. 1).
FA012C10F4C9325A CRC64;
                                                                                                                                                    PRINTS; PRO0237; GPCRRHODOPSN.
PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.
PROSITE; PS0262; G_PROTEIN RECEP F1 2; 1.
G_PTCTein coupled receptor; Transmembrane.
DOMAIN 1 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
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01-0c7-1996 (Rel. 34, Last sequence update)
01-0c7-1936 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 8 (C-C CKR-8) (CR-CKR-8)
(GFRCY6) (Chemokine receptor-like 1) (CKR-L1) (TER1)
CCR8 OR CMXBR8 OR CKRL1.
            GO; GO:0006954; P:inflammatory response; IMP.
O; GO:0003334; P:regulation of cell migration; IMP.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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MEDLINE-98129363; PubMed=9469461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 OWDFGNTMCQLLTGLYFIGFF 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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TRANSMEM
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W. MEDLINE=97026720; PubMed=8872898;

W. MEDLINE=97026720; PubMed=8872898;

A. Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,

A. Post T.W., Gerard C., Dorf M.E.,

R. Tanscriptase-polymerase chain reaction does not detect mRNA for the

RT transcriptase-polymerase chain reaction does not detect mRNA for the

RT transcriptase-polymerase chain reaction does not detect mRNA for the

RT or new MCP-1 receptor.";

R. J. Neurosci. Res. 45:382-391(1996).

C. -- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5

C. Calcium ions level.

C. -- SUBCELLUIAR LOCATION: Integral membrane protein.

C. -- SUBCELLUIAR LOCATION: Integral membrane protein.

C. -- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,

C. -- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,

C. -- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=96205938; PubMed=8631787;
Bering L., Gosling J., Monteclaro F.S., Lusis A.J., Tsou C.-L.,
Charo I.F.;
"Molecular cloning and functional expression of murine JE (monocyte
chemoatractant protein 1) and murine macrophage inflammatory protein
lalpha receptors: evidence for two closely linked C-C chemokine
receptors on chromosome 9.";
J. Blol. Chem. 271:7551-7558(1996).
            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) MCS:106185; CCr2.
GO:0016493; F:C-C chemokine receptor activity; IDA.
GO:0019955; F:Cytckine binding; IPI.
GO:0019065; F:cytckine defense response (sensu Vertebrata); IMP.
GO:0030097; P:hemopoiesis; IMP.
GO:0006959; P:humoral immune response; IMP.
                                                                                                                                                                                                                                                                                                                                                                    P51683, Q61172, DANIELLO, PALI, 373 AR., P51683, Q61172, DANIELLO, DANIELLO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kurihara T., Bravo R.;
Cloning and functional expression of mCCR2, a murine receptor for
the C-C chemokines JB and FIC.";
J. Biol. Chem. 271:11603-11606(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
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            Indels
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B
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    Mismatches
                                                                                                                        121 QWIFGNILCKIMSVLYYVGFFS 142
                                                                        1 OWDFGNIMCQLLTGLYFIGFFS 22
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MEDLINE=96216064; PubMed=8662823;
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EMBL; U51717; AAC52557.1; -.
EMBL; U56819; AAC52784.1; -.
    Conservative
                                                                                                                                                                                                                                                                                                                                            STANDARD;
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12;
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Gaps

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Length 373;

(GPR-CY6)

(CCR-8) (GPR-C (CMKBRL2) (CC-

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CKR8 MACMU
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TRANSMEM
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CKR8 MACMU
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GO; GO:0004950; F:chemokine receptor activity; TAS.
GO; GO:0004950; F:chemokine receptor activity; TAS.
GO; GO:00155; P:cell adhesion; TAS.
GO; GO:0007155; P:cell adhesion; TAS.
GO; GO:0006935; P:chemotaxis; TAS.
GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.
InterPro; IPR004068; CG & receptor.
InterPro; IPR004068; CG & receptor.
InterPro; IPR000276; GPGR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification of the CC chemokines TARC and macrophage inflammatory protein-1 beta as novel functional ligands for the CCR8 receptor.";

Eur. J. Immunol. 28:582-588(1998).

-!- FUNCTION. Receptor for the chemokines SCYA1/I-309, SCYA4/MIP-1-beta and SCYA1/TARC. May regulate monocyte chemotaxis and thymic cell line apoptosis. Alternative coreceptor with CD4 for HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                          SEQUENCE FROM N.A.
MEDLINE=97131825; PubMed=8977299;
MEDLINE=97131825; PubMed=8977299;
Samson M., Stordeur P., Labbe O., Soularue P., Vassart G.,
Pamson M., Stordeur T., Thompoore M., "Molecular cloning and chromosomal mapping of a novel human gene,
"Molecular cloning and chromosomal mapping of a novel human gene,
"Molecular cloning and chromosomal mapping of a novel human gene,
"Molecular cloning and chromosomal mapping of a novel human gene,
"Molecular cloning and chromosomal mapping of a novel human gene,
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"Molecular cloning and chromosomal mapping of a novel human gene,"
"Molecular cloning and chromosomal mapping of a novel human gene,"
"Molecular
      "Molecular cloning and RNA expression of two new human chemokine
                                                                                                                                                                                                                                                                                                                                                                                   Bernardini G., Hedrick J., Sozzani S., Luini W., Spinetti G., Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A., Napolitano M.;
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Pfam; PF00001; 7rm 1; 1.

PRINTS; PR01530; CFEMOKINER8.

PRINTS; PR01537; GPERHENDOPSN.

PROSITE; PS00237; GPRTENDOPSN.

PROSITE; PS00237; GPROTEIN RECEP F1_1; 1.

PROSITE; PS00262; GPROTEIN RECEP F1_1; 1.

PROSITE; PS00262; GPROTEIN RECEP F1_1; 1.

PROSITE; PS00262; GPROTEIN RECEP F1_2; 1.

PROSITE; PS00262; GPROTEIN RECEP F1_2; 1.

PROSITE; PS00262; GPROTEIN RECEP F1_2; 1.

PROSITE: 1 (POTENTIAL).
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Nakajima T., Yoshida R., Harada S.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
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2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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                             receptor-like genes.";
Biochem. Biophys. Res. Commun. 227:846-853(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
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TRANSMEM
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-!- FUNCTION: Receptor for the chemokines SCYA1/I-309, SCYA4/MIP-1-beta and SCYA1/TARC. May regulate monocyte chemotaxis and thymic call line apoptosis (By similarity).
-!- SUBCELLUIAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae, Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Spleen; MEDLINE=21354176; PubMed=11461684; MEDLINE=21354176; PubMed=11461684; Margulies B.J., Hauer D.A., Clements J.E.; Margulies B.J., Hauer D.A., Clements J.E.; "Identification and comparison of eleven rhesus macaque chemokine
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R PEAN, PROGOL, TEM. 1, 1.

R PAINTS; PRO1330; CHEMOKINER8.

DR PRINTS; PRO1337; GPCRHODOPSN.

DR PROSITE; PSO1237; GPROTEIN RECEP.FI. 1; 1.

DR PROSITE; PSO1237; GPROTEIN RECEP.FI. 2; 1.

DR PROSITE; PSO1237; GPROTEIN RECEP.FI. 2; 1.

FT PRANSMEM 36 63 1. (POTENTIAL).

FT TRANSMEM 36 63 1. (POTENTIAL).

FT TRANSMEM 74 93 2 (POTENTIAL).

FT TRANSMEM 74 93 2 (POTENTIAL).

FT TRANSMEM 19 107 EXTRACELULAR (POTENTIAL).

FT TRANSMEM 19 107 EXTRACELULAR (POTENTIAL).

FT TRANSMEM 19 4 107 EXTRACELULAR (POTENTIAL).

FT TRANSMEM 19 107 EXTRACELULAR (POTENTIAL).

FT TRANSMEM 19 172 4 (POTENTIAL).
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
2-C chemokine receptor type 8 (C-C CKR-8) (CC-CKR-8)
                                                                                                                                                                                                                                                                                                 Length 355;
                                                                                                            EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                             Y SIMILARITY.
BC14A153CF695361 CRC64;
                                                                                                                                                                    (POTENTIAL).
                                                       CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                       Score 82; DB 1; I
Pred. No. 4.5e-05;
6; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       356 AA.
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InterPro; IPR004068; CC 8 receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 QWVFGTVMCKVVSGFYYIGFYS 119
                                                                                                                                                                                                                                                                                                                                                                                                                1 OWDEGNIMCOLLIGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                                            40844 MW;
                                                                                                                                                                                                                                                                                             Match 65.1%;
Local Similarity 54.5%;
les 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
      172
203
223
223
264
281
305
106
355 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptors.";
AIDS Res. Hum. Retroviruses 17:981-986(2001).
-!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
Transduces a signal by increasing the intracellular calcium ions
                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003. (Rel. 41, Last annotation update)
C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR2)
(Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF013958; AAD11572.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF0001; 7tm 1; 1.
PR00137; GPCRRHODDPSN.
PROSITE; PS00237; GPRRHODPSN.
PROSITE; PS00262; GPROTEIN RECEP F1 1; 1.
PROSITE; PS50262; GPROTEIN TRECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=A;
IsoId=018793-2; Sequence=Not described;
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=21354176; PubMed=11461684;
Margulies B.J., Hauer D.A., Clements J.E.;
"Identification and comparison of eleven rhesus macaque chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                         .;
0
                                                                                                                                            Length 356;
S (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                         4; Indels
                                                                                                           1979628DEE44845B CRC64;
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                       Score 82; DB 1; I
Pred. No. 4.6e-05;
5; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=018793-1; Sequence=Displayed;
                                                                                                                                                                                                                     98 QWVFGTVMCKVVSGFYYIGFYS 119
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                                                                                                           41210 MW;
                                                                                                                                       Match 65.1%;
Local Similarity 54.5%;
es 12; Conservative 6
                                                                                                                                                                                                                                                                                                            STANDARD;
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   204
224
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282
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018793;
TRANSMEM
DOMAIN
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"Molecular cloning and functional expression of murine JB (monocyte chemoattractant protein 1) and murine macrophage inflammatory protein lalpha receptors: evidence for two closely linked C-C chemokine receptors on chromosome 9.1;
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                  CKRS MOUSE STANDARD; PRT, 354 AA.
PS1662; 035313; 035891; P97308; P97405; Q61867;
01-0CT-1996 (Rel. 34, Created)
15-UTU-1998 (Rel. 36, Last sequence update)
10-0CT-2003 (Rel. 42, Last sequence update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (MIP-1 CCRS OR CMKRRS.
                                                     S (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
SULFATION (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCEI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6, and NIH Swiss; TISSUE=Kidney, Liver, and Spleen; MEDLINE=98001387; PubMed=934222; Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.; "Polymorphisms in the CGR5 genes of African green monkeys and mice implicate specific amino acids in infections by simian and human
                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C57BL/6 X CBA; TISSUB=Thymus;
MEDLINE=96278910; Pubmed=8662890; Meyer A., Coyle A.J., Proudfoot A.B.I., Wells T.N.C., Power Cloning and characterization of a novel murine macrophage
                                                                                                                                                                                                         Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.,
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                            4 (POTENTIAL). EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                            4B2552BCE913FE9F CRC64;
               (POTENTIAL)
                                                                                                                                                                                                    Score 81; DB 1; L
Pred. No. 6.5e-05;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammatory protein-1 alpha receptor."; J. Biol. Chem. 271:14445-14451(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptors on chromosome 9.";
J. Biol. Chem. 271:7551-7558(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-129/SvJ; TISSUE-Spleen;
MEDLINE-96205938; PubMed-8631787;
                                                                                                                                                                                                                                                                         1 OWDFGNTMCQLLTGLYFIGF 20
                                                                                                                                                                             41139 MW;
                                                                                                                                                                                                                   65.0%;
                                                                                                                                                                                                      64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nunodeficiency viruses.";
Virol. 71:8642-8656(1997)
                                                                                                                                                                                                                                13; Conservative
  1136
1133
1133
1130
114
1156
114
1156
                                                                                                                                                                            360 AA;
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DOMAIN
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CKR3 CAVPO
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                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                            PRINTS; PR0001; 7tm 1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS00262; GPROTEIN TRANSMEMDZABA; Glycoprotein; Polymorphism.

G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
                                                          MEDLINE-97404635; PubMed-9261347;
Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H.,
Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.;
"Two distinct CCR5 domains can mediate coreceptor usage by human
immunodeficiency virus type 1.";
J. Virol. 71:6305-6314 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                               4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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(IN REF. 2).
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                                                                                                                                                                                    EMBL, U47036, AACS2454.1; -.
EMBL, S4151; CAA63867.1; -.
EMBL, U68565, AAB37273.1; -.
EMBL, U83327; AACS3386.1; -.
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1126
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                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i. FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin, MCP-3, MCP-4 and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level (By similarity).
-i. SUBCELLULAR LOCATION: Integral membrane protein.
-i. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-9904984699; MEDLINE-99049845; PubMed-9934999; Grand N.P., Li Y., Collins P.D., Post T.W., Jose P.J., Williams T.J., Gerard N.P., Li Ponath P.D.; "Cloning and characterization of the guinea pig ecsinophil ectaxin "Cloning and characterization of the guinea pig ecsinophil antibody in vivo."; Leceptor. 3: blockade using a monoclonal antibody in vivo."; Jimmunol. 161:6139-6147(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                        CKR3 CAVPO STANDARD; PRT; 358 AA.
092213;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cavia porcellus (Guinea pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Cavidae, Cavia.
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RIBL, AF060698; AAC80428.1; -...

RIGEATIO: IPRO0024; GFCR. Rhodpsn.

R PRINTS; PR00237; GFCREHODOPSN.

R PRINTS; PR00237; GFCREHODOPSN.

R PROSITE; PS00237; GFOTEIN RECEP_F1_1; 1.

DR PROSITE; PS50252; G PROTEIN RECEP_F1_2; 1.

KW G-Drotein coupled receptor; Transmembrane.

NAM G-DROTEIN RECEP_F1_2; 1.

A3 EXTRACELLULAR (POTENTIAL).

FAM G-DROTEINIAL).
                                                                                                                                 63.5%; Score 80; DB 1; Length 354; 57.1%; Pred. No. 9.1e-05;
145 N -> I (IN REF. 5).
190 H -> Y (IN REF. 3).
208 P -> S (IN REF. 1).
40863 MM; B4A6B942E88F9CF0 CRC64;
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                                                                                                                                                                                         12; Conservative
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     145
190
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354 AA;
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RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Ehate N.K.,

RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Ehate N.K.,

RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Ehate N.K.,

RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Ehat N.K.,

RA Stapleton M., Soaces M.B., Bonaldo M.F., Canavant T.L., Scheetz T.E.,

RA Bosak S.A., McGwan P.U., McKernan K.J., Malek J.A., Gunlany S.J.,

RA Bosak S.A., McMany D.M., Sodergren E.J., Lu X., Gabbs R.A.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Yillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodriques S., Sanchez A.C., Garimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RT "Generation and initial analysis of more than 15,000 full-length

RANTES, AND LESS EFFICIBNILY TO MIP-1-BETA OR MCP-1 AND

SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR

C. PLOTTER PARTION RESEPONSIBLE FOR AFFECTING STEM CELL
                                                                                                                                                                                     CKR1_MOUSE STANDARD; PRT; 355 AA.
P51675; Q91VP9;
01-0CT-1996 (Rel. 34, Created)
01-0CT-21996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
C-C chemokine receptor type 1 (C-C CKR-1) (CC-CKR-1) (CCMacrophage inflammatory protein-1 alpha receptor) (MIP-1alpha-R)
(RANTES-R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gao J.-L., Murphy P.M.,
"Cloning and differential tissue-specific expression of three mouse
beta chemokine receptor-like genes, including the gene for a
functional macrophage inflammatory protein-1 alpha receptor.";
J. Biol. Chem. 270:17494-17501(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecular characterization of two murine eosinophil beta chemokine
                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia, Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=129/6v, TISSUE=Peritoneal macrophage;
MEDLINE=96072806; PubMed=7594543;
Post T.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
Gerard C.;
                                                            ;
0
                                Length 358;
                                   0.00013;
... 3; Indels
358 AA; 41623 MW; 7B73FAB7A3BC3670 CRC64;
                                                          8; Mismatches
                           62.7%; Score 79; 50.0%; Pred. No.
                                                                                                       102 KWVFGHFMCKIISGLYYVGLFS 123
                                                                                   1 OWDFGNTMCOLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=129/SvJ;
MEDLINE=9534054; PubMed=7542241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptors.";
J. Immunol. 155:5299-5305(1995).
                Query Match
Best Local Similarity 50.09
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SEQUENCE
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CKR1_MOUSE
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Bukaryota, Metazoa; Chordata; Cramiata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxiD=10116;
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-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Detected in the heart, spleen, lung, peritoneal exudate cells and leukceytes.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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054814; 055169;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)
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R EMBL; U28644; AAA89153.1; -

R EMBL; U28404; AAA89153.1; -

R EMSL; BAJ339; I49339.

R PIR; I49339; I49339.

R GO; GO: 0005515; P: protein binding; IPI.

GO; GO: 0005515; P: protein binding; IPI.

GO; GO: 0005515; P: protein binding; IPI.

R GO; GO: 0005954; P: inflammatcry response; IMP.

GO; GO: 0003099; P: inflammatcry response; IMP.

R GO; GO: 0001099; P: inflammatcry response; IMP.

R GO; GO: 0001009; P: inflammatcry response; IMP.

R FRINTS; PS00237; GFRHODOPSN.

R PROSITE; PS00237; GPROTEIN RECEP F1 1; I.

R PROSITE; PS00237; G PROTEIN RECEP F1 1; I.

R G-protein coupled receptor; EXTRACELLULAR (POTENTIAL).

TRANSWEM 35 60 1 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

EXTRACELLUIAR (POTENTIAL).

3 (POTENTIAL).

4 (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLUIAR (POTENTIAL).

6 (POTENTIAL).

EXTRACELLUIAR (POTENTIAL).

7 (POTENTIAL).

EXTRACELLUIAR (POTENTIAL).

6 (POTENTIAL).

EXTRACELLUIAR (POTENTIAL).

TO (POTENTIAL).

SY (POTENTIAL).

A > V (IN REF. 2 AND 3).

I - > V (IN REF. 2 AND 3).

I - > V (IN REF. 3).
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Best Local Similarity
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AC 0548

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                                                              Jiang Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K., Defiebre C.M., Pennell N.A., Streit W.J., Harrison J.K.; "Chemokine receptor expression in cultured glia and rat experimental
                                                                                                                                                                SEQUENCE FROM N.A.
STRATSWISTERAT; TISSUB-Spleen;
STRATNSWISTERAT; TISSUB-Spleen;
STRATNSWISTERAT; TISSUB-Spleen;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to ectaxin,
MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level (By similarity)
-!- SUBCELIULAR LOCATION: Integral membrane protein.
-!- TISSUB SPECIFICITY: Expressed in spleen but not in astrocytes or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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01-00T-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor 1-like protein 1 (Macrophage inflammatory
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41643 MW; 880F682984F501DA CRC64;
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45.5%; Pred. No. 0.00052;
            SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
STRAIN=Wistar; TISSUE-Spleen;
MEDLINE-98318173; PubMed=9655467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 356 AA.
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EMBL; Y13400; CAA73830.1; --
INTECPEO; IPR000276; GPCR_Rhodpsn.
PEAM; PF00001; 7tm 1; 1.
PRINYS; PR00237; GPCREHODPSN.
PROSTITS; PS00237; GPCREHODPSN.
PROSTITS; PS00237; GPCREHOLPSN.
GPROTEIN RECEP_F1 1; 1.
G-protein coupled receptor; Transmembrane.
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102 EWGFGHCMCKMLSGLYYLALYS 123
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                                                                                                              allergic encephalomyelitis.";
J. Neuroimmunol. 86:1-12(1998).
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Best Local Similarity 45.5
Matches 10, Conservative
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359 AA;
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P51676;
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                                                                                                                                                                  Gao J.-L., Murphy P.M.;
"Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.";
J. Biol. Chem. 270:17494-17501(1995).
-!- FUNCTION: Probable receptor for a C-C type chemokine.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Detected in the spleen, liver and leukocytes.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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01-0CT-1993 (Rel. 27, Last sequence update)
01-SMAR-2004 (Rel. 43, Last annotation update)
C-C chemokine receptor type 1 (C-C CKR-1) (CC-CKR-1) (CCR-1) (MP-1alpha-R)
(Macrophage inflammatory protein-1 alpha receptor) (MIP-lalpha-R)
                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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PROSITE; PS00237; G-PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G-PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Transmembrane.
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PIR; 149340; 149340.
MGD; MGT:104617; CCT111.
INTEXPLO; IPRO00276; GPCR_Rhodpsn.
Pfam; PP00001; 7tm_1; 1.
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                                                                                                                                     STRAIN=129/SvJ;
MEDLINE=95340546; PubMed=7542241;
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protein-1 alpha receptor-like 1).
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                                 Mus musculus (Mouse).
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                                                                                                                  SEQUENCE FROM N.A.
                                                                                 NCBI_TaxID=10090;
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ID CKR1_HUMAN
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P56482;
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CARBOHYD
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CKR1 MACMU
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W. MEDLINE=94095629; PubMed=7505609;

W. MEDLINE=94095629; PubMed=7505609;

W. MEDLINE=94095629; PubMed=7505609;

W. Molecular Cloning of CDNAs encoding a LD78 receptor and putative

T "Molecular cloning of CDNAs encoding a LD78 receptor and putative

T "Molecular cloning of CDNAs encoding a LD78 receptor and putative

W. Molecular CDNAs encoding a LD78 receptor and putative

T I = the North CONTRON Receptor for a CC type chemokine. Binds to MIP-1-alpha,

T I = the North CONTRON Receptor for a CC type chemokine. Binds to MIP-1-alpha,

MIP-1 delta, RANTES, and MCP-3 and, less efficiently, to MIP-1-

Deta or, MCP-1 and subsequently transduces a signal by increasing

the intracellular calcium ions level. Responsible for affecting

CC -1- SUBCELULAR LOCATION: Integral membrane protein.

CC -1- TISCE ESPECIFICITY: Widely expressed in different hematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL; L10918; AAA36543.1; --
EMBL; D10925; BAA01723.1; --
PIR; A45177; A45177
Genew; HGNC:1602; CCR1.
                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=92240122; PubMed=7683036;

MEDLINE=9240122; PubMed=7683036;

Murphy P.M.;

Murphy P.M.;

"Structure and functional expression of the human macrophage inflammatory protein 1 alpha/RANTES receptor.";

J. Exp. Med. 177:1421-1427(1993).
                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                        SEQUENCE FROM N.A.
MEDLINE=93161416; PubMed=7679328;
Neote K., Digregorio D., Mak J.Y., Horuk R., Schall T.J.;
Molecular cloning, functional expression, and signaling
characteristics of a C-C chemokine receptor.";
Cell 72:415-425(1993).
(RANTES-R) (HM145) (LD78 receptor) CCR1 OR CMKER1.
                      Homo sapiens (Human)
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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AIDS Res. Hum. Retroviruses 17:981-986(2001).

-! FUNCTION: RECEPTOR FOR A C-C TYDE CERMOKINE. BINDS TO MIP-1-ALPHA,
-! FUNCTION: RECEPTOR FOR STORING TO MIP-1-BETA OR MCP-1 AND
SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING STEM CELL
PROLIFERATION.
-! SUBCELLULAR LOCATION: Integral membrane protein.
-! SUMICARITY: Belongs to family 1 of G-protein coupled receptors.
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15-UUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemckine receptor type 1 (C-C CKR-1) (CCR-1) (CCR1).
CCR1 OR CMKBR1.
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                                                                                                                       4 (POTENTIAL).

EXTRACELULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
7 (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
BY SIMILARITY.
E -> D (IN REF. 3).
E -> D (IN REF. 3).
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SEQUENCE FROM N.A.
SEQUENCE=21354176; PubMed=11461684;
Margulies B.J., Hauer D.A., Clements J.E.;
"Identification and comparison of eleven rhesus macaque chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Macaca mulatta (Rhesus macaque).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
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InterPro; IPR00021; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PR0121; PS00237; GPCRRHODDPSN.
PROSITE; PS00237; GPROTEIN RECEP_F1 1; 1.
PROSITE; PS00237; GPROTEIN RECEP_F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
TRANSMEM 35 60 1 (POTENTIAL).
DOMAIN 61 64 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.3%; Score 71; DB 1; Length 355; 47.6%; Pred. No. 0.0021; ive 6; Mismatches 5; Indels
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 WVFGDAMCKILSGFYYTGLYS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41172 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 47.6
Matches 10; Conservative
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EMBL; U29677; AAA86118.1; -. EMBL; U28406; AAA89155.1; -. MGD; MGI:104616; Ccr3.
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01-OCT-1996 (Rel. 34, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Probable C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3)
Probable 3) (MCR3) (MR3) (Macrophage inflammatory protein-1 alpha receptor-like 2) (MIP-1 alpha RL2).
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDITRE 5540546; PubMed=7542241;

Gao J.-L., Murphy P.M.;

Gao J.-L., Murphy P.M.;

"Cloning and differential tissue-specific expression of three mouse "Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.";

J. Biol., Chem. 270:17494-1750[1995].

-I. FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin, MCP-3, MCP-4 and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level.

-I. SUBCELLULAR LOCATION: Integral membrane protein.

-I. TISSUE SPECIFICITY: Detected in skeletal muscle and in trace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular characterization of two murine eosinophil beta chemokine
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                        Length 355;
                                                                                                                                                                                                                                                                                          Score 71; DB 1; Length 355
Pred. No. 0.0021;
5; Indels
                                                                      EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
                                                                                                                                                    6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                BY SIMILARITY.
41CAEA7CC19D23D4 CRC64;
                    EXTRACELLULAR (POTENTIAL)
                                        3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                            (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunol. 155:5299-5305(1995).
                                                                                                                                                                                                                                                                    41198 MW;
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 47.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCR3 OR CMKBR3 OR CMKBR1L2.
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  91
1129
1146
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106
355 AA;
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P51678;
  TRANSMEM
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DOMAIN
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TRANSMEM
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SEQUENCE
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MEDLINE=95348056; PubMed=7622448;
Combadiere C., Ahuja S.K., Murphy P.M.;
"Cloning and functional expression of a human eosinophil CC chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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CKR3 HUMAN STANDARD; Q9ULV8;

P51677; Q15748; Q86WD2; Q9ULV8;

01-OCT-1996 (Rel. 34, Last sequence update)

15-MAR-2004 (Rel. 43, Last annotation update)

C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3)

(CKR3) (EOSINOPhil ectaxin receptor).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
GO; GO:0016493; F:C-C chemokine receptor activity; IDA. GO; GO:0005515; F:protein binding; IPI. GO; GO:0006935; P:chemotaxis; IDA. InterPro; IPR000276; GPCR_Rhodpsn.
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AC11ED66E283CEAF CRC64;
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CYTOPLASMIC (POTENTIAL).
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Pred. No. 0.003;
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                                                                                                        PEAM, PRO0001; 7tm 1; 1.
PRINTS; PR00037; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP_F1 1; 1.
PROSITE; PS50252; G PROTEIN RECEP_F1 2; 1.
G-protein coupled receptor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. Chem. 270:16491-16494(1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41825 MW;
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Local Similarity 40.9%;
les 9; Conservative
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276 S
41043 MW;
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Local Similarity 52.4%;
les 11; Conservative
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355 AA;
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018983;
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REAL SEQUENCE FROM N.A.

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REAL SEQUENCE FROM N.A.

REAL SETABLE SEAS SEAST; Pubmed=1247932;

REAL SETABLE SEAS SEAST; Pubmed=1247932;

REAL SETABLE R.D., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang L.,

RA Bornstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Parage C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gab L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gab L.J., Hulyk S.W.,

RA Nilalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,

RA Pabey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Mitting M., Madan A., Youchman J.W., Green E.J., Dickson M.C.,

RA Schriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Schriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Schriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Schriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R. Proc. Natl. Acad. Sci. U.S.A., 99:1689-16903 (2002).

- I- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,

c. - FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,

c. - FUNCTION: Receptor for a C-C type chemokine. Sinds to eotaxin,

c. - FUNCTION: Receptor for a C-C type chemokine.

R. Proc. Natl. Acad. Sci. U.S.A., 99:1689-16903 (2002).

- - FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,

c. - FUNCTION: Receptor for a C-C type chemokine.

C. - FUNCTION: Receptor for a C-C type chemokine.

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- - FUNCTION: Receptor for a C-C type chemokine.

- - - FUNCTION: Receptor for a C-C type chemokine.

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                                                        MEDLINE=9621895; PubMed=8676064;
Ponath P.D., Qin S., Post T.W., Wang J., Wu L., Gerard N.P.,
Newman W., Gerard C., Mackay C.R.;
Nolecular cloning and characterization of a human ectaxin receptor
expressed selectively on eosinophils.";
J. Exp. Med. 183:2737-2748(1996).

SEQUENCE FROM N.A.
Xiao L., Weiss S., Qari S., Rudolph D., Hodge T., Lal R.;
"Partial resistance to infection by syncytium-inducing primary HIV-1
in exposed uninfected individuals homozygous for CCR5 32bp deletion.";
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                        H.
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-22074933; PubMed=12079287;
Wijh S., Dayhoff D.E., Wang C.E., Imam Z., Ehrenberg P.K.,
Michael N.L.;
"Transcription regulation of human chemokine receptor CCR3: evidence
for a rare TATA-less promoter structure conserved between Drosophila
and humans.";
                                                                                                                                                                                                                                                  [6] SEQUENCE FROM N.A., AND VARIANT SER-218.
MEDLINE=21040311; PubMed=1119669;
KARO H., TSUGHIYA N., Izumi S., Miyamasu M., Nakajima T., Kawasaki Hirai K., Tokunaga K.;
"New variations of human CC-chemokine receptors CCR3 and CCR4.";
Genes Immun. 1:97-104(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kopatz S.A., Aronstam R.S., Sharma S.V.; arons clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdma.org)."; Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
eotaxin receptor.";
J. Exp. Med. 183:2349-2354(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomics 80:86-95(2002).
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SEQUENCE FROM N.A.
                                              SEQUENCE FROM N.A.
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EWEL; U28694; AACSO469-1; -

REMEL; U49277; AAB0726-1; -

REMEL; U49277; AAB0726-1; -

REMEL; U49277; AAB0726-1; -

REMEL; AF02635; AAB65964-1; -

REMEL; AF021092; AAC65970-2; -

REMEL; AF271092; AAC65970-2; -

REMEL; AF1000456; GO2436; GO2436; GO2436; GO2406; GO3600004950; F:chemokine receptor activity; TAS.

RO; GO:00004950; F:chemokine receptor activity; TAS.

RO; GO:00004950; F:chemokine response; TAS.

RO; GO:0000535; P:chemotaxis; TAS.

RO; GO:0000535; P:chemotaxis; TAS.

RO; GO:0000535; P:inflammatory response; TAS.

RO; GO:0000555; P:inflammatory response; TAS.

RO; GO:0000125; P:inflammatory response; TAS.

RO; GO:000125; P:inflammatory response; TAS.

RO; GO:0000125; P:inflammatory response; TAS.

RO; GO:0000125; P:inflammatory response; TAS.

RO; GO:00001707: F:inflammatory response; TAS.

RO; GO:00001707: F:inflammatory response; TAS.
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C -> S (polymorphism found in about 7%
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Pred. No. 0.0083;
4; Mismatches 6; Indels
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
7 (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
7 (POTENTIAL).
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S -> T (IN REF. 4 AND 5).
E95DCD7A6C643874 CRC64;
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15-JTL-1998 (Rel. 36, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
C-X-C chemokine receptor type 6 (CXC-R6) (CXR-6)
receptor bonzo).
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CCR6 CERAB
TO CCR6 CE
DT 15-UUL
DT 15-UUL
DT 15-UUL
DE C-C CE
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14.7 - A

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              CBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                      chemokine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CKR4 HUMAN STANDARD; PRT; 360 AA.
PST579; OSULY6; OSULY7;
01-OCT-1996 (Rel. 34, Last sequence update)
01-AR-2004 (Rel. 34, Last annotation update)
C-C chemokine receptor type 4 (C-C CKR-4) (CCR-4) (CCR4)
(K5-5).
                                                                                                                                           -!-FUNCTION: Receptor for the C-X-C chemokine CXCL16. Used as a coreceptor by SIVs and by strains of HIV-2 and m-tropic HIV-1.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCR4 OR CMKBR4.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Cercopithecus aethiops (Green monkey) (Grivet).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae;
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                                                                                SEQUENCE FROM N.A.
MEDLINE=97373958; PubMed=9230441;
Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.;
Expression cloning of new receptors used by simian and human "Expression cloning of new receptors used by simian and human nature 388:296-300(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 66; DB 1; Length 342;
                                                                                                                                                                                                                                                                             EMBL; AF007859; AAB64255.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PF00237; GPCRHODDSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1 1; 1.
PROSITE; PS00267; G_PROTEIN_RECEP_F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Indels
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                  Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39226 MW;
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Best Local Similarity 45.5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16
342 AA;
                                                             NCBI_TaxID=9534;
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DOMAIN
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HUMAN
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PUNCION, TISSUE SPECIFICITY, AND PHOSPHORYLATION.

RA MEDLINE-20219238; PubMed=10754227;
RA Inngjerdingen M. Damaj B., Maghazachi A.A.;
Inngman NK cells express CC chemokine macrophage-derived

RT chemokine, and 1-399.";
Unmunol 164:408-4054(2000)

J. Immunol 164:408-4054(2000)

J. Immunol 164:408-4054(2000)

J. Immunol 164:408-4054(2000)

J. Immunol 164:408-4054(2000)

Mediated by G(I) protectins which activate a phosphatidylinositcle calcium second messenger system. Can function as a chemokine colored primary HIV-2 isolates. In the CNS, could mediate hippocampal-neuron survival.

Mediate hippocampal-neuron survival.

J. SUBCELULAR LOCATION: Integral membrane protein.

J. SUBCELULAR LOCATION: Integral membrane protein.

J. SUBCELULAR LOCATION: Integral membrane protein.

J. TISSUE SPECIFICITY: Predominantly expressed in the the spleen and basophils, and in platelets; at lower levels, in the spleen and basophils, and in platelets; at lower levels, in the spleen and basophils, and in platelets; at lower levels, in the spleen cand in monocytes. Detected also in macrophages, IL-2-activated natural killer cells and skin-homing memory T cells, mostly the ones expressing the cutaneous lymphocyte antigen (CLA). Expressed in brain microravacular and coronary artery endothelial cells.

J. PHOSPHORYLAIDEN CRECEPTOR KINASES I AND 2.

BY BETA ADRENBERGIC RECEPTOR KINASES I AND 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98104168; PubMed=9430724; Inai T., Chantry D., Raport C.J., Wood C.L., Nishimura M., Godiska R., Yoshie O., Gray P.W.; P.W.; Macrophage-derived chemokine is a functional ligand for the CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-21040311; PubMed-11196669; KabLine-21040311; PubMed-11196669; Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H., Hirai K., Tokunaga K.; Indunaga K.; Indunaga K.; Indunasa K.; Indunasa K.; Indunasa K.; Indunasa C. Chemokine receptors CCR3 and CCR4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION.
MEDINE-99194604; PubMed=10466728;
MEDINE-99194604; PubMed=10466728;
Andrew D.P., Warnke R., Ruffing N., Kassam N., Wu L., Butcher E.C.;
The chemckine receptor CCR4 in vascular recognition by cutaneous but
not intestinal memory T cells.";
Nature 400:776-780(1999).
                                                           MEDLINE-953707

MEDLINE-95370289; PubMed=7642634;

POWER C.A., Meyer A., Nemeth K., Bacon K.B., Hoogewerf A.J.,

Proudfoot A.E.I., Wells T.N.C.;

"Mollecular cloning and functional expression of a novel CC chemokine

"receptor cDNA from a human basophilic cell line.";

J. Biol. Chem. 270:19495-19500(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDDINE-97313486; PubMed-9169480; Imai T., Baba M., Nishimura M., Kakizaki M., Takagi S., Yoshie O.; Imai T., Baba M., Nishimura M., Kakizaki M., Takagi S., Yoshie O.; Time T cell-directed CC chemokine TRRC is a highly specific biological ligand for CC chemokine receptor 4."; J. Biol. Chem. 272:15036-15042(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kopatz S.A., Aronstam R.S., Sharma S.V.; "Copatz S.A., Aronstan B.S., Sharma proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org)."; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND VARIANTS VAL-130 AND SER-178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            emokine_receptor 4.";
Biol. Chem. 273:1764-1768(1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
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                                                                                                                                                                                         EMBL; X85740; CAA59743.1; ---
DR EMBL; AB023889; BAA86965.1; --
DR EMBL; AB023890; BAA86965.1; --
DR EMBL; AB023890; BAA86966.1; ---
DR EMBL; AB023890; BAA86966.1; --
DR EMBL; AB023891; BAA86969.1; --
DR EMBL; AS023891; BAA86969.1; --
DR EMBL; AS7160; A57160;
DR Genew; HAGNC:1605; CCR4.

MIM, 604836; --
DR GO: GO:0008987; C:chemotxine receptor activity; TAS.

GO; GO:0008987; C:chemotxine response; TAS.

GO; GO:0009987; P:chemotxine response; TAS.

GO; GO:0009987; P:imflammer response; TAS.

GO; GO:0009954; P:imflammer response; TAS.

RO; GO:0009954; P:imflammer response; TAS.

CO; GO:0009954; P:imflammer response; TAS.

RO; GO:0009564; P:imflammer response; TAS.

RO; GO:0009564; P:imflammer response; TAS.

RO; GO:00095654; P:imflammer response; TAS.

RO; GO:0009567; GPRCRENCOPSN.

RROSITE; PRO0237; GPRCRENCOPSN.

RROSITE; PRO0237; GPRCTEIN RECEP F1 1; 1.

RROSITE; PRO0237; GPRCTEIN RECEP F1 2; 1.

RROSITE; PRO0337; GPRCTEIN RECEP F1 2; 1.
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EXTRACELLUIAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
BY SIMILARITY.
  SIMILARITY: Belongs to family 1 of G-protein coupled receptors
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Pred. No. 0.012;
8; Mismatches 5; Indels
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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/FTId=VAR_010670.
51EBE12AD1FAFABF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 40.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178
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CARBOHYD
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RESULT 38
CCR6\_HUMAN STANDARD; PRT; 342 AA.
AC 000574; 000575;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update) 102 QWVFGLGLCKMISWMYLVGFYS 123 1 OWDFGNTMCQLLTGLYFIGFFS 22

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Gaps

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REDINE=Pancreas;

RX MEDINE=2388257; Pubmed=12477932;

RX Altaschar R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altaschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altaschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altaschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heng L.,

RA Boach S.S., Logdellano K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raba S.S., Logdellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratue P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,

RA Pilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Pilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Pilalon D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Scheerch A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RT "Generation and initial analysis of more than 15,000 full-length

RT "Generation and initial analysis of more than 15,000 full-length

RT Proc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).

- "FUNCTION: Receptor for the C.A.-C chemokine CXCL16. Used as a coreceptor by SIVs and by strains of HIV-2 and m-tropic HIV-1.

C. "FUNCTION: Receptor for the C.A.-C chemokine CXCL16.

- TISSUE SPECIFICITY: Expressed in lymphoid tissues and activated T.

- "ISSUE SPECIFICITY: Expressed in lymphoid tissues and activated T.

- "ISSUE SPECIFICITY: Expressed in lymphoid tissues and activated T. C-X-C chemokine receptor type 6 (CXC-R6) (G protein-coupled receptor bonzo) (G protein-coupled receptor STRL33), CXCR6 OR BONZO OR STRL33 OR TYMSTR. MEDLINE=97431687; PubMed=9285716; MEDLINE=97431687; MEDLINE=97431687; M., Meara A., Oberlin B., Brass N., Legler D.F., Loctscher P., D'Apprazo M., Meese B.U., Rousset D., Virelizier J.L., Baggiolini M., Arenzana-Seisdedos F., Moser B.; Maser B.; Metarive chemckine receptor selectively expressed in activated T cells, exhibits HIV-1 coreceptor function."; Curr. Biol. 7:652-660(1997). -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors. "STRL33, A novel chemokine receptor-like protein, functions as a fusion cofactor for both macrophage-tropic and T cell line-tropic HIV-1."; Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. Kopatz S.A., Aronstam R.S., Sharma S.V.; "cDM clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org)."; Submitted (UUN-2003) to the EMBL/Genbank/DDBJ databases. SEQUENCE FROM N.A.
MEDLINE=97373958; PubMed=9230441;
MEDLINE=97373958; PubMed=9230441;
Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.;
"Expression cloning of new receptors used by simian and human immunodeficiency viruses."; SEQUENCE FROM N.A., AND VARIANT ALA-25. DEDLINE-97311099; PubMed-9166430; Liao F., Alkhatib G., Peden K.W.C., Sharma G., Berger E.A., Farber J.M.; Exp. Med. 185:2015-2023(1997) Nature 388:296-300(1997) (Human) SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. NCBI\_TaxID=9606 sapiens 

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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                      . .; TAS.
                                                                                                                                                                                                                     15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-X-C chemokine receptor type 6 (CXC-R6) (G protein-coupled
CXCR-6 DOIZO).
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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D -> A (in STRL33.3).
/FIId=VAR_003506.
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MEDLINE=97373958; PubMed=9230441;
Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.;
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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5; Mismatches
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N-LINKED (GLCN
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CYTOPLASMIC (
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                                                                                              EMBL; U73529; AAB61456.1; -...
EMBL; V73531; AAB61457.1; -...
EMBL; Y13249; CAA73698.1; -...
EMBL; AY322543; AAP84336.1; -...
EMBL; BC033584; AAH33584.1; -...
                                                                                 EMBL; AF007545; AAB64221.1; -.
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Best Local Similarity 45.5
Matches 10; Conservative
                                                                                                                                                                             HGNC:16647; CXCR6.
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CCR6_MACNE
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MEDLINE=99433499; PubMed=10505680;
MEDLINE=99433499; PubMed=10.Li., Girard M., Butor C.;
"Sequences and predicted structures of chimpanzee STRL33 (Bonzo) and gpr15 (BOB).";
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15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation u
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                                                                                                               -i- FUNCTION: Receptor for the C-X-C chemokine CXCL16. Used as a coreceptor by SIVs and by strains of HIV-2 and m-tropic HIV-1.
-i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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Expression cloning of new receptors used by simian and human
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InterPro; IPR000276; GPCR_Rhodpsn.
Prim; PF00001; Ttm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; GPROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; GPROTEIN RECEP_F1_2; 1.
PROSITE: PS50262; GPROTEIN RECEP_F1_2; 1.
TRANSMEM 33 CPROTEINIAN.
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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1800 BY SIMILARITY.
16 N-LINKED (GLCNAC. . ) (PA
39297 WW, 55F9F68CB62D2DF5 CRC64;
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Local Similarity 45.5%;
les 10; Conservative
                                                 immunodeficiency viruses.";
Nature 388:296-300(1997).
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342 AA;
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coreceptor by SIVs and by strains of HIV-2 and m-tropic HIV-1.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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N-LINKED (GLCHAC. . ) (POTENTIAL).
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JR EMBL; AF084229, AAD52041.1;

DR INTERPO; IPRO00276, GPGR_Rhodpsn.

DR PRINTS; PRO0277; GPGRAHODPSN.

DR PROSITE; PS50262; G_PROTEIN_RECEP_FI_2; I.

WW G-protein coupled receptor; Transmembrane; Glycoprotein.

DOMAIN

1 32 EXTRACELLULAR (POTENTIAL).

SAMEM 3 STRACELLULAR (POTENTIAL).

ONAIN

1 32 CYTOPLASMIC (POTENTIAL).

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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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342 AA;
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Best Local Similarity
Matches 10; Conserv
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Tage L., Ehrenberg P.K., Chang G., Michael N.L.;

Tage L., Ehrenberg P.K., Chang G., Michael N.L.;

Tage L., Ehrenberg P.K., Chang G., Michael N.L.;

RT Tage L., Ehrenberg P.K., Chang G., Michael N.L.;

Transcription Unit for the Chemokine Receptor CCR-5, a Major Entry Co-
RT Receptor for HIV1.;

Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.

BR GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0001584; F:receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor protein signalin. .; IEA.

BR GO; GO:0001584; F:rhodopsin-like receptor protein signalin. .; IEA.

BR FROW FROW THE 1.

BR REMINTS; PRO0021; GPCRRHODOSN.

BR PROSITE; PS50262; G-RROTEIN_RECEP_FI_2; I.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Score 126; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels
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SEQUENCE 215 AA; 23946 MW; 3C9146C76BA416F7 CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
CC-chemokine receptor.
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                                                                                                              PRELIMINARY;
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Maximum Match 100%
Listing first 45 summaries
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1 QWDFGNTMCQLLTGLYFIGFFS 22
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species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161920; AA47677.1; -
GO; GO:00016021; C:integral to membrane; IEA.
GO; GO:00018872; F:receptor activity; IEA.
GO; GO:000186; F:rporcein coupled receptor activity; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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339 AA, 39115 MW, 3C6369F922C91AA7 CRC64;
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339 AA, 39066 MW, 8BAF02E19423BF79 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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100.0%; Pred. No. 3.1e-11;
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PROSITE; PS00237; GPROTEIN RECEP FI 1; 1.
PROSITE; PS50262; GPROTEIN RECEP FI 2; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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            STTTS
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Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
Ho D.D.;
HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism.";
AIDS Res. Hum. Retroviruses 0:0-0(1997).
AIDS Res. Hum. Retroviruses 0:0-0(1997).
Remai, AF00116021; C:integral to membrane; IEA.
GO; GO:00016021; F:receptor activity; IEA.
GO; GO:0001184; F:rhodopsin-like receptor activity; IEA.
RO; GO:0001186; P:G-protein coupled receptor protein signalin. ..; IEA.
RITERPRO; IRRO0276; GPCRRHODOFSN.
RITERPRO; IRRO0237; GFCRRHODOFSN.
ROSITE; PS00237; GFRRHODOFSN.
ROSITE; PS00237; GFRRHODOFSN.
ROSITE; PS00262; G_PROTEIN_RECEP_FI_2; 1.
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EMBL; AF161919; AAD47676.1; -.
EMBL; AF161919; AAD47676.1; -.
GO; GO:0004812; F:receptor activity; IEA.
GO; GO:000186; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. ..; IEA.
InterPro; IPR000276; GPCR_Rhodpsin.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   333 AA; 38174 MW; AEFBA07A67893AEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QUN24;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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                                                                                                                                                           333 AA
                                                                                                                                                                                                                  Created)
               QWDFGNTMCQLLTGLYFIGFFS 114
                                                                                                                                                           PRT;
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Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
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Best Local Similarity 100.0%;
Matches 22; Conservative 0
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                                                                                                                                                                                                                                                                                                     CCR5 receptor (Fragment).
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Ry Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

Shibata R., Toder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;

Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;

Standard R., Submitted (Jul.1999) to the EMBL/GenBank/DDBJ databases.

EMBL, Arielald, AAD47611.1; -.

BR GO, GO:0004872; Fireceptor activity; IEA.

GO, GO:0004872; Fireceptor activity; IEA.

GO; GO:0001884; Firhodopsin-like receptor activity; IEA.

GO; GO:0001886; Pirhodopsin-like receptor protein signalin. .; IEA.

BR GO; GO:000188; Pirhodopsin-like receptor protein signalin. .; IEA.

BR GO; GO:000188; Pirhodopsin-like receptor protein signalin. .; IEA.

BR FRINTS; PRO0227; GPCR-RHODOPSN.

PROSITE; PSSC0237; GPCR-RHODOPSN.

Receptor.

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SEQÜENCE 339 AA; 39086 MW; 88ADBB44E2CB4ECZ CRC64;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NOBI_TaxID=9606;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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nes 22; Conservative
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Homo sapiens (Human)
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ERQUENCE FROM N.A.

SEQUENCE FROM N.A.

Author C., Marx P., Wolinksy S.;

Author C., Marx P., Wolinksy S.;

"Sequences of the CCRS genes from diverse simian and prosimian
"Sequences of the CCRS genes from diverse simian and prosimian
"Sequences of the CCRS genes from diverse simian and prosimian
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"Sequences of the CCRS genes from diverse simian and prosimian
"Sequences of the CCRS genes from diverse simian and prosimian
"Bubmitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF161921; AAD47678.1; -.

BREMBL; AF161921; AAD47674.1; -.

"A GO; GO:00016021; C:integral to membrane; IEA.

GO; GO:00016021; C:integral to membrane; IEA.

GO; GO:0001884; F:rhodopsin-like receptor protein signalin. .; II

ROSITE; PRO0226; GPRRHODOPSN.

PROSITE; PRO0227; GPROTEIN_RECEP_F1_2; 1.

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SEQUENCE 339 AA; 33128 MW; 9C3369FFFIF2PZ7A CRC64;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity 100.0%; Pred. No. 3.16-11;
Matches 22; Conservative 0; Mismatches 0; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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86 QWDFGNTMCQLLTGLYFIGFFS 107 1 OWDFGNTMCQLLTGLYFIGFFS 22 RESULT 8 셤

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SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCR5 genes from diverse simian and prosimian
species."; (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                             Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                         01-MAY-2000 (TrEMBLrel. 13, Created)
11-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
               PRT;
                 PRELIMINARY;
                 Q9UBT9
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EQUIENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
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GO; GO:0001891; F:receptor activity; IEA.

GO; GO:0001894; F:receptor activity; IEA.

GO; GO:0001894; F:receptor activity; IEA.

GO; GO:0001894; F:receptor activity; IEA.

GO; GO:000186; P:-protein coupled receptor protein signalin. .; IEA.

InterPro; IPRO0027; GPCR.Rhodpsn.

PRENTY; PRINTS; PRO00237; GPCRRHODOPSN.

PROSITE; PS00237; GPCRRHODOPSN.

PROSITE; PS00237; GPROTEIN\_RECEP\_FI\_1; 1.

NCBI\_TaxID=9606;

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EMBL; AF161915; AAD47672.1; -.
EMBL; AF161909; AAD47666.1; -.
EMBL; AF161910; AAD47667.1; -.
EMBL; AF161911; AAD47668.1; -.
EMBL; AF161912; AAD47669.1; -.
GO; GO:0016021; C:integral to membrane; IEA.

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Query Match
100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels (

1 QWDFGNTMCQLLTGLYFIGFFS 22

1 1 339 339 339 AA; 39146 MW; 10FE05FE5371D4B3 CRC64;

Receptor. NON TER NON TER SEQUENCE

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EMBL; AF162024; AAD4779.1; -...
EMBL; AF162024; AAD4779.1; -...
EMBL; AF16189; AAD47646.1; -...
EMBL; AF16189; AAD47646.1; -...
GO; GO:0016872; F:receptor activity; IEA.
GO; GO:000186; P:cprotein coupled receptor protein signalin. ..; IEA.
INCEPPRO; PR000276; GPCR, Rhodpsn.
PRINTS; PR00217; GPCR, Rhodpsn.
PROSITE; P800217; GPCR, Rhodpsn.
PROSITE; P800217; GPCR, RHODPSN.
PROSITE; P800217; GPCR, RHODPSN.
PROSITE; P8502627; GPROFEIN RECEP_F1_2; 1.
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF161887; AAA47644.1; -.
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0001872; F:receptor activity; IEA.
GO, GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO, GO:000186; P:G-protein coupled receptor protein signalin. . .; IEA.
InterPro; IPRO00276; GFCR_Rhodpsn.
                                             Hylobates concolor (crested gibbon).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hylobatidae, Hylobates.
                                                                                                                                                                                   SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCR5 genes from diverse simian and prosimian
species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hylobates concolor (crested gibbon).
Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hylobatidae, Hylobates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy P. Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S. Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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339 339
339 AA; 39075 MW; 09257FBFB834C4AE CRC64;
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339 339
339 AA; 39036 MW; 5555FEAR2614D35C CRC64;
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Last annotation update)
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Pred. No. 3.1e-11;
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PRINKS: PR00231; GPCMFHODPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last seq 01-VMY-2003 (TrEMBLrel. 24, Last ann C-C chemokine receptor 5 (Fragment).
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C-C chemokine receptor 5 (Fragment)
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                                                                                                                                  NCBI_TaxID=29089;
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Q9TUX1;
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Q9TUX1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
GO, GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:00011884; F:rhodopsin-like receptor protein signalin.
InterPro; IPR00027; GFO. TOTCE Rhodopsn.
PRINTS; PR00021; 7tm 1; 1.
PROSITE; PR00237; GPREIN RECEP F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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                                                                                                                                                                                                                                                                                                                                                     Score 126; DB 4; Length 339;
Pred. No. 3.1e-11;
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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339 339
339 AA, 39114 MW, 3C6369F92C29F4A7 CRC64;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemckine receptor 5 (Fragment).
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nes 22; Conservative
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Matches 22; Conserv
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The Sep 28 13:49:56 2004
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ô ò Gaps Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.

L Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.

R GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:001684; P:rhodopsin-like receptor activity; IEA.

GO; GO:0001584; P:rhodopsin-like receptor protein signalin...;

R GO; GO:0001786; P:G-protein coupled receptor protein signalin...;

R Fam; PRO0237; GPCRRHODOPSN.

R PROSTIE; PRO0237; GPRRHODOPSN.

R PROSTIE; PSO0237; GPROTEIN\_RECEP\_F1\_1; 1. SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCRS genes from diverse simian and prosimian SEQUENCE FROM N.A.
Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCRS genes from diverse simian and prosimian
species."; Gorilla gorilla gorilla (Lowland gorilla). Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla. Macaca nemestrina (Pig-tailed macaque).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates; Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca. ö . 0 Query Match 100.0%; Score 126; DB 6; Length 339; Best Local Similarity 100.0%; Pred. No. 3.1e-11; Matches 22; Conservative 0; Mismatches 0; Indels ( 100.0%; Score 126; DB 6; Length 339; 100.0%; Pred. No. 3.1e-11; tive 0; Mismatches 0; Indels 1 1 339 339 339 AA, 39079 MW; A4A79753DA2F7AAF CRC64; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-UUN-2003 (TrEMBLrel. 24, Last annotation update) C-C chemokine receptor 5 (Fragment). 01-MAY-2000 (TrEMBirel. 13, Created)
01-MAY-2000 (TrEMBirel. 13, Last sequence update)
01-UJN-2003 (TrEMBirel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment). 339 AA 86 QWDFGNTMCQLLTGLYFIGFFS 107 PRT; PRT; 1 OWDFGNTMCQLLTGLYFIGFFS 22 Query Match
Best Local Similarity 100.00
-008 22; Conservative PRELIMINARY; PRELIMINARY; Receptor. NON TER NON TER SEQUENCE Q9TUT4 RESULT 12 Q9TUW8 RESULT 13
209TUT4
1D 09TUT9
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REGUINCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibara R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
Sequences of the CCR5 genes from diverse simian and prosimian

The Species.";
S ö ö Gabs Hylobates concolor (crested gibbon).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia; Butheria, Primates; Catarrhini; Hylobatidae; Hylobates. ; 0 ö Match
Local Similarity 100.0%; Score 126; DB 6; Length 339;
Local Similarity 100.0%; Pred. No. 3.1e-11;
tes 22; Conservative 0; Mismatches 0; Indels 100.0%; Score 126, DB 6, Length 339; 100.0%; Pred. No. 3.1e-11; ive 0, Mismatches 0; Indels ( 1 1 339 339 339 AA, 39092 MW, 84B51B9548E0703C CRC64; 1 339 339 339 AA; 39024 MW; EC4CE48DEEEF107E CRC64; 01-MXY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-UNN-2003 (TrEMBLrel. 24, Last annotation update) C-C chemokine receptor 5 (Fragment). 339 AA PROSITE, PSO0237, G PROTEIN RECEP F1 1, 1.
PROSITE, PSS0262, G\_PROTEIN\_RECEP\_F1\_2; 1. PRT; 86 QWDFGNTMCQLLIGLYFIGFFS 107 1 QWDFGNTMCQLLTGLYFIGFFS 22 PRELIMINARY; Best Local Similarity 100. Matches 22, Conservative PRELIMINARY; Receptor. NON TER NON TER SEQUENCE Receptor. NON TER NON TER SEQUENCE Query Match Query Match Q9TUUB Q9TUUB; Q9TUW9; Best Loca Matches RESULT 15 Q9TUU8 ID Q9TUU AC Q9TUU RESULT 14 Q9TUW9 ଟ ACCOCK ON THE PROPERTY OF T 셤

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Cercopithecus nictitans (white-nosed guenon).
Eukaryota; Metazoa; Chordata; Craniaca; Vertebrata; Euteleostomi;
Bamaalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
NCBI_TaxID=36228;
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EMBL, AF161903, AAD47660.1; -..

EMBL, AF161903, AAD47660.1; -..

EMBL, AF161903, AAD47660.1; -..

EMBL, AF161903, AAD47660.1; -..

GO, GO:0016621; C:integral to membrane; IEA.

GO, GO:0001884; F:rhodopsin-like receptor activity; IEA.

GO, GO:0001884; F:rhodopsin-like receptor protein signalin...

InterPro; IPR000276; GPRCE, Rhodopsn.

PROMOTIC: PRO0277; GPRCE, Rhodopsn.

PROSTIE; PS00237; GPCRPEIN RECEP F1 1; 1.

PROSTIE; PS50262; G_PROTEIN RECEP F1 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
NCBI_TaxID=9598;
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Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy F.
"Sequences of the CCRS genes from diverse simian and prosimian species.",
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339 339
339 AA; 39129 MW; 4A88F8BB601D46A4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         01-WAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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01-NAY-2000 (TrEMBLrel. 13, Created)
01-NAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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100.0%; Pred. No. 3.1e-11;
iive 0; Mismatches 0;
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Q9TQU7
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Q9TUW4
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161905; AAD47662.1; -.
EMBL; AF161901; AAD47663.1; -.
EMBL; AF161901; AAD47661.1; -.
EMBL; AF161904; AAD47661.1; -.
GO; GO:001621; C:integral to membrane; IEA.
GO; GO:00184; F:receptor activity; IEA.
GO; GO:000184; F:rhodopsin-like receptor activity; IEA.
GO; GO:000186; P:d-protein oupled receptor protein signalin. .; IEA.
InterPro; IFR000276; GPCR_Rhodpsn.
Pfan; PF00001; 7tm 1; 1.
PRINTS; PR000237; GERRHOOPSN.
PROSITE; PS00237; GERRHOOPSN.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                             Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                           Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                          species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AFIG1949; AAD47705.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0007186; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:rhodopsin-like receptor activity; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
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Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 126; DB 6; Length 339;
; Pred. No. 3.1e-11;
0; Mismatches 0; Indels C
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UMY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemckine receptor 5 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00001; 7tm 1; 1.
PROMINS; PRO0237; GPCRHODOSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
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                                                                                                                                 Cercopithecus diana (Diana monkey)
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AC 09TOW
AC 09TOW
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P SEQUENCE FROM N.A.

A KURRHAMAN K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Anibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; T "Sequences of the CCRS genes from diverse simian and prosimian species.", Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.

E RBL; API62047; AAD47799.1; -.

R EMBL; API62044; AAD47799.1; -.

R EMBL; API62044; AAD47799.1; -.

R GO; GO:00016021; C:integral to membrane; IEA.

GO; GO:0001872; F:receptor activity; IEA.

GO; GO:000186; P:C-protein coupled receptor activity; IEA.

GO; GO:0001186; P:C-protein coupled receptor protein signalin. ..; I.

R MENTS; PRO0021; 7m 1; 1.

P FAM: PRO0001; 7m 1; 1.

P FAM: PRO0001; 7m 1; 1.

P RRSITE; PS00237; GPCRRHODOPSN.

R PRINTS; PRO0237; GPCRRHODOPSN.

R PROSITE; PS00237; GPCRRHODOPSN.

R PROSITE; PS00237; GPROTEIN RECEP FI 1; 1.
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCRS genes from diverse simian and prosimian
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Bukaryota, Metazoa; Chordata; Craniata, Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels (
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339 339
339 AA, 39150 MW; 847D5F92BB03E6E2 CRC64;
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SEQUENCE 339 AA; 39121 MW; AFBGE3EE4D6D3484 CRC64;
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01-MAY-2000 (TrEWBLrel. 13, Last sequence update)
01-ULM-2003 (TrEWBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OWDFGNTMCQLLTGLYFIGFFS 22
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Best Local Similarity 100...
Best 22; Conservative
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DT 091-MA
DT 01-MA
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                                                                                                                                                                   Saguinus sp.
Eukaryota, Hatazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
NCBI_TaxID=100754;
                                                                                                                                                                                                                                                                        Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; T. Sequences of the CCRS genes from diverse simian and prosimian species."; (JUL-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AF16,2015; AAD47770.1; — GO, GO,0016892; Fireceptor activity; IEA. GO; GO:0004872; Fireceptor activity; IEA. GO; GO:0001584; Firhodopsin-like receptor activity; IEA. GO; GO:0001584; Firhodopsin-like receptor protein signalin. ..; Finer.; PR00237; GPCR-Rhodpsn. PRINTS; PR00237; GPCR-Rhodpsn. PRINTS; PR00237; GPRNHODOPSN. PROSITE; PS00237; GPRNTEN RECEP_FI_1; 1.
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinkey S., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinkey S., Sequences of the CGR5 genes from diverse simian and prosimian species.";

Submitted (JUL.1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF161954; AAD47706.1;

EMBL; AF161952; AAD47706.1;

EMBL; AF161952; AAD47708.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mamalia, Eutheria, Primates, Catarrhini, Cercopithecidae;
Cercopithecinae, Macaca.
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339 339
339 AA; 39063 MW; 78BCE7A84B877085 CRC64;
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Q9TQT0;
Q01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
Q9TUR9 PRELIMINARY; PRT; 339 AA.
Q9TUR9;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2003 (TrEMBLrel. 13, Last sequence update)
01-UMY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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Matches 22, Conser
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339 AA.

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Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; "Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cercopithecus aethiops vervet.

Ekaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates; Catarrhini, Cercopithecidae,
Cercopithecinae, Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                           339 339 39137 NW; 9E626ED3288607C1 CRC64;
01-WAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) C-C chemokine receptor 5 (Fragment).
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U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UMY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 126; DB 6;
Pred. No. 3.1e-11;
); Mismatches 0;
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Les 22, Conservative
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O9TUR6;
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    GO, GO:0016021; C:integral to membrane; IEA.

GO, GO:0001891; F:receptor activity; IEA.

GO, GO:0001894; F:rhodopsin-like receptor activity; IEA.

GO; GO:0007186; F:receptor activity; IEA.

InterPro; IPR000276; GPCR_Rhodosn.

PRINTS; PR000217; GPCRRHODOPSN.

PRINTS; PR000217; GPCRRHODOPSN.

PROSITE; PS500237; GPCRRHODOPSN.

PROSITE; PS500262; G_PROTEIN_RECEP_FI_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ARIG1972; AAD47727.1; -
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:001684; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001186; P:G-protein coupled receptor protein signalin. .; IEA.
InterPro; IRRO0276; GER.Rhodpsn.
PRINTS; PRO0237; GFCRRHODDRN.
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
MCBI_TaxID=9544;
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339 AA; 39067 MW; SBFCBCSBA96C2F9B CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                        PRT; 339 AA.
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Q9TSN2
ID Q9TSN2
AC Q9TSN2,
DI 01-MAY-2000 (TrEMBLrel. 13, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 OWDFGNIMCOLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                             1 QWDFGNTMCQLLTGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                  . Match 100.0%;
Local Similarity 100.0%;
es 22; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22; Conservative
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Gaps

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339 AA.

Length 339; Indels

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A KURSTER FROM N.A.

A KURSTEAN K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillais S., Kulken C., Marx P., Wolinksy S.;
T "Sequences of the CCRS genes from diverse simian and prosimian
T "Sequences of the CRS genes from diverse simian and prosimian
T Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF161900; AAD47657.1; -. Commerce of the EMBL/GenBank/DDBJ databases.

EMBL; AF161900; AAD47657.1; -. Commerce of the EMBL/GenBank/DDBJ databases.

EMBL; AF161900; AAD47657.1; -. Commerce of the EMBL/GenBank/DDBJ databases.

EMBL; AF161900; AAD47657.1; -. Commerce of the EMBL/GenBank/DDBJ databases.

EMBL; AF161900; AAD47657.1; -. Commerce of the EMBL/GenBank/DDBJ databases.

EMBL; AF161900; AAD47657.1; -. Commerce of the EMBL/GenBank/DDBJ databases.

EMBL; AF161900; AAD47657.1; -. Commerce of the EMBL/GENBANG of the EMBL/GENBANG
  Eutheria; Primates; Catarrhini; Hominidae; Pan.
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339 339
339 AA, 39103 MW, 4038C132D024C5A4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
les 22; Conservative
                           NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Colobus guereza (Black-and-white colobus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pan troglodytes (Chimpanzee).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M. Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S. "Sequences of the CCR5 genes from diverse simian and prosimian species.",
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                  Length 339;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 126; DB 6; Length 3 100.0%; Pred. No. 3.1e-11; tive 0; Mismatches 0; Indels
                                                                                                                                Indels
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339 339
339 AA; 39168 MW; GA4BF72FEBFF566F CRC64;
'339 339
339 AA; 39178 MW; 9DF2A6F446C55AED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  017076;
01-MAY-2000 (TYEMBLEE]. 13, Created)
01-MAY-2000 (TYEMBLEE]. 13, Last sequence update)
01-JUN-2003 (TYEMBLEE]. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                          Query Match 100.0%; Score 126; DB 6; Best Local Similarity 100.0%; Pred. No. 3.1e-11; Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                              PRT; 339 AA.
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                                                                                                                                                                                                                QWDFGNTMCQLLTGLYFIGFFS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QWDFGNTMCQLLTGLYFIGFFS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OWDFGNIMCOLLIGLYFIGFFS 22
                                                                                                                                                                                  1 OWDFGNIMCOLLIGLYFIGFFS 22
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Best Local Similarity 100,0
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                                                                                                                                                                                                                                                                                                     RESULT 25
09TQV6
10D Q9TQVV
AC Q9TQVV
AC Q9TQVV
AC Q0TQVV
DT O1.-MA
DT O1.-M
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Q9TUM6
ID Q9TUM
AC 09TUM
DT 01-MA
DT 01-MA
DT 01-MA
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GN CCRS.
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CCC C
GN CCRS.
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100.0%; Score 126; DB 6; Length 339; 100.0%; Pred. No. 3.1e-11; ive 0; Mismatches 0; Indels (

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EQUIENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

Runstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

A Shibara R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;

Sequences of the CCRS genes from diverse simian and prosimian

ST Sequences of UTL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL. API62041; AAD47796-1;

SCHOOL621; Cintegral to membrane; IEA.

GO; GO:001621; Cintegral to membrane; IEA.

GO; GO:001621; Cintegral to membrane; IEA.

GO; GO:001621; Fireceptor activity; IEA.

GO; GO:00186; Pi-G-protein coupled receptor protein signalin. .; IEA.

InterPro; IPR00276; GPCR.Rhodopsn.

PRAMTS; PR00217; GFCRRHODOPSN.

PROSITE; PS00237; GFCRRHODOPSN.

PROSITE; PS00262; G_PROTEIN_RECEP_FI_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                         Cercopithecus mona.

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
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339 339
339 AA; 39019 MW; 7176F940AF11F3ED CRC64;
                                                                                                                                                                                                              OFTUG9;
01-YAY-2000 (TrEMBLrel. 13, Created)
01-YAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
86 QWDFGNTMCQLLTGLYFIGFFS 107
                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                    PRELIMINARY;
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Species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161989; AAD47744.1;
EMBL; AF161989; AAD47743.1;
EMBL; Freeeptor activity; IEA.
GO; GO:0001584; F:receptor activity; IEA.
GO; GO:0001584; F:receptor activity; IEA.
EMBL; F:rec
GO, GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:000186; P:G-protein coupled receptor protein signalin. . .; IEA.
InterPro; IPR000276; GPCR Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PROMITE; PR00273; GPCRENDODPSN.
PROSITE; PS00277; GPCREND RECEP. FI 1; 1.
PROSITE; PS50262; G_PROTEIN RECEP. FI 2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Papio papio (Guinea baboon).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCR5 genes from diverse simian and prosimian
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339 339
339 AA, 39097 MW, C576E7AA492D7080 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              339 339 339 3313 MW; 7F9803EA0E0AF9ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
02-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 100.0%; Score 126; DB 6; Similarity 100.0%; Pred. No. 3.1e-11; 22; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 3.1e-11;
trive 0; Mismatches 0;
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01-MAY-2000 (TrEMBLrel. 13, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QWDFGNTMCQLLTGLYFIGFFS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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Gest Local Similarity 100...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Kunstman K., Chen Z., Kouther B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinksy S.; Shibata R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinksy S.; Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
NCBI_TaxID=9542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161951; AAD47707.1;
GO; GO:00016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
INCEPRO; GO:0007186; P:G-protein coupled receptor protein signalin.
PF00001; 7tm_1; 1.
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100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161955; AAD47711.1; -.
GO: GO:0016021; C:integral to membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339 AA; 39098 MW; F0132E8BC44EF829 CRC64;
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                         339 AA.
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PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
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                                                         86 QWDFGNTMCQLLTGLYFIGFFS 107
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                    1 QWDFGNIMCQLLIGLYFIGFFS 22
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Q9TSN3
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Query Match 100.0%; Score 126; DB 6; Best Local Similarity 100.0%; Pred. No. 3.1e-11; Matches 22; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                      1 OWDFGNIMCQLLIGLYFIGFFS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ppecies.",
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF162046; AAD47801.1; ...
ENBL; AF162043; AAD47798.1; ...
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001884; F:rhodopsin-like receptor protein signalin. ..; IEA.
InterPro; IRR000276; GFCR_Rhodops.
Pfan; PPO0001; Thu 1; ...
PRINTS; PR00237; GFCRRHODOPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1 2; 1.
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EMBL, AF161995; AAD47750.1; -.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016121; F:receptor activity; IEA.

GO; GO:0001284; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001284; F:rhodopsin-like receptor protein signalin. . .; IEA.

InterPro; IPR000276; GPCR_Rhodopsn.

PRINTS; PR00237; GPCRHODOPSN.

PROSITE; PS50262; G_PROTEIN_RECEP_FI_2; 1.

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Papio.
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCR5 genes from diverse simian and prosimian species.";
                                                                                                                        Cercopithecus nictitans (white-nosed guenon).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Fillai S., Kuiken C., Marx P., Wollinkey S., "Sequences of the CCR5 genes from diverse simian and prosimian
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) C-C chemokine receptor 5 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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22; Conservative
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09TUS7
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AC 09TUS
DT 01-MA
DT 0
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species.; submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases. Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF161899; AAD47656.1; George (July 1997) to membrane; IEA. GO; GO:0016201; C:integral to membrane; IEA. GO; GO:0001584; F:rhodopsin-like receptor activity; IEA. GO; GO:0007186; P:chrotein coupled receptor protein signalin. . .; IEA. InterPro; IPR00027; GPCR_Rhodopsn. PEAM; FP00001; Trul.; Jrul.; PRINTS; PR000237; GPCRRHODOPSN. PROSITE; PS500237; GPROTEIN_RECEP_FI_1; 1.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pongo.
                                                                                                                                                                                                CCR5.
Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.
"Sequences of the CCR5 genes from diverse simian and prosimian
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Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy
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339 339
339 AA, 39157 MW, 4A9EBAD183E8E72D CRC64;
                        Q9TUW7;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UMY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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339 AA
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PRT;
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Gaps

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Length 339; Indels

339 339 34, 39068 MW; 84EB018085DC0A62 CRC64;

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1001-71-610-100-01-01

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Best Loc Matches

RESULT 35 Q9TUS5

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SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinksy S.;
Shibata R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CrS genes from diverse simian and prosimian
species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161991; AAA97748.1; -.
EMBL; AF161991; AAA97745.1; -.
EMBL; AF161991; AAA97745.1; -.
EMBL; AF161991; Fireceptor activity; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0001884; F:indoopsin-like receptor activity; IEA.
GO; GO:0001884; F:indoopsin-like receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFF61970; AAA47725.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0001862; F:receptor activity; IEA.
GO; GO:000186; F:receptor activity; IEA.
InterPro; IPR000276; GPCR_Rhodpsin.
PRINTS; PR000277; GPCR_Rhodpsin.
PRINTS; PR000277; GPCRRHODPSN.
PROSITE; PS002377; GPCRRHODPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                               Macaca mulatta (Rhesus macaque).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
Shibates of the CCR5 genes from diverse simian and prosimian
species."
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339 339
339 AA; 39155 MW; 3D1B5039B9E24C82 CRC64;
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UMY-2003 (TrEMBLrel. 24, Last annotation update)
0-C chemokine receptor 5 (Fragment).
                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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100.0%; Pred. No. 3.1e-11;
trive 0; Mismatches 0;
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                            Species...;
Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.
Lymitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.
R GO; GO:0016021; C:integral to membrane; IEA.
R GO; GO:001684; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
R GO; GO:0001786; P:rhodopsin-like receptor protein signalin. ..;
R InterPro; IPR000276; GPCR_Rhodpsn.
R FILM: PR00017; GPCRRADOPSN.
R PRINTS; PR00237; GPCRRADOPSN.
R PROSITE; PS00237; GPRRADOPSN.
R PROSITE; PS00237; GPRRADOPSN.
R PROSITE; PS002237; GPRRADOPSN.
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Bukaryota, Metazota, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Papio.
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCRS genes from diverse simian and prosimian
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
BMBL, PR161997; AAD47752.1; ...
GO, GO:0004872; Fireceptor activity; IEA.
GO, GO:000186; F:Greceptor activity; IEA.
GO, GO:000186; F:Greceptor activity; IEA.
InterPro; IPR000276; GPCR-Rhodpsn.
Fram; PR0001; 7tm 1; 1.
PRINTS; PR00237; GPCR-RHODPSN.
PROSITE; PS00237; GPCR-RHODPSN.
PROSITE; PS00237; GPCR-RHODPSN.
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"Sequences of the CCR5 genes from diverse simian and prosimian
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339 339
339 AA; 39103 NW; 4350C4625FB0657C CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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les 22; Conservative
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Length 339; Indels

Best Loc Matches

RESULT 36

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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                            Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.

Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.

GO, GO:0016021; C:ntegral to membrane; IEA.

GO; GO:0018872; F:receptor activity; IEA.

GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001886; F:Gerctein coupled receptor protein signalin.

InterPro; IPR00276; GPCR_Rhodpsn.

PFam; PF00001; 7tml; 1.

PRINTS; PR00237; GFCRRHODOFN.

PROSITE; PS00237; G_PROTEIN_RECEP_FI_1; 1.
                      Cercopithecus nictitans (white-nosed guenon).
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Best Local Similarity 100.
Matches 22; Conservative
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339 AA;
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                                                                                              NCBI_TaxID=36228;
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinksy S.;
M. Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
T. Sequences of the CCR5 genes from diverse simian and prosimian

IT Species.";
Species.";
Species.";
EMBL; AF162040; AAD47795.1;
EMBL; AF162040; AAD47795.1;
EMBL; AF162040; AAD47793.1;
EMBL; AF164040; AAD47793.1;
EMBL; AF164040; AAD47793.1;
EMBL; AAD47793
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Cercopithecus.
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                                                                                                                                                                             ch 100.0%; Score 126; DB 6; Length 339; Similarity 100.0%; Pred. No. 3.1e-11; 22; Conservative 0; Mismatches 0; Indels (
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.339 339 MW; 7176E3EAOEO0F3ED CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                              339 AA.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR000237; GFCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Matches 22, Conservative
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Q9TUQ8
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March Front Front E., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; Sequences of the CCRS genes from diverse simian and prosimian pecies.";

"Sequences of the CCRS genes from diverse simian and prosimian to be consisted (ULL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; APIG1907; ADAP4664-1; -.

EMBL; AF161907; ADAP4664-1; -.

GO; GO:00016021; C:integral to membrane; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001586; P:G-protein coupled receptor protein signalin. .; IEA.

InterPro; IPR000276; GPCR\_Rhodpsn.

PROSITE; PS00237; GPCR\_Rhodpsn.

PROSITE; PS00237; GPCR\_RHOGPSI\_1; 1. Pongo pygmaeus (Orangutan). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pongo. Length 339; 339 39117 MW; 4C4E35825BD54E9C CRC64; 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
C-C\_chemokine receptor 5 (Fragment). 100.0%; Score 126; DB 6; 339 AA. PRT; PRELIMINARY;

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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kulken C., Marx P., Wolinksy S., "Sequences of the CCR5 genes from diverse simian and prosimian

1 339 339 339 AA; 39148 MW; OCA289CDDEEDE831 CRC64;

Gaps ó Length 339; 100.0%; Score 126; DB 6; Length 3 100.0%; Pred. No. 3.1e-11; arive 0; Mismatches 0; Indels

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1 OWDFGNTMCOLLTGLYFIGFFS 22

0; Gaps Best Local Similarity 100.0%; Pred. No. 3.1e-11; Matches 22; Conservative 0; Mismatches 0; Indels

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Search completed: September 28, 2004, 09:06:18 Job time : 36.2 secs

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Abg92880 Human G-p

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Aab88995 HIV 95120
Aaw27407 Human CCR
Aaw27835 Human G-p
Aaw36325 Human G-p
Aay80128 Human G-p
Aag79089 Amino aci
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Aag79089 Human G-p
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Aab7039 Human G-p
Aab4688 Human G-p
Aab4688 Human G-p
Aab46898 Human G-p
Aab46898 Human G-p
Aab46898 Human G-p
Aab468999152 Human G-p
Aab83284 Human G-p
Aab83289 Human G-p
Aab87150 Human G-p
Aab87152 Human G-p
Aab87152 Human G-p
Aab87159 Human G-p
Aab87159 Human G-p
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118.345 Million cell updates/sec
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                                                                                                                                                                                                   1586107
        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
                                                 - protein search, using sw model
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AAW27407
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1 SOYOFWKNFQTLKIVILG 18
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Gapop 10.0 , Gapext 0.5
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geneseq1200s:*
geneseq2000s:*
geneseq2001s:*
geneseq2002s:*
geneseq2003s:*
geneseq2003bs:*
                                                                                                                                                                                                                                                                                          A_Geneseq_29Jan04:*
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seq length: 200000000
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Query
Match Length DB
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Perfect score:
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AMEZESOS  AMEZES	; 18 AA. peptide #47. CD4; HIV; glycoprotein 120; gp120; antagonist; CD4; STRL33.  ' OS. OP.	nger C; 2001-244398/25.  It polypeptides useful for treating HIV infection, have homology to ons of domains of human chemokine receptors CCR5, CXCR4 and STRL33, binds to HIV gp120 under physiological conditions.  The l; Page 37; 114pp; English.  Present invention describes a number of peptides which are able to ito HIV glycoprotein 120 (gp120). These are similar to the human obvine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are inl in the treatment of HIV, as they prevent replication of the virus. present sequence is an example of a peptide of the invention nence 18 AA;  Tatch  100.0%; Score 96; DB 4; Length 18;  Accord Similarity 100.0%; Pred. No. 4.2e-08;  1 SQYQFWKNFQTLKIVILG 18
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0 1 2 2 3 4 8 8 8 8 8 8 8 8 8 8 4 4 4 4 4 4 4 4	. 0 0 04 4 4 0 0 0 0	xing  11; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;
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Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour; asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy; diagnosis; leukocyte trafficking; G protein coupled receptor; ligand; modulator; antibody; human.
                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is human CC (Cys-Cys) chemokine receptor 5 (CCR5), which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES Chemokines, but not by monocyte chemoattractant protein 1 (MCP-1), MCP-2, MCP-3, interleukin-8 (IL-8) or growth related gene product alpha (GRO alpha) chemoxines. Active CCR-5 is also a receptor of human immunodeficiency virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can used to diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid psoriasis, viral infections, especially HIV-1 or HIV-2 infection, cancer, atherosclerosis and autoimmune disorders
                                                                                                                                                                                                                                                                                                    Active and inactive forms of human CC chemokine receptor CCR-5 - useful to diagnose, prevent and/or treat inflammatory disorders, autoimmune disease and viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 96; DB 2; I 100.0%; Pred. No. 8.9e-07;
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56. .67
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                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Fig 1b-c; 94pp; English.
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                                                                                         97WO-BE000023.
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                                                                                                                          96EP-00870021.
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Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 352 AA;
                                                                                         28-FEB-1997;
                                                                                                                          01-MAR-1996;
06-AUG-1996;
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                 WO9732019-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a number of peptides which are able to bind to HIV glycoprotein 120 (gp120). These are similar to the human chemokine receptors CRSP, CXCR4 and STRL131, as well as CD4. These are useful in the treatment of HIV, as they prevent replication of the virus. The present sequence is an example of a peptide of the invention
                                                                                                                                                                                                                                                      Human chemokine receptor; CD4; HIV; glycoprotein 120; gpl20; antagonist; replication; CCR5; CXCR4; CD4; STRL33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention; inflammatory disease; rheumatorid arthritis; glomerulonephritis; asthma; idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer; atherosclerosis; autoimmune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gpl20 under physiological conditions.
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100.0%; Pred. No. 4.2e-08;
ttive 0; Mismatches 0;
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                                                                                                                                                                                                                     HIV gp120 protein binding peptide #88.
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                                                                                                            AAB88995 standard; peptide; 18 AA
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SQYQFWKNFQTLKIVILG 18
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                                                                                                                                                                                  23-MAY-2001 (first entry)
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nes 18; Conservative
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Gaps

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Domain

Homo sapiens

Length 352; Indels

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95WO-US007173.
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           06-JUN-1995;
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                                  06-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                           This polypeptide sequence comprises novel human chemokine receptor 88C, a grotein coupled receptor that is involved in leukocyte trafficking. Its amno sequence was deduced from a cDNA clone (AAAT85161) isolated from a macrophage library. Its shows 62% identity to CCCKR1. Chemokine receptor 88-2B (see AAW27124) has also been identified. 88C and 88-2B receptors and their polypeptide fragments can be produced in transformed host cells. The receptors, peptides comprising one or more of the extracellular or intracellular domains, and anti-receptor antibodies can be used to modulate receptor activities, particularly ligand and G protein binding, and are potentially potentially useful in the treatment of atheroslerosis, inemmatoid arthritis, tumours, asthma, viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G-protein chemokine receptor; HDGNR10; signal transduction; haematopoiesis; leukaemia; inflammation; rheumatoid arthritis; diagnosis;
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          /label= Intracellular_domain
259. .280
/label= Extracellular_domain
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/label= Intracellular_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           abnormal haematopoietic processes etc
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                                                                                                                              96WO-US020759
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96US-00661393
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                                                                                                                                                                                                               Gray PW, Schweickart VL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infection, AIDS,
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                                                                                NO9722698-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC chemokine receptor 5; CCR5; G-protein coupled receptor;
human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.
                                                                                                                                                Human G-protein chemokine receptor, HDGNR10 - useful to identify (ant)agonists, for treatment of haematopoiesis, leukaemia, chronic and acute inflammation, rheumatoid arthritis, etc.
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note= "transmembrane domain"
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note= "transmembrane domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human CC chemokine receptor 5 (CCR5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW23835 standard; protein; 352 AA.
                                                                                                                                                                                                                     Claim 1; Page 44-46; 61pp; English
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95WO-US007173.
                                (HUMA-) HUMAN GENOME SCI INC.
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/label= IV
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Best Local Similarity 100.
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                                                                                               WFI; 1997-043072/04.
N-PSDB; AAT44042.
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TGA

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c co-receptor for infection by macrophage-tropic (M-tropic) strains of HIV-1. The invention relates to the identification of a CRS variant (see AAW88131), designated CRRAM303, comprising the first two transmembrane domains of wild-type CCRS, but lacking transmembrane domains 3-7. The command of wild-type CCRS, but lacking transmembrane domains 3-7. The command of wild-type CCRS, but lacking transmembrane domains 3-7. The command of wild-type CCRS allele shows a prostence of the CCRSM303 variant with the wild type CCRS allele shows a command may indicate slower progression of the disease. The strains, and may indicate slower progression of identify individuals at lower command of the confidence of the command of the command of the confidence of the command of the confidence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; G-protein coupled receptor; G-protein chemokine receptor; HDGNR10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New CCRS variant protein of the HIV-1 co-receptor - useful in developing resistance of CCRS-expressing cells to {
m HIV-1} infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is the amino acid sequence of wild-type human CCRS, which serves as
                in wild-type CCR5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Braun J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human G-protein chemokine receptor HDGNR10 SEQ ID NO:2.
                /note= "corresponds to TGT (Cys)
(Stop) in CCr5m303"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
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                                               103. .124
/note= "rransmembrane domain 3"
142. .167
/note= "transmembrane domain 4"
                                                                                                                                                                      236. .260
//note= "rransmembrane domain 6"
275. .301
/note= "transmembrane domain 7"
                                                                                                                                                     "transmembrane domain 5"
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                                                                                                                                                                                                                                                                                                                                                                                                                          (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Page 34-35, 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY80128 standard; protein; 352 AA
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                                                                                                                                 .223
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                                                                                                                                                     'note=
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N-PSDB; AAV84126.
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  Misc-difference
                                                                                                                                                                                                                                                                        WO9854317-A1
                                                                                                                                                                                                                                                                                                                                                  29-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-1997;
                                                                                                                                                                                                                                                                                                               03-DEC-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This protein sequence comprises of a novel human macrophage-selective CC chemokine receptor that has been designated CCR5. The sequence was deduced from an isolated DNA clone (see Abr7620). An Ala127Leu variant (see WA38810 of CCR5 was also identified. The susceptibility of human macrophages to HIV infection depends on cell surface expression of CD4 protein coupled cell surface molecules. The susceptibility of figure in coupled cell surface molecules. It plays an essential role in the membrane fusion step of infection by some HIV isolates. The establishment of stable, non-human cell lines and transgenic mammals having cells that coexpress human CD4 and CCR5 provides valuable tools for research of HIV infection. Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding agents capable of blocking membrane fusion between HIV and target cells represent potential anti-HIV therapeutics for macrophage tropic strains
                                                                                                                                                                                                                                                                                                                                                                                                                            CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion between HIV and a target cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                             Berger EA, Alkhatib G, Murphy PM;
261. .276
/note= "extracellular loop-3 (Claim 19)"
7. .300
/label= VII
/note= "transmembrane domain"
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                                                                                                                                                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 68; Fig 1C; 70pp; English.
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/note= "
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Broder CC, Kennedy PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIV-1 co-receptor CCR5
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Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT76920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy;
                                                                                                                                                                                                28-MAY-1997;
                                                                                                                                                                                                                                     28-MAY-1996;
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                                                                                                                  W09745543-A2
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Domain
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Gaps

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An antibody for the treatment or prevention of HIV-infection comprises a gpl20 portion which binds to DC-SIGN or is exposed upon gpl20 binding of DC-SIGN due to concomitant conformational change.

Disclosure; Page 118-119; 131pp; English

Geijtenbeek T;

Van Kooyk Y,

Kwon D,

Littman DR,

WPI; 2001-602565/68.

28-FEB-2001; 2001WO-US006322. 02-MAR-2000; 2000US-00517605. (UYNY ) UNIV NEW YORK STATE. (UTN1-) UNIV NIJWEGEN.

Homo sapiens. WO200164752-A2

07-SEP-2001

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The present sequence represents a human G-protein chemokine receptor designated HDGNR10. HDGNR10 polynucleotides are useful in methods of screening to compounds which bind to and either: (1) activate the HDGNR10 polypeprides causing stimulation of haematopoiesis, wound healing, coagulation, and angiogenesis; treatment of solid tumours, chronic infections, leukaemia, T-cell mediated autoimmune diseases, parasitic infections, psoriasis, and to stimulate growth factor activity, or (2) inhibit activation of the HDGNR10 polypeptides which is useful for preventing and/or treating allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation, histamine and immunoglobulin B-mediated allergic reactions, prostaglandin-independent fever, bone marrow failure, silicosis, sarcoidosis, rheumatoid arthritis shock and hyper-eosinophilia syndrome. The polynucleotides are also useful for diagnostic assays for detecting the polypeptides and for detecting an altered level of the soluble form of the receptor polypeptides. The polynucleotides are also useful for in vittor purposes related to mutations in the polynucleotides are also useful for in vittor purposes related to going the polynucleotides. The polynucleotides are also useful for in vittor purposes related to scientific research, synthesis of DNA and manufacture of DNA vectors
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C-type lectin; ICAM3; HIV entry; T cell; macrophage; HIV infection; CCR5.
                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acid encoding human G-protein chemokine receptor useful for diagnostic assays, scientific research and screening for compounds which bind to and activate or inhibit activation of the receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
diagnosis; haematopoiesis; wound healing; coagulation; angiogenesis;
               tumour, infection; leukaemia; psoriasis; allergy;
T-cell mediated autoimmune disease; atherogenesis; anaphylaxis;
inflammation; allergic reaction; silicosis; sarcoidosis;
rheumatoid arthritis; hyper-eosinophilia syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 1; 22pp; English
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nes 18; Conservative
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                                                                                                                                                                                                                                                                                 Li Y, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 352 AA;
                                                                                                                                                                                       06-JUN-1995;
                                                                                                                                                                                                                     06-JUN-1995;
                                                                                                                         US6025154-A.
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The specification describes an antibody which is specific for an antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN or is exposed upon gp120 binding of DC-SIGN due to concomitant conformational change. DC-SIGN is a receptor that is specifically expressed on dendritic cells and facilitates infection of T lymphocytes with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin. DC-SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes) with high affinity. The antibody of the invention inhibits the trans enhancement of HIV entry into a T cell or macrophage facilitated by dendritic cells. The antibody is useful to treat or prevent HIV infection. The present sequence represents a human CGS protein, which is a translocation promoting agent that interacts with CD4. This receptor functions in HIV-1 entry into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV; human immunodeficiency virus; antimicrobial; vascdllator; vulnerary; vytostatic; immunosuppressive; noctropic; neuroprotective; gene therapy; neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative collitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                              Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 96; DB 4; Length 35
100.0%; Pred. No. 8.9e-07;
iive 0; Mismatches 0; Indels

    .36
    /label= Extracellular domain

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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                            Sequence 352 AA;
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Domain
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Extracellular\_loop\_1

Extracellular\_loop\_2

Intracellular loop 3

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// Note- --- 59 ... / Jabel= Intracellular_loop_1 68 ... 88 / Jabel= Transmembrane_domain / Note= "Segment 2"
7. .305
label= Transmembrane_domain
                                                                    label= Transmembrane_domain
note= "Segment 3"
                                                                                          .96. .223
|Tabel= Transmembrane_domain
                                                                                                                                              36. .260
|abel= Transmembrane_domain
note= "Segment 6"
                                                                                                                                                              61. .274 _
label= Extracellular_loop_3
         17. .58
|| Transmembrane_domain
                                                                                    label= Intracellular loop 2
                    note= "Segment 1"
                                                                                                    note= "Segment 4"
                                                                                                                                note= "Segment 5
                                                                                                         167. .195
/label= Ex
                                                                                                                                    224. .235
/label= In
                                                    19. .102
|label= E
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                                                                                                                                                                                                                                                                         Rosen CA, Roschke V,
                                                                                                                                                                                                                                                                                    WPI; 2001-488966/53.
N-PSDB; AAD13282.
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The invention relates to human G-protein chemokine receptor (CCR5) HDGNR10 polypeptides and polymucleotides. CCR5 HDGNR10 antibodies are useful for treating, preventing or ameliocating a disease or disorder associated with inflammation, defective or aberrant chemotaxis of immune cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's sarcomal or defective or aberrant T-cell antigen presenting cell interaction. The disease or disorder may also be an infectious disease (e.g. a viral infection such as an early stage HIV infection, a cytomegalovirus infection, or a poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The disease or disorder may be associated with aberrant CCR5 expression, lack
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197. .305
| Transmembrane_domain
| Inote= "Segment 7"
                                                                                                                                                                         /label= Intracellular domain
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09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
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of CCR5 function, aberrant CCRS ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein is used as a food additive or preservative to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA, protein, antibodies, agonists and antagonists are also useful in the diagnosis, trearment and prevention of cancer (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract, liver, lung, urogenital); immune disorders (Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's lisease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular disorders (Mpocardial ischaemias) and wound healing. The present sequence is human CCR5 HDGNR10 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  solated nucleic acid encoding a human G-protein chemokine receptor (CCRS) HDGNR10 polypeptide, useful for preventing or treating autoimmune liseases e.g. rheumatoid arthritis, hyperproliferative disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation, HIV; human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; cytostatic; immunosuppressive; notropic, neuroprotective; gene therapy; neurodegenerative disorder; Kaposi's sarcoma, autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.
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09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
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N-PSDB; AAD13299.
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                                                                                                                                                                                                                                                                            Sequence 352 AA;
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cassociated with inflammation, defective or aberrant chemotaxis of immune cells, HIV infection (Such as Pneumocystis carinii pneumonia or Kaposi's aracoma) or defective or abermant T-cell antigen presenting cell interaction. The disease or disorder may also be an infectious disease (e.g. a viral infection, such as an early stage HIV infection, a cytomegalovirus infection, or a poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The disease or disorder may be associated with aberrant CCRS expression, lack of CCRS function. aberrant CCRS ligand expression, or lack of CCRS ligand function. CCRS HOCKNIO procein is used as a food additive or preservative to increase or decrease storage capabilities. CCRS HDGNRIO DNA, protein, antibodies, agonists and antagonists are also useful in the diagnosis, treatment and prevention of cancer (breast, ovary, adrenal angonists, treatment and prevention of cancer (breast, ovary, adrenal used bone, bone marrow, gastrointestinal tract, liver, lung, crops.) the continuum disorders (Addison's disease, allergies, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular disorders (myocardial isohaemias) and wound healing. The present sequence is human CCRS HDGNRIO protein
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Sequence 352 AA;

Gaps ö 100.0%; Score 96; DB 4; Length 352; 100.0%; Pred. No. 8.9e-07; 0; Indels Mismatches , 0 1 SOYOFWKNFOTLKIVILG 18 Conservative Local Similarity les 18; Conserv Query Match Matches

185 SQYQFWKNFQTLKIVILG 202

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Ş AAG80111 standard; protein; 352 AAG801: 

AAG80111;

(first entry) 17-JAN-2002

Human CCR5 protein.

Chemokine, tumour diagnosis, colorectal, prostatic, organ rejection, inflammation; autoimmune disease, metastasis, bronchial asthma, lupus, chronic bowel inflammation; rheumatoid arthritis; cytostatic; antinflammatory; antiasthmatic; immunosuppressive; dermatological; antirheumatic; antiarthritic.

Homo sapiens

WO200172830-A2.

04-OCT-2001.

02-APR-2001; 2001WO-EP003708.

31-MAR-2000; 2000DE-01016013.

(IPFP-) IPF PHARM GMBH. (FORS/) FORSSMANN U.

Forssmann W, Adermann K,

WPI; 2001-626256/72.

Diagnostic agent containing two or more receptor-specific ligands, useful for detecring tumors, inflammation etc., also therapeutic use of ligand inhibitors.

Spodsberg N;

Heitland A,

Disclosure, Page 10; 26pp; German.

at least in This invention describes a novel diagnostic agent (A) comprising two different ligands (I) for receptors (II) that are implicated

or prostatic), organ rejection, inflammation and autoimmune diseases.
Also inhibitors of (I) are used therapeutically against tumors (and their metastases), inflammation (particularly bronchial asthma or chronic bowel inflammation), or autoimmune diseases (Theumatcoid arthritis or lupus), where the (cardio) vascular, lymphatic, respiratory, nervous, digestive, endocrine, motor or urogenital systems or skin are affected, and bone marrow diseases. The products of the invention are chemokine derivatives which have cytostatic, antiinflammatory, antiasthmatic. Chemokines act on specific tumor and inflammatory calls through a conscellation of chemokine receptors (CR), which control migration and prollferation of these cells. AAG80045 AAAG80128 represent human chemokine (A) are used for the diagnosis of tumors (especially colorectal fragments used to illustrate the method of the invention 88888888888888888888

Sequence 352 AA;

Gaps ; 0 Length 352; 0; Indels 100.0%; Score 96; DB 4; I 100.0%; Pred. No. 8.9e-07; iive 0; Mismatches 0; Local Similarity 100. Les 18; Conservative Query Match Best Loca Matches

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RESULT 13 AAE0432

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AAE04321 standard; protein; 352 AA

AAE04321;

(first entry) 04-SEP-2001

Human; transformed mammalian cell; CD4; reporter gene; translocation; human immuno deficiency virus; HIV; long terminal repeat; LTR; therapy; chemokine receptor; CKR; cellular dysfunction; HIV infection; cofactor; CC-CKR-5; envelope glycoprotein; anti-HIV. Human chemokine receptor (CKR), CC-CKR-5 related protein #2.

Homo gapiens

US6258527-B1 

10-JUL-2001.

97US-00861105 21-MAY-1997;

96US-0017157P. 96US-0020043P. 97US-00858660. 20-MAY-1996;

19-JUN-1996;

(AARO-) AARON DIAMOND AIDS RES CENT. (UYNY ) UNIV NEW YORK STATE.

Liu R;

Ellmeier W, Landau NR,

Deng H,

Littman DR,

WPI; 2001-417127/44.

N-PSDB; AAD08577

mammalian cell (I) that contains a CD4 gene, reporter gene for identification of drugs and antibodies for treatment of Transformed and HIV LTR

Disclosure; Col 47-50; 37pp; English.

The present invention relates to a transformed mammalian cell that contains a gene encoding CD4, a construct encoding a reporter gene under the regulation of an human immuno deficiency virus (HIV) long terminal repeat (LTR) and that has been transduced with a vector encoding a human chemokine receptor (CKR) where the CD4 and the CKR are present on the call surface of transformed mammalian cell. The invention is useful for

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AAE07039 standard; protein; 352 AA.
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identifying drugs or antibodies that interfere with the translocation of HIV into transformed mammalian cell or for identifying a human chemokine receptor that facilitates the infection of a particular HIV strain into the transformed mammalian cell. Compounds identified can be used to tract cellular dysfunction and to prevent or combat HIV infection. The present Sequence is a human chemokine receptor (CKR), CC-CKR-5 related protein. CC-CKR-5 is the principal cofactor for entry mediated by the envelope glycoproteins of primary macrophage-tropic strains of HIV-1
                                                                                                                                                                                                                                                                                                                      Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV; human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; cytostatic; immunosuppressive; noctropic; neuroprotective; gene therapy; neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative collitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia.
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                                                                                                                       100.0%; Score 96; DB 4; I 100.0%; Pred. No. 8.9e-07;
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/label= Transmembrane_domain
/note= "Segment 3"
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/label= Transmembrane_domain
/note= "Segment 5"
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/label= Transmembrane_domain
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/label= Intracellular_loop_3
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/label= Extracellular_domain
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/label= Transmembrane_domain
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| label= Intracellular_loop_1
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/label= T
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/label= 7
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The present sequence is human G-protein chemokine receptor (CCRS) HDGNR10 protein. CCRS HDGNR10 cDNA is included in ATCC Deposit No: 97183. CCRS HDGNR10 antibodies are useful for treating, preventing or amaliorating a disease or disorder associated with inflammation, defective or aberrant chemotaxis of immune cells, HTV infection (such as Pneumocystis carini presenting cell interaction. The disease or disorder may also be an infectious disease (e.g. a viral infection such as an early stage HIV infection, a cytomegalovirus infection, or a poxvirus infection, an autofunue disease (e.g. rheumatoid arthritis) or a neurodegenerative continum disease or disorder may be associated with aberrant CCRS disorder. The disease or disorder may be associated with aberrant CCRS carpression, lack of CCRS function. CCRS HDGNR10 protein is used as a food additive or preservative to increase or decrease storage capabilities. CCRS HDGNR10 DNA are useful for chromosome identification and in gene conternation or carbon are also useful in the diagnosis, treatment and prevention of cancer (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract, cutori, diabetes mellitus, continum abemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, continum and unitiple sclerosis, rheumatoid arthritis and ulcerative continum is candiovascular disorders (myocardial ischaemias) and wound continue then also designed to continue the diagnostic removed arthritis and ulcerative continue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated nucleic acid encoding a human G-protein chemokine receptor (CCRS) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders.
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/label= Intracellular_domain
                                         261. .274
/label= Extracellular_loop_3
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/label= Transmembrane_domain
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'note= "Segment 6"
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09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
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Matches 18; Conservat
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AAE07039;

16-OCT-2001 · (first entry)

Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.

human immunodeficiency virus; antimicrobial; vasodilator; valnerary; cytostatic; immunosuppressive; nootropic; neuroprotective; gene therapy; neurodegenerative disorder; Kaposis sarcoma; autoimmune disease; rhemmatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative colitis; Crobn's disease; wound healing; cardiovascular disorder; myocardial ischaemia. Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;

Homo sapiens.

WO200158915-A2

16-AUG-2001,

09-FEB-2001; 2001WO-US004152.

09-FEB-2000; 2000US-0181258P. 09-MAR-2000; 2000US-0187999P. 22-SEP-2000; 2000US-0234336P.

(HUMA-) HUMAN GENOME SCI INC

Li Y, Ruben SM; Roschke V, Rosen CA,

WPI; 2001-488965/53. N-PSDB; AAD13198.

Isolated nucleic acid encoding a human G-protein chemokine receptor (CCRS) HOGNRIO polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders

Example 40; Page 486-487; 495pp; English.

The present sequence is human d-protein chemokine receptor (CCR5) HDGNR10

C protein. CCR5 HDGNR10 antibodies are useful for treating, preventing or
ameliotating a disease or disorder associated with inflammation,
defective or aberrant chemotaxis of immune cells, HTV infection (such as
C decrive or aberrant chemotaxis of immune cells, HTV infection (such as
CC derrant T-cell antigen presenting cell interaction. The disease or
C disorder may also be an infectious disease (e.g. a viral infection such
cs an early stage HIV infection, a dytemegalovirus infection, or a
CC disorder may also be an infection, a dytemegalovirus infection, or a
CC disorder may also be an infection, a disease or decrease
CC a neurodegenerative disorder. The disease or disorder may be associated
CC with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5
CC ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein
CC is used as a food additive or preservative to increase or decrease
CC storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome
CC identification and in gene therapy. CCR5 HDGNR10 DNA, protein,
CC antibodies, agonists and antagonists are also useful in the diagnosis,
CC treatment and prevention of cancer (breast, ovary, adrenal gland, bone,
CC bone marrow, gastrointestinal tract, liver, lung, urogenital); immune
CC disorders (Addison's disease, allergies, autoimmune haemolytic anaemia,
CC disorders (Malbaches mallitus, CCPA) is disease, multiple
CC disorders (myocardial ischaemias) and wound healing

Sequence 352 AA;

; 0 Query Match 100.0%; Score 96; DB 4; Length 352; Best Local Similarity 100.0%; Pred. No. 8.9e-07; Matches 18; Conservative 0; Mismatches 0; Indels ; 0

1 SQYQFWKNFQTLKIVILG 18

185 SQYQFWKNFQTLKIVILG 202

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RESULT 16 AAB46858

AAB46858 standard; protein; 352 AA

AAB46858;

(first entry) (revised) 02-AUG-2001 04-MAY-2001 16-AUG-2001

Human HDGNR10 protein.

HDGNR10; human; G-protein chemokine receptor; antiinflammatory; imminosuppressive; imminosuppressive; cytostatic; antiparasitic; antialregic; immunosuppressive; cytostatic; antiparasitic; antipsoriatic; antirheumatic; antiarthritic; vasotropic; gene therapy; haematopolesis; wound healing; coagulation; anapidogenesis; solid tumour; infection; leukemia; growth factor activity; T-cell mediated autoimmune disease; psoriasis; allergy; atherogenesis; anaphylaxis; malignancy; inflammation; histamine; IgE; silicosis; shock; prostaglandin-independent fever; bone marrow failure; sarcoidosis; hyper-eosinophilic syndrome; vulnerary.

Homo sapiens.

US2001000241-A1.

12-APR-2001.

29-NOV-2000; 2000US-00725285

95US-00466343. 98US-00195662. 99US-00339912. 06-JUN-1995; 18-NOV-1998;

25-JUN-1999;

(LIYY/) LI Y. (RUBE/) RUBEN S M.

Li Y, Ruben SM;

WPI; 2001-226317/23. N-PSDB; AAF26390.

New human G-protein chemokine receptor polypeptides and polynucleotides, useful for identifying (ant)agonists to the G-protein chemokine receptor

Claim 1a; Page 15; 22pp; English.

This invention describes a novel receptor polypeptide (1) selected from (1) a fully defined 329 amino acid sequence (II) fully disclosed in the epecification; and (ii) a polypeptide encoded by the DNA contained in a plasmid, and fragments, analogs and derivatives of the polypeptide. The products of the invention have antiinflammatory, immunomodulatory, antiporate, antiallergic, immunosuppressive, vulnerary, orfosteric, antiporate, antiporate, antiantinematic, antianthic and vasotropic activity and can be used for gene therapy. The G-protein chemokine activity and can be used for gene therapy. The G-protein chemokine activity and can be used for gene therapy. The G-protein chemokine activity and can be used for gene therapy. The G-protein chemokine also be used for stimulating of uncourse, chronic infections, leukemia, T-cell mediated autoimmune diseases, paraditic infections, psoriasis, and stimulating growth factor activity. HDGNRIO is useful for treating allergic reactions, prostaglandin-independent fever, bone marrow failure, estimulating syndrome. (N.B. This record was resubmitted to correct errors in the keyword formatting)

Sequence 352 AA;

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This sequence represents the human CCRS protein sequence. The invention relates to a method for determining whether an agent is capable of modulating the interaction of chemotractic chemokine receptor 5 (CCR5) with gp120, comprising incubating the agent with CCRS and gp120 and determining whether the agent modulates the interaction, where gp120 is associated with CDR, and where the interaction is a low affinity binding. The method is used to identify an agent capable of modulating the interaction of CCRS with gp120. An agent identified by the method is used to prepare a pharmaceutical composition for the treatment of a disease or condition associated with CCRS and gp120 interaction, to treat a subject with a disease or condition associated with CCRS and gp120 interaction, and for preparing a pharmaceutical for treating human immunodeficiency virus (HIV). It can also be treat anti-inflammatory diseases. The method is commercially useful, amenable to high throughput screening, and elects interaction of gp120 with cells expressing only CCR5.
                                                                                                                                                                                                                                                                                                                                                                                                           Determining if an agent can modulate CCR5-gp120 interaction, comprises incubating the agent with CCR5 and gp120 and determining if the agent modulates the interaction.
                                       Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5; human immunodeficiency virus; anti-inflammatory disease; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 96; DB 4; Length 352; 100.0%; Pred. No. 8.9e-07; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                   12-JAN-2000; 2000GB-0000659.
12-JAN-2000; 2000GB-0000661.
12-JAN-2000; 2000GB-0000663.
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                                                                                                                                                                                       03-JAN-2001; 2001EP-00300020
             Human CCRS protein sequence
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Best Local Similarity 10v...
Best Local Similarity 10v...
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                                                                                                                                                                                                                                                                                   (PFIZ ) PFIZER LTD (PFIZ ) PFIZER INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying agonists of G protein-coupled receptors (GPCRs) for use in disease treatment, comprises contacting candidate compounds with versions of GPCRs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to G protein-coupled receptors (GPCRs) for which the endogenous ligand has been identified. Non-endogenous constitutively activated versions of known GPCRs are used in the invention for the direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists. Such agonists are useful as therappeutic agents for diseases or disorders associated with GPCRs. The present sequence is a non-endogenous version of a known human GPCR
                                             Gaps
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                                                                                                                                                                                                                                                                                                                    Human, G protein-coupled receptor; GPCR; non-endogenous; mutant; constitutively activated GPCR; agonist; disease.
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             100.0%; Score 96; DB 4; Length 352; 100.0%; Pred. No. 8.9e-07; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                       Non-endogenous human GPCR protein, SEQ ID NO: 477
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                                                                            ABB56342 standard; protein; 352
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                                                                                                                                                                                                                                                          (first entry)
                 Query Match 100.
Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lehmann-Bruinsma K,
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N-PSDB; ABI97978.
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                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
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  Gaps
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                                                                                                                                                                                                                  AAB82948 standard; protein; 352 AA.
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us-10-084-813-13.rag

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The present sequence is that of human HIV-1 co-receptor CCR5. Amino acids 2-18 in the N-terminal region of CCR5 comprise an HIV-1 gpl20-binding 2-18 in the N-terminal region of CCR5 comprise an HIV-1 gpl20-binding 2 HIV-1 gpl20. Post-translational sulfation of the tyrosine residues in the HIV-1 gpl20. Post-translational sulfation of the tyrosine residues in the CCR5 N-terminal is required for gpl20 binding and may critically modulate the susceptibility of target cells to HIV-1 infection in vivo. The invention provides claimed sulfated peptides (see AAB8294) that are based on the CCR5 N-terminal region and which are effective for inhibiting HIV-1 binding to CCR5. These optides are used in claimed methods of inhibiting HIV infection of CD4+ cells, of preventing CD4+ cells from becoming infected with HIV, of tracating a subject whose CD4+ cells are infected with HIV, and of identifying an agent which inhibits binding of a CCR5 ligand to a CCR5 receptor. The methods may be carried cout in a subject, especially a human, infected (therapeutic method), not infected with HIV (prophylactic method), or in a subject who is not infected with, but has been exposed to, HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel compounds comprising specific amino acids within CCR5 (HIV 1 coreceptor) amino terminal domain including negatively charged and two sulfated tyrosine residues is useful for treating HIV infection in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Length 352;
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100.0%; Score 96, DB 4; I
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0;
                                            2. .18 //note= "binds to HIV-1 gp120"
                                                                                                                                                                                                                                                                                                                 (PROG-) PROGENICS PHARM INC. (AARO-) AARON DIAMOND AIDS RES CENT.
                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 30; 163pp; English.
                                                                                                                                                                                                                              29-FEB-2000; 2000US-018567P.
19-MAY-2000; 2000US-0205839P.
07-FEB-2001; 2001US-0267231P.
                                                                                                                                                                                     28-FEB-2001; 2001WO-US006699.
                                                                                                                                                                                                                                                                                                                                                                                                                        2001-611273/70.
                                                                                                                                                                                                                                                                                                                                                                                Dragic T, Olson WC;
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                                                                                                  WO200164710-A2
                    Key
Binding-site
                                                                                                                                               07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        humans.
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New nucleic acid encoding an antibody specific for the G-protein chemokine receptor CCR5, useful for treatment and diagnosis of e.g.

Claim 61; Fig 1; 180pp; English.

inflammation.

Li Y, Ruben SM;

Rosen CA, Roschke V, WPI; 2002-434754/46.

N-PSDB; ABK51853.

09-FEB-2000; 2000US-0181258P. 09-MAR-2000; 2000US-0187999P. 22-SEP-2000; 2000US-0234336P. 09-FEB-2001; 2001US-00779879.

US2002048786-A1

25-APR-2002

Homo sapiens.

(ROSE/) ROSEN C A. (ROSC/) ROSCHKE V. (LIYY/) LI Y. (RUBE/) RUBEN S M.

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The present invention relates to the isolation of a novel human G-protein chemokine receptor (CCR5) designated HDGNR10, and polynucleotide sequences encoding it. The invention also describes antibodies that bind human G-protein chemokine receptor (CCR5) HDGNR10 and polynucleotide chuman G-protein chemokine receptor (CCR5) HDGNR10 and polynucleotide sequences encoding the antibodies. The antibodies are useful for treating or preventing inflammation, defective or aberrant chemotaxis of immune cells and T-cell/antigen-presenting cell interactions, infections and autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral infections despecially early-scage human immune deficiency virus (HIV), cytomegalovirus or pox virus infections, Kapoes sarcoma, or conditions associated with aberrant or deficient expression of the CCR5 receptor or its ligands. The antibodies are also useful to determine CCR5 expression, e.g. for diagnosis, prognosis and monitoring of cancer and other cyproricitic cent chemokine receptor, and in the treatment of a wide range of diseases such as infectious diseases (e.g. influenza), neurological diseases (e.g. combinant receptor, and in the treatment of a wide range of diseases such as infectious diseases (e.g. influenza), neurological diseases (e.g. HDGNR10 #1).
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Best Local Similarity 100.
Matches 18; Conservative
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Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; immune cell chemotaxis; autoimmune disease; rheumatoid arthritis; neurodeceneation; viral infection; Kaposi sarcoma; cancer; hyperproliferative disease; neurological disease; receptor.

Human G-protein chemokine receptor (CCR5) HDGNR10 #1.

(first entry)

13-AUG-2002

AAU97150;

AAU97150 standard; protein; 352 AA.

1 SOYOFWKNFOTLKIVILG 18

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human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome; drug screening; identification; variant.
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                                                                                                      Misc-difference
                                                                                                                                           WO200171346-A2
                                          Homo sapiens
                                                                                                                                                                    27-SEP-2001
                                                                                                                                                                                                                                                                                                                                  Westor JJ,
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AAM52828
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                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to the isolation of a novel human G-protein chemokine receptor (CCRS) designated HDGNR10, and polymucleotide sequences encoding it. The invention also describes antibodies that bind human G-protein chemokine receptor (CCRS) HDGNR10 and polymucleotide sequences encoding the antibodies. The artibodies are useful for treating sequences encoding the antibodies. The artibodies are useful for treating cells and T-cell/antigen-presenting cell interactions, infections and autoimmune diseases, rheumatoid arthritis, neurodegameration, viral infections (especially early-stage human immune deficiency virus (HIV), cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions associated with aberrant or deficient expression of the CCRS receptor or its ligands. The antibodies are also useful to determine CCRS exceptor or its ligands. The antibodies are also useful to determine CCRS exceptor or its ligands. The diseases The polymucleotide sequences encoding human crombinant receptor, and in the treatment of a wide range of diseases such a infectious diseases (e.g. intluenza), neurological diseases (e.g. present sequence represents human G-protein chemokine receptor (CRS) HDGNR10 can be used to produce the present sequence represents human G-protein chemokine receptor. (CRS) Edecative diseases (e.g. cancer)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                          New nucleic acid encoding an antibody specific for the G-protein chemokine receptor CCRS, useful for treatment and diagnosis of e.g.
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     hyperproliferative disease; neurological disease; receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 165-166; 180pp; English
                                                                                                                                                                                                                                              Ruben SM;
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                                                                                                                               09-FEB-2000; 2000US-0181258P.
09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
                                                                                                                                                                                                                                              Li Y,
                                                                                                        09-FEB-2001; 2001US-00779879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human CCR5 Gln 55 variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18; Conservative
                                                                                                                                                                                                                                                Rosen CA, Roschke V,
                                                                                                                                                                                                                                                                      WPI; 2002-434754/46.
N-PSDB; ABK51870.
                                                                                                                                                                                 (ROSE/) ROSEN C A.
(ROSC/) ROSCHKE V.
(LIYY/) LI Y.
(RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 352 AA;
                                                          US2002048786-A1
                                   Homo sapiens,
                                                                                                                                                                                                                                                                                                                                   inflammation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HDGNR10 #2
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The invention relates to a method for identifying a binding compound for chemokine receptor 5 (CCR5). The method involves screening a library of ctest molecules (particularly peptides) with immobilised CCR5, and then identifying those molecules which bind. The invention also relates to identifying those molecules identified using the method of the invention. CC cRE-binding molecules identified using the method of the invention of transfer vector encoding tagged CCR5, a computer-aided methods for transfer vector encoding tagged CCR5, a computer-aided methods for a computer aided furug screening assay that utilises the three-dimensional structure of CCR5. Compounds identified using the methods of the invention are useful for treating or preventing HJV (human computer aided furug screening assay that utilises the three-dimensional structure of CCR5. Compounds identified using the methods of the invention are useful for treating or preventing HJV (human computer and patient. The methods of the invention may also be used to identify agonists or antagonists of the interaction of CCR5. The present screening and the interaction of CCR5. The present sequence represents a naturally or a binding motif for CCR5. The present sequence represents a naturally a leucine, at position 55 there is a glutamine, rather than a leucine, at position 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying CC chemokine receptor 5 binding compound for treating AIDS, comprises binding a molecule from library to a molecule having binding property corresponding to CCR5 and identifying bound molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                      note= "Glu replaces wild-type Leu; encoded by CTG'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tan Hehir CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                         /note= "Encoded by AGC"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM52828 standard; protein; 352 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   See RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2000; 2000US-0190946P.
21-MAR-2000; 2000US-0190996P.
21-MAR-2000; 2000US-0191299P.
20-MAR-2001; 2001US-00813613.
20-MAR-2001; 2001US-00813653.
                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-2001; 2001WO-US009155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONS-) CONSENSUS PHARM INC.
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wilson CJ,
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                                         Misc-difference 55
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haematopolesis; wound healing; coagulation; angiogenesis; solid tumour; chronic infection; leukaemia; T-cell mediated autoimmune disease; parasitic infection; pooriasis; growth factor activity; allergy; atherogenesis; anaphylaxis; malignancy; inflammation; histamine; immunoglobulin E; IgE-mediated allergic reaction; sarcoidosis; prostaglandin-independent fever; bone marrow failure; shock; rheumatoid arthritis; hyper-eosinophilic syndrome; cytostatic; immunosuppressive; antiparastic; antiparastic; antiparastic; antiparastic; antiparatory; antirheumatory; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human G-protein chemokine receptor polypeptide useful for identifying modulators for stimulating hematopoiesis, wound healing, leukemia, for treating allergy, rheumatoid arthritis, shock and as
   Human; G-protein chemokine receptor; HDGNR10; CCR5 receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; Fig 1; 22pp; English.
                                                                                                                                                                   antipyretic; receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-690494/74.
N-PSDB; ABS54272.
                                                                                                                                                                                                                                                                                                                                                           (LIYY/) LI Y.
(RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                           Li Y, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           leukemia, for tr
research agents.
                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                             25-JUN-1999;
                                                                                                                                                                                                                                                                                                                            06-JUN-1995;
                                                                                                                                                                                                                                                              25-JUL-2002
   The invention relates to a method for identifying a binding compound for CC chemokine receptor 5 (CCR5). The method involves screening a library of test molecules (particularly peptides) with immobilised CCR5, and then identifying those molecules which bind. The invention also relates to corps. Prinding those molecules identified using the method of the invention, methods for identifying consensus motified to CCR5-binding peptides, a transfer vector encoding tagged CCR5, a computer-aided methods for determining the relative binding affinity of a test molecule to CCR5 and a computer aided drug screening assay that utilises the three-dimensional structure of CCR5. Compounds identified using the methods of the invention are useful for treating or preventing HIV (human immunodeficiency virus) infection or AIDS (acquired immunodeficiency syndrome) in a patient. The methods of the invention may also be used to identify agonists or antagonists of the interaction of CCR5 with its natural ligand, and to determine a binding motif for CCR5. The present sequence represents human CCR5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                    CCR5; CC chemokine receptor 5; human; HIV infection; human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome; drug screening; identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying CC chemokine receptor 5 binding compound for treating AIDS, comprises binding a molecule from library to a molecule having binding property corresponding to CCR5 and identifying bound molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 96; DB 5; I 100.0%; Pred. No. 8.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                          Tan Hehir CA;
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             Human CC chemokine receptor 5 (CCR5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Fig 4A; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                          See RH,
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21-MAR-2000; 2000US-019129P.
20-MAR-2001; 2001US-00813448.
20-MAR-2001; 2001US-00813651.
20-MAR-2001; 2001US-00813653.
                                                                                                                                                                                                          21-MAR-2001; 2001WO-US009155
                                                                                                                                                                                                                                                                                                                                                         (CONS-) CONSENSUS PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      Nestor JJ, Wilson CJ,
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N-PSDB; ABA02317.
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                                                                                                                                           WO200171346-A2
                                                                                                              Homo sapiens.
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99US-00339912. 95US-00466343,

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The present invention relates to the isolation of human G-protein chemokine receptor, HDGNR10 (CCR5 receptor), and the polynucleotide sequences sequence encoding it. HDGNR10 polypeptide and polynucleotide sequences rate or useful for diagnosing a disease or a susceptibility to a disease rate or useful for diagnosing a disease or susceptibility to a disease care or useful for identifying modulators for stimulating haematopolesis, wound healing, coagulation, angiogenesis, to treat solid tumours, chronic infections, psoriasis, or for stimulating growth factor activity. The sequences are also useful for preventing and/or treating allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation, histamine and immunoglobulin E (IgE)-mediated allergic reactions, prostaglandin-independent fever, bone marrow failure, sarcoidosis, rheumatoid arthritis, shock and hypercosning philic syndrome. Polynucleotide sequences encoding HDGNR10 can be used in gene therapy to treat conditions related to underexpression of HDGNR10. The present sequence represents human G-protein chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 96; DB 5; Length 352; 100.0%; Pred. No. 8.9e-07; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor, HDGNR10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 352 AA;
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Matches
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Human G-protein chemokine receptor, HDGNR10.

(first entry)

03-DEC-2002

12225232 22252323

ABG70597;

ABG70597 standard; protein; 352 AA

RESULT 24 ABG70597

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Human immunoglobulin variable heavy domain #1
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histicoycosis; chemotaxis; infectious disease; autoimmune disease; Addison's disease; dermatitis; rheumatoid arthritis; allergy; neurodegenerative discorder; viral infection; poxvirus infection; HIV; human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma; pneumocystis carnii infection; cardiovascular disorder; atherosclerosis; Immunoglobulin, variable heavy chain, variable light chain, human, G-protein chemokine receptor, CCR5, HDGNR10, cancer, inflammation, immunologic deficiency syndrome, blood protein disorder, nephritis, ataxia telangiectasia, endotoxin lethality, inflammatory bowel disease, lymphocytopenia

Homo sapiens.

WO200264612-A2

22-AUG-2002

08-FEB-2002; 2002WO-US003634

09-FEB-2001; 2001US-00779880

09-FEB-2001, 2001WO-US004153. 12-UUN-2001, 2001US-0297257P. 08-AUG-2001, 2001US-0310457P. 12-OCT-2001, 2001US-034447P. 21-DEC-2001, 2001US-0341725P.

(HUMA-) HUMAN GENOME SCI INC.

Roschke V, Rosen CA, Ruben SM;

WPI; 2002-643455/69. N-PSDB; ABS68606 New human G-protein Chemokine Receptor gene (HDGNR10) useful for treating, preventing, ameliorating or monitoring diseases or disorders associated with aberrant expression of HDGNR10 e.g. cancer.

Example 55; Fig 4; 562pp; English.

The invention describes an isolated polynucleotide encoding a first antibody at least 95-100% identical to a second antibody consisting of antibody at least 95-100% identical to a second antibody consisting of antibody at least 95-100% identical to a second antibody consisting of a variable heavy (VH) or variable light (VL) domain of thee antibody expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8, XF37.68.1885, XF37.68.2851, XF27.28.36412. XF27.788.1885, XF27.28.2610, XF27.28.36412. XF27.28.36711 or XF27.78.18185. The antibody is useful treating, preventing, ameliorating, prognosing or monitoring cancers or other diseases or disorders e.g. immunologic deficiency inflammation associated disorders such as endotoxin lethality, nephritis and inflammatory bowel disease, conditions associated with an increase in certain haematopoietic cells such as histocytosis, defective or aberrant chemotaxis of immune cells or T-cell antigen presenting cell interaction, an infectious disease, an autoimmune disease such as Addison's disease, dermatitis and rheumatoid arthritis, allergies, a neurodegenerative or addisorder, a viral infection e.g. HIV infection, Cytomegalovirus or poxvirus infection, a Phenocytis carnii infection, Kaposi's sarcoma, cardiovascular disorder associated with aberrant expression of novel human Green content of human immunoglobulin sequence associated with the antibodies sequence of humagainst HDGNR10

Sequence 352 AA;

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                                                 Gaps
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0
Query Match 100.0%; Score 96; DB 5; Length 352; Best Local Similarity 100.0%; Pred. No. 8.9e-07; Matches 18; Conservative 0; Mismatches 0; Indels
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185 SQYQFWKNFQTLKIVILG 202

RESULT 26 ABG92880

ABG92880 standard; protein; 352 AA.

ABG92880;

19-NOV-2002 (first entry)

Human G-protein chemokine receptor (CCR5) HDGNR10 #1.

Immunoglobulin; variable heavy chain; variable light chain; human; G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation; immunologic deficiency syndrome; blood protein disorder; nephritis; ataxia telangiectasia; endocrain lethality; inflammatory bowel disease; histiocytosis; chemotaxis; infectious disease; autoimmune disease; hadison's disease; dermatitis; nemmatory bowel disease; neurodegenerative disorder; viral infection; poxvirus infection; human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma; pheumocystis carnii infection; cardiovascular disorder; atherosclerosis; lymphocytopenia

Homo sapiens.

WO200264612-A2.

22-AUG-2002.

08-FEB-2002; 2002WO-US003634. 

09-FEB-2001; 2001US-00779880 09-FEB-2001; 2001WO-US004153. 12-UUN-2001; 2001US-0297257P. 08-AUG-2001; 2001US-0328447P. 12-OCT-2001; 2001US-0328447P.

(HUMA-) HUMAN GENOME SCI INC.

21-DEC-2001; 2001US-0341725P.

Roschke V, Rosen CA, Ruben SM;

WPI; 2002-643455/69. N-PSDB; ABS68553. New human G-protein Chemokine Receptor gene (HDGNR10) useful for treating, preventing, ameliorating or monitoring diseases or disorders associated with aberrant expression of HDGNR10 e.g. cancer.

Disclosure, Fig 1A-B; 562pp; English.

The invention describes an isolated polymucleotide encoding a first attibody at least 95-100% identical to a second antibody consisting of an extibody at least 95-100% identical to a second antibody consisting of amino acid sequence comprising at least one, two or three CDR regions of a variable heavy (VH) or variable light (VL) domain of the antibody consisting of XF3.512. XF21.086, XF22.362. XF22.362. XF22.362. XF22.362. XF22.362. XF22.362. XF22.362. XF22.362. XF22.362. XF22.263. XF22.263.

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us-10-084-813-13.rag

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Gaps

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Indels

Pred. No. 8.9e-07; Mismatches 0;

100.08; Pr.

Best Local Similarity 100. Matches 18; Conservative

185 SQYQFWKNFQTLKIVILG 202

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18

1 SQYQFWKNFQTLKIVILG

AAE25811 standard; protein; 352 AA

RESULT 28 AAE25811

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The invention relates to human G-protein chemokine receptor (CCR5), antibodies are used for the treatment or prevention of inflammation, defective or aberrant chemotaxis of immune cells or T cell antigen. presenting cell interaction, viral infections (specifically human immune deficiency (including its early stages), cytomegalo or pox viruses), autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis carinii infection, Kaposi's sarcoma or any condition associated with detection, diagnosis, prognosis aroman or any condition associated with detection, diagnosis, prognosis and monitoring of cancers or other hyperproliferative diseases. The present sequence is human G-protein chemokine receptor (CCR5), HDGNR10 DNA
protein chemokine receptor (CCRS) HDGNR10. This is an amino acid sequence of Human G-protein chemokine receptor (CCRS) HDGNR10 #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding antibodies to the human CCR5 receptor HDGNR10, useful for treatment, prevention and diagnosis of e.g. cancer, also related antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                    Human; G-protein chemokine receptor; CCR5; HDGNR10 protein; cancer;
inflammation; viral infection; autoimmune disease; neurodegeneration;
rheumatoid archirits; Pneumocystis carinii infection; Kaposi's sarcoma;
hyperproliferative disease; receptor.
                                                                                                                    Gaps
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                                                                                    Length 352;
                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                    Human G-protein chemokine receptor (CCR5), HDGNR10 #1
                                                                               Query Match
100.0%; Score 96; DB 5; I
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                 AAE25808 standard; protein; 352 AA
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09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
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                                                                                                                                                                                                                                                                                                                                   (first entry)
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(ROSC/) ROSCHKE V.
(LIYY/) LI Y.
(RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-499674/53.
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                                                 Sequence 352 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to human G-protein chemokine receptor (CCR5), HDGNR10 proteins and nucleic acid molecules encoding such proteins. CCR5 antibodies are used for the treatment or prevention of inflammation, defective or aberrant chemotaxis of immune cells or T cell antigenpresenting cell interaction, viral infections (specifically human immune deficiency (including its early stages), cytomegalo or pox viruses), autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis carinii infection, Raposi's sarcoma or any condition associated with detection, diagnosis, prognosis and monitoring of cancers or other hyperproliferative diseases. The present sequence is human G-protein chemokine receptor (CCR5), HDGNR10 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding antibodies to the human CCR5 receptor HDGNR10, useful for treatment, prevention and diagnosis of e.g. cancer, also
                                                                                                                Human; G-protein chemokine receptor; CCR5; HDGNR10 protein; cancer; inflammation; viral infection; autoimmune disease; neurodegeneration; rheumatoid arbhritis; Pneumocystis carinii infection; Kaposi's sarcoma; hyperproliferative disease; receptor.
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                                                                                     Human G-protein chemokine receptor (CCRS), HDGNR10 #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 96; DB 5; 1
100.0%; Pred. No. 8.9e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 170; 186pp; English.
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09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
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                                                       (first entry)
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Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         related antibodies.
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ROSCHKE V.
LI Y.
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RUBEN S M.
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                                                                                                                                                                                                                       US2002061834-A1.
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                                                                                                                                                                                            Homo sapiens.
                                                       24-FEB-2003
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                          AAE25811;
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(LIYY/) I
(RUBE/) F
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Length 352;

2: В

100.0%; Score 96;

Tue Sep 28 15:49:56 2004

The invention relates to a novel human 7-transmembrane receptor, HDGNR10, which has been identified as a G-protein chemokine receptor. The dPCR HDGNR10 polypeptide can be expressed by standard recombinant methodology. Compounds that activate or inhibit the receptor polypeptide, optionally expressed from DNA in gene therapy vectors, are used to treat diseases that requires (a) activation of the receptor (e.g. stimulation of hasmatopoiseis, treatment of solid tumours, T-cell mediated autoimmune diseases, parasitic infections, psoriasis etc.); or (b) inhibition of the receptor (e.g. allergy, inflammation, rheumatoid arthritis, silicosis etc.). The present sequence represents the human HDGNR10 receptor New polynucleotide encoding a human G protein chemokine receptor HDGNR10, useful e.g. for treating tumors. Claim 7; Fig 1; 22pp; English. 

Sequence 352 AA;

Gaps . 0 100.0%; Score 96; DB 5; Length 352; 100.0%; Pred. No. 8.9e-07; ive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 18; Conservative

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SOYOFWKNFOTLKIVILG 202 SOYOFWKNFOTLKIVILG 18

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ABB08343 standard; protein; 352 ABB08343; ABB08343 LID ABB083 XX ABB083 XX ABB083 XX ABB083 XX DT 18-JUD XX DB Human

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Human chemokine (C-C motif) receptor 5 polypeptide. (first entry) 18-JUN-2002

Human chemokine C-C motif receptor 5; CCR5; haplotype pair; isogene; single nucleotide polymorphism; SNP; human immunodeficiency virus 1; HIV-1 infection; acquired immunodeficiency syndrome; AIDS; antiviral; genotype; polymorphic variant; transgenic; drug screening; gene therapy; chromosome 3p21 

Homo sapiens

Location/Qualifiers 'label= Leu, /label= Arg, /label= Phe, Key Misc-difference Misc-difference Misc-difference

WO200177125-A2

18-OCT-2001

04-APR-2001; 2001WO-US010708.

05-APR-2000; 2000US-0194361P.

(GENA-) GENAISSANCE PHARM INC.

Choi JY, Kliem SE,

N-PSDB; ABA97318, ABA97319. WPI; 2002-041282/05

New haplotypes of the human chemokine (C-C motif) receptor 5 gene, useful to diagnose and treat diseases associated with its abnormal expression or function, including human immunodeficiency virus-1 infection.

Claim 29; Fig 3; 61pp; English

The present sequence is that of a polypeptide encoded by the human chemokine (C-C motif) receptor 5 (CCR5) gene of the invention (see Chemokine, (C-C motif) receptor 5 (CCR5) gene of the invention (see Gene of an individual by determining if the individual has one of the CCR5 haplotypes or haplotype pairs fully defined in the specification.

CCR5 haplotypes or haplotype pairs fully defined in the specification.

CC CR5 haplotypes or haplotype pairs fully defined in the specification.

CC cr6 specification also describes an isogene defined in the specification of the servence CCR5 gene sequence and comprises an isogene defined by a haplotype described control of the specification and its sencoded polypeptide. The methods of the invention are useful to diagnose and develop treatment for diseases associated with abnormal expression or function of the gene. The CCR5 isogenes and the screened compounds are useful for treating human immunodeficiency virus (HrV)-1 infection and the progression to acquired immunodeficiency syndrome (AIDS). The invention has antiviral applications. The specification has antiviral and individual; predicting a haplotype pair for the CCR5 gene of an individual; predicting an association between a trait and a haplotype or composition comprising a genoryping oligonuclectide for detecting a CCR5 polymorphism; a recombinant non-human organism transformed with CCR5 conformed with CCR5 protein encoded by the variant sequence; an isolated antibody specific for the CCR5 polymorphism; and a method for correcting drugs targeting the CCR5 polymorphism; sequence of an isolated antibody specific for the CCR5 polymorphism; sequence of an isolated antibody specific for the CCR5 polymorphism; sequence of an isolated antibody specific for the CCR5 polymorphism; sequence of the CCR5 polymorphism; sequ

Sequence 352 AA;

Gaps ; 0 100.0%; Score 96; DB 5; Length 352; 100.0%; Pred. No. 8.9e-07; ive 0; Mismatches 0; Indels Local Similarity 100. les 18; Conservative Query Match Best Loc Matches

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185 SQYQFWKNFQTLKIVILG 202 SOYOFWKNFQTLKIVILG 18 н

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RESULT 31

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ABG75540 standard; protein; 352 AA.
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ABG75540;

(first entry) 16-APR-2003

Human G-protein chemokine receptor, HDGNR10, protein.

Human; receptor; G-protein chemokine receptor; 7-transmembrane receptor; HIGMN10; signal transduction; gene therapy; haematopoissis; wound healing; coagulation; angiogenesis; tumour; chronic infection; leukaemia; T-cell mediated auto-inmune disease; parasitic infection; psoriasis; growth factor; allergy; atherogenesis; anaphylaxis; malignancy; inflammation; histamine; Igg-mediated, prostaglandin-independent fever; bone marrow failure; silicosis; sarcoidosis; rheumatoid arthritis; shock; hyper-eosinophilic syndrome.

Homo sapiens.

US2002132269-A1

19-SEP-2002

11-FEB-2000; 2000US-00502783

95US-00466343 06-JUN-1995; (HUMA-) HUMAN GENOME SCI INC.

Li Y, Ruben SM;

WPI; 2003-208944/20. N-PSDB; ABX10635.

Novel human G-protein chemokine receptor polypeptide useful for diagnostic purposes and for identifying modulators of the polypeptide useful for treating leukemia, autoimmune diseases, psoriasis and allergic reactions. 

Claim 7; Fig 1; 22pp; English.

The invention discloses a G-protein chemokine receptor (sometimes referred to as a 7-transmembrane receptor) polypeptide, HDGNR10, and the polymynolacidectide encoding it. G-protein chemokine receptors are involved in signal transduction pathways. The polymucleotide and polypeptide can be compounds which activate or inhibit activation of the compounds are useful for treating a patient having need to activate or inhibit a G-protein chemokine receptor. The compound is administered by providing to the patient DNA encoding the agonist or catagonist and expressing them in vivo (gene therapy). The compound is disease or susceptibility to a disease related to an under-expression of the protein, for chromosome identification or as immunogens for producing attribodies. Agonists are useful in stimulating haematopoiesis, wound healing, coagulation, angiogenesis, to treat solid tumours, chronic infections, psoriasis and to stimulate growth factor activity.

Antagonists are useful in the prevention and steatement of allergy, antagonists are useful in the prevention and treatment of allergy, thistamine and ISB-mediated allergic reactions, prostaglandin-independent fewer, bone marrow failure, silicosis, sarcoidosis, rheumatoid arthritis, content of an dhypaption, and hypaptic sarcoidosis, rheumatoid arthritis, content of an hypothemial silicosis, sarcoidosis, rheumatoid arthritis, content of an hypothemial silicosis, sarcoidosis, rheumatoid arthritis, content of the provention and secution in the prevention content of the provention and coute inflammation, content of allergy contents and hypertonesis.

Sequence 352 AA;

Gaps ö Length 352; 100.0%; Score 96; DB 6; Length 35z 100.0%; Pred. No. 8.9e-07; Query Match 100. Best Local Similarity 100. Matches 18; Conservative

1 SQYQFWKNFQTLKIVILG

Ź ABR58602 standard; protein; 352

ABR58602

RESULT 32

ABR58602;

Human cancer related protein SEQ ID NO:259.

(first entry)

09-JUL-2003

Human, cancer; diagnosis; screening; modulator; leukaemia; ischaemia; heart disease; atherosclerosis; endometriosis.

Homo sapiens.

WO2003025138-A2

27-MAR-2003

17-SEP-2002; 2002WO-US029560.

20-SEP-2001; 2001US-0323887P. 13-NOV-2001; 2001US-0350666P. 08-FEB-2002; 2002US-0355145P. 17-SEP-2001; 

12-APR-2002; 2002US-0372246P.

(EOSB-) EOS BIOTECHNOLOGY INC.

Wilson KE; Gish KC, Hevezi PA, Mack DH, Aziz N, Zlotnik Mfar D,

2003-354600/33. N-PSDB; ACC72740. New genes that are up-regulated or down-regulated in cancers, useful a markers for diagnosing e.g. cancer, ischemia or heart diseases, or as therapeutic targets for screening drugs for treating these diseases.

Claim 12; Page 745; 767pp; English.

The present invention describes an isolated nucleic acid molecule, which comprises the sequence of any of the genes that are up-regulated or down-regulated in specific cancers (e.g. about 1013 genes up-regulated in culture lamphocytic leukemia). ACC72641 to ABC702860 represent cancer related gene nucleotide sequences which encode the proteins given in ABC80502. Also described: (1) determining the presence or apsence of a pathological cell in aptient; (2) an expression vector comprising a nucleic acid molecule described above; (3) a host cell comprising the vector; (4) an isolated polypeptide, which is encoded by the nucleic acid; (5) an antibody that specifically binds the polypeptide of (4); (6) specifically targeting a compound to a pathological cell in a patient by administering to the patient the antibody above; and (7) a patient by administering to the patient the antibody above; and (7) a patient by administering to the patient, the nucleic acid is useful for diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow, bladder, brain, breast, cervix, colon/rectum, kidney, lung, overy, colon/rectum, kidney, lung, overy, colon/rectum, kidney, lung, overy, and colon and uterus), wounds, ischaemia, heart diseases, and endometriosis. The nucleic acid is also useful in a pathology, as a pathology, and uterus), wounds, ischaemia, heart diseases, and and endometriosis. The nucleic acid is also useful in a pathology, pathology, pathology, and uterus), wounds, ischaemia, heart diseases, and endometriosis. The nucleic acid is also useful in pathologies

Sequence 352 AA;

ö 100.0%; Score 96; DB 6; Length 352; 100.0%; Pred. No. 8.9e-07; 0; Indels Mismatches 0; Query Match Best Local Similarity 100. Matches 18; Conservative

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Gaps

1 SOYOFWKNFOTLKIVILG 18

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Human G-protein chemokine receptor (HDGNR10) polypeptide Human; G-protein chemokine receptor; receptor; HDGNR10;

7-transmembrane receptor

US2003023044-A1.

10-JAN-2003

Homo sapiens

95US-00466343. 98US-00195662. 99US-00339912.

06-JUN-1995; 18-NOV-1998; 25-JUN-1999;

(HUMA-) HUMAN GENOME SCI INC.

WPI; 2003-456307/43. N-PSDB; ACA61721.

Li Y, Ruben SM;

03-SEP-2002; 2002US-00232686.

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The invention relates to a method for treating an urological disorder which comprises assaying the ability of the compound to modulate 313, 313, 5464, 188717 or 3354 mucleic acid expression or polypeptide activity. The method is useful for identifying a compound for treating urological disorder comprising urinary incontinence e.g., overactive/oversensitive bladder, overflow uninary incontinence, stress urinary incontinence caused by defunction of the bladder, urethra or central/peripheral nervous system, prostatitis, benign prostatic hyperplasia, prostate cancer or kidney disorders. It is also used in gene therapy. The present sequence is human C-C chemokine receptor type 5 (CCRS, 333) protein. This sequence is used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                          Human; urological disorder; stress urinary incontinence; prostate cancer; benign prostatic hyperplasia; overactive bladder; oversensitive bladder; overflow urinary incontinence; gene therapy; nephrotropic; prostatitis; kidney disorder; C-C chemokine receptor type 5; CCR5; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying a compound, capable of treating urological disorder e.g., benign prostatic hyperplasia, by assaying the ability of the compound to modulate 313, 333, 5464, 188717 or 33524 nucleic acid expression or polypeptide activity.
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100.0%; Pred. No. 8.9e-07;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                           Human C-C chemokine receptor type 5 (333) protein.
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ID ABU61654 standard; protein; 352 AA.
AC ABU61654;
XX
OR-AUG-2003 (first entry)
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                                                                                                         AAO29514 standard; protein; 352 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-NOV-2001; 2001US-0344552P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                           27-AUG-2003 (first entry)
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N-PSDB; AAL59912.
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                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                          AA029514;
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                    185
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The invention relates to a method of producing an antibody, involving immunising an animal with a human G-protein chemokine receptor (HDGNR10) polypeptide (also referred to as a human 7-transmembrane receptor) and recovering an antibody which binds the polypeptide. The method is useful for producing an antibody which binds specifically to the human G-protein chemokine receptor polypeptide. This sequence represents the HDGNR10 polypeptide of the invention
                                                                                                                                                                                                                                                                                                                        Producing an antibody, involves immunizing an animal with a polypeptide or with a polypeptide encoded by the human G-protein chemokine receptor clone in ATCC 97183, and recovering the antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, chemokine receptor, CCR5, viral infection, surface protein,
respiratory virus infection, respiratory syncytial virus infection,
RSV infection, bronchiolitis, bronchitis, pneumonia, asthma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of human chemokine receptor CCR5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP97728 standard; protein; 352 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SOYOFWKNPOTLKIVILG 18
                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 1; 23pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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Best Local Similarity 100.7
Matches 18, Conservative
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ABP97728
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10-AUG-2001; 2001US-0311088P.

G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atheroselerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma; The present sequence represents human chemokine receptor CCR5. The specification describes a method for modulating viral infection of a cell. the method comprises modulating a binding interaction between a cell chemokine-receptor and a surface protein of the virus. The provise is that the cell chemokine-receptor is not CX3CR1 and that the virus is not HIV. The method is useful for treating or preventing respiratory virus infection in vertebrates, more particularly respiratory syncytial virus (RSV) infections, and related diseases, e.g. bronchiolitis, Modulating viral infection of a cell, for treating or preventing respiratory virus infections, bronchitis, pneumonia or asthma, by modulating a binding interaction between a cell chemokine-receptor 100.0%; Score 96; DB 6; Length 352; 100.0%; Pred. No. 8.9e-07; ive 0; Mismatches 0; Indels Human C-C chemokine receptor 5 protein SEQ ID NO:352. Disclosure; Page 96-98; 120pp; English. ABP81933 standard; protein; 352 AA. SQYQFWKNFQTLKIVILG 202 SOYOFWKNFOTLKIVILG 18 surface protein of the virus. (first entry) (TOPI-) TOPIGEN PHARM INC. Query Match Best Local Similarity 100.' Zemzoumi K; WPI; 2003-256541/25. N-PSDB; ABZ68881. Sequence 352 AA; WO200261087-A2 Homo sapiens. 04-MAR-2003 08-AUG-2002 Renzi P, 185 ABP81933; ulcer. 원 ð

The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino caids. Also described: (I) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (i) an isolated antibody having high specificity and high affinity or anticly for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR. (I) can be useful for detecting an antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell regeneration-related diseases, growth-related diseases, cell regeneration-related diseases, growth-related diseases, cell corresponding GPCRs. The antigenic peptides for treating immune-related diseases, growth-related diseases, cell atherosclerosis, bacterial, fungal, protozoan or viral infections, atherosclerosis, bacterial, fungal, protozoan or viral infections, cesecoarthritis, osteoporosals, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, graft versus host disease, parkinson's disease, multiple sclerosis, pain, psoriasis, constitution, allergies, cancer, cardiomyopathy, chronic and acute circliammation, rehard disorders, rheumatoid arthritis, trauma, ulcers, or any other disorders in which GPCRs are involved. The antibodies may be used in immunoassays and immunoaisapness, ABP82523 to ABZ42869 encode GPCR proteins given in ABP81675 to ABZ42869 encode ceremonic and acute invention of the present invention ö Gaps .; 0 Length 352; 0; Indels 100.0%; Score 96; DB 6; L 100.0%; Pred. No. 8.9e-07; ive 0; Mismatches 0; 1 SQYQFWKNFQTLKIVILG 18 185 SQYQFWKNFQTLKIVILG Query Match
Best Local Similarity 100.
Matches 18; Conservative Sequence 352 AA; 셤 ઠે

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Gaps

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New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or

Disclosure, Fig 1; 523pp; English.

and a

autoimmune diseases.

N-PSDB; ABZ42781

ADC03341 standard; protein; 352 AA. Human chemokine receptor 88-C. (first entry) 18-DEC-2003

receptor; human; anti-HIV; virucide; HIV; SIV; 88-C; 88-2B; chemokine receptor; envelope protein; atherosclerosis; rheumatoid arthritis; tumour growth suppression; asthma; viral infection; AIDS; inflammatory condition.

95US-00575967. 96US-00661393. 96US-00771276. 26-MAR-2002; 2002US-00106623. US2002150888-A1. Homo sapiens. 20-DEC-1995; 07-JUN-1996; 20-DEC-1996; 17-0CT-2002. 

(LIFE-) LIFESPAN BIOSCIENCES INC

19-DEC-2000; 2000US-0257144P. 19-DEC-2001; 2001WO-US050107

Brown JP;

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WPI; 2003-046718/04 Burmer GC, Roush

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This protein sequence comprises an Ala127Leu variant of a novel human macrophage-selective CC chemokine receptor (see also AAW23835) that has been designated CCR5. The sequence was deduced from an isolated cDNA clone (see AAT76919). The conservative variation should not affect the activity of CCR5. The susceptibility of human macrophages to HIV activity of CCR5. The susceptibility of human macrophages to HIV activity of CCR5. The susceptibility of depends on call surface expression of CD4 and CCR5. CCR5 is a comper of the 7-transmembrane superfamily of G-protein coupled cell surface molecules. It plays an essential role in the membrane fusion step of infection by some HIV isolates. The establishment of stable, non-human CCR infection by some HIV isolates. The establishment of stable, non-human cCR provides valuable tools for research of HIV infection.

Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding agents capable of blocking membrane fusion between HIV and target cells represent potential anti-HIV therapeutics for macrophage tropic strains of HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prostaglandin; PG; E2EP3 receptor; E2EP2 receptor; CCR-5; human; chemokine receptor; ss2 adrenergic receptor; small G-protein rho; renal outer medullary potassium ion channel protein; ion-channel protein; lambda phage repressor protein; G-protein coupled receptor; bacteria; biochemical; vaccine; immunohistochemical; orphan receptor; HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion between HIV and a target cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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100.0%; Score 96; DB 2; Length 371;
Best Local Similarity 100.0%; Pred. No. 9.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berger EA, Alkhatib G, Murphy PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fusion protein containing human chemokine receptor CCR-5.
                                            /note= "transmembrane domain"
                                         note= "transmembrane domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Combadiere C, Feng Y,
Broder CC, Kennedy PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-032650/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAT76919
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                                                                                                                                                                                                                                                                                                                                          8-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to screening for a modulator of human immunodeficiency virus (SIV) or simian immunodeficiency virus (SIV) or simian immunodeficiency virus (SIV) infection, comprising contacting a first composition having an European of the Second composition having an HV or SIV envelope protein in the second composition having an HV or SIV envelope protein in the presence or absence of a compound. Also included are screening for a modulator of HIV infection, detecting HIV infection of cells (comprising contacting a cell that has been recombinantly modified to express at cast one of human chemokine receptors 86 and 88-28 with HIV, and detecting HIV infection in the cell) and inhibiting HIV infection of cells (comprising contacting cells with an antibody to at least one of numan chemokine receptors 88 and 88-28 with HIV, and detecting HV infection of the cell after the contacting step). The methods and compositions of the present invention are useful for the diagnosis and treatment of disorders associated with the aberrant expression or activity of 88C or 88-2B chemokine receptors, such as atherosolerosis, rheumatoid arthritis, tumour growth suppression, as the conditions. Also and other inflammatory conditions. The genes for human 88-C and 88-C an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                  Screening for a modulator of HIV and SIV infection utilizing polynucleotides that encode the 88C or 88-2B chemokine receptors, useful for diagnosing and treating disorders such as atherosclerosis, arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC chemokine receptor 5; CCR5; G-protein coupled receptor; human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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/label= IV
/note= "transmembrane domain"
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|label= III
|note= "transmembrane domain"
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                                                                                                  Raport CJ;
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                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 17-18; 29pp; English.
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/label= I
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                                                                                                  Gray PW, Schweickart VL,
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Best Local Similarity 100.
Matches 18, Conservative
(GRAY/) GRAY P W.
(SCHW/) SCHWEICKART V L.
(RAPO/) RAPORT C J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chemokine receptor 88-C.
                                                                                                                                                 WPI; 2003-182491/18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention provides isolated nucleic acid sequences that encode rabbit prostaglandin (PG) E2EP3 receptor, human PG E2EP2 receptor, rat renal outer chemokine receptor CRF-5, human se2 adranergic receptor, rat renal outer medullary potassium ion channel protein or human small G-protein rho, together with deduced protein sequences. Also provided is a method for the production of enkaryctic proteins by culturing bacteria transformed with vectors containing the above mucleic acid sequences or a nucleic acid (I) that comprises: (i) first sequence that encodes either a DNA-binding protein, or a lambda phage repressor protein, placed upstream of, and in frame with, (ii) a sequence encoding a protein, placed upstream of, and in frame with, (ii) a sequence encoding a protein, (I) are used for recombinant production of eukaryctic proteins, particularly membrane proteins groteins are useful for biochemical or structural studies; and the encoding a protein sin vaccines, and diagnostic and screening assays and as antigens for use in vaccines, and for raising antibodies that are useful can encode second completed and proteins are useful for proper or complete capence against the chemokine receptor CCR-5 can be used (when administered as antiserum or generated in vivo) to prevent complete complete capence or used (when administered as antiserum or generated in vivo) to prevent complete capence or capence capence or complete capence or capence capence or c
                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid constructs for high level expression of eukaryotic proteins in bacteria, for producing e.g. chemokine receptor CCR-5 for preventing HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 49-53; 81pp; English
                                                                                                                                                                                                                                                                                        Breyer RM, Ma L, Kennedy C;
                                                                                                                                                                                                        98US-0081989P.
                                                                                                                                                               99WO-US008214
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                                                                                                                                                                                                                                                                                                                              WPI; 1999-620416/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 439 AA;
                                           Homo sapiens.
                                                                                                                                                                 16-APR-1999;
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                                                                                 WO9953033-A1
                                                                                                                        21-OCT-1999
                     Synthetic.
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100.0%; Score 96; DB 2; Length 439; 100.0%; Pred. No. 1.1e-06; tive 0; Mismatches 0; Indels
Query Match 100.
Best Local Similarity 100.
Matches 18; Conservative
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AAW27125 standard; protein; 352 AA Macaque chemokine receptor 88C. (first entry) 14-DEC-1997 AAW27125; 40 RESULT 40 

Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour; asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy; diagnosis; leukocyte trafficking; G protein coupled receptor; ligand; modulator; antibody.

Macaca

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This polypeptide sequence comprises macaque chemokine receptor 88C, a G protein coupled receptor that is involved in leukocyte trafficking. Its amino sequence was deduced from a 88C DNA (AAR82163) isolated by PCR amplification. It shows 97% identity to human 88C (AAM27123). 88C receptors and their polypeptide fragments can be produced in transformed host cells. The receptors, peptides comprising one or more of the extracellular or intracellular domains, and anti-receptor antibodies can be used to modulate receptor activities, particularly ligand and G protein binding, and are potentially potentially useful in the treatment of atheroslerosis, rheumatoid arthritis, tumours, asthma, viral infection, AIDS, inflammatory conditions, pathological immune response, abnormal haematopoietic processes etc. A hybridoma that produces an antibody that specifically binds to macaque 88C is claimed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding chemokine receptors 88-2B and 88C - used modulate leukocyte trafficking, e.g. for treatment of inflammation, tumours, viral infections, auto-immune diseases, etc.
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Pred. No. 2.6e-06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                      Gray PW, Schweickart VL, Raport CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 36; Page 57-58; 65pp; English.
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94.4%; Pred
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N-PSDB; AAT85163.
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WO9722698-A2
                                                                                                                          20-DEC-1996;
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07-JUN-1996;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Sequence 13, Appl	Sequence 77, Appl	11,	Sequence 11, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 22, Appl	Sequence 2, Appli	Seguence 22, Appl	Sequence 15, Appl	Sequence 17, Appl
ID	US-10-084-813-13	US-10-084-813-77	US-10-661-798-11	US-10-612-791-11	US-09-938-719-11	US-09-939-226-11	US-09-938-703-11	US-09-725-285-2	US-09-759-841-2	US-09-779-879A-2	US-09-779-879A-22	US-09-779-880A-2	US-09-779-880A-22	US-09-813-653-15	US-09-813-653-17
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## ALIGNMENTS

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Publication No. US20030068615A1

Publication No. US20030068615A1

Publication No. US20030068615A1

GENERAL INRORMATION:

APPLICANT: SAXINGEN:

TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC

TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND METHODS OF USE

TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE

TITLE OF INVENTION: 218075

CURRENT APPLICATION NUMBER: US/10/084,813

CURRENT APPLICATION NUMBER: PCT/US00/23505

PRIOR FILING DATE: 2000-08-25

PRIOR FILING DATE: 1999-08-27

NUMBER OF SEQ ID NOS: 1242

SEQ ID NO 13

LENGTHENE: Patentin version 3.1

LENGTHENE:
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; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-13
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 18; Conserva
US-10-084-813-13
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RESULT 2 US-10-084-813-77 Sequence 77, Application US/10084813 Publication No. US20030068615A1

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APPLICANT: SAMON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOXINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,719
FILING DATE: 24-Mg-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 96; DB 16; Length 49; 100.0%; Pred. No. 7.9e-08;
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ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
                                                                                                                              GENERAL INFOGRATION:
APPLICANT: Samson, Michael
APPLICANT: Parmentier, Marc
APPLICANT: Parmentier, Marc
APPLICANT: Vassart, Gilbert
CORNENT: Vassart, Gilbert
FILE REFERENCE: 9409/2023E
CURRENT APPLICATION NUMBER: US/10/612,791
CURRENT FILING DATE: 2001-08-24
FRIOR APPLICATION NUMBER: 09/938,703
FRIOR FILING DATE: 2001-08-24
FRIOR FILING DATE: 2001-08-24
FRIOR FILING DATE: 1997-04-09
FRIOR FILING DATE: 1997-03-03
FRIOR APPLICATION NUMBER: 08/810,028
FRIOR FILING DATE: 1997-03-03
FRIOR FILING DATE: 1996-03-01
FRIOR FILING DATE: 1996-03-01
FRIOR FILING DATE: 1996-03-01
FRIOR RELING DATE: 1996-03-01
FRIOR RELING DATE: 1996-03-01
FRIOR FILING DATE: 1996-03-01
FRIOR SEQIONOS: 18
SOFTWARE: PATENTIN UNFERS: EP 96870102.9
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FILING DATE: 27-JULY-2000
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/09938719
Patent No. US20020106742A1
GENERAL INFORMATION:
                                                   Sequence 11, Application US/10612791 Publication No. US20040161739A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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ZIP: 92660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-612-791-11
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Best Local Similarity
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GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Sameon, Michael
APPLICANT: Sameon, Michael
APPLICANT: Parmentier, Marc
APPLICANT: Prederic, Libert
TITLE OF INVENTION: Screening Methods for Identifying Compounds which Decrease HIV En
TITLE OF INVENTION: A Cell
FILE REFERENCE: 9409/2023F
CURRENT PEDFLICATION NUMBER: US/10/661,798
CURRENT PEDFLICATION NUMBER: US/10/661,798
CURRENT FILING DATE: 2003-09-12
PRIOR FILING DATE: 2000-07-27
PRIOR FILING DATE: 2000-07-27
PRIOR FILING DATE: 1907-04-09
PRIOR FILING DATE: 1997-04-09
PRIOR FILING DATE: 1997-04-09
PRIOR PILING DATE: 1996-03-01
PRIOR PILING DATE: 1996-03-01
PRIOR PILING DATE: 1996-03-01
PRIOR FILING DATE: 1996-03-01
GENERAL INFORMATION:

APPLICANT: SAXINGER, CARL
TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
TITLE OF INVENTION: POLYPEPTIDES, COMPOSITIONS, AND METHODS OF USE
FILE REFERENCE: 218875
CURRENT APPLICATION NUMBER: US/10/084,813
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: PCT/US00/23505
PRIOR FILING DATE: 2000-08-25
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 1242
SOFTWARE: Patentin version 3.1
SEQ ID NO 77
LENGTH: 18
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100.0%; Pred. No. 7.9e-08;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 96; DB 14; Length 18; 100.0%; Pred, No. 3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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Publication No. US20040110127A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 18; Conservative
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Best Local Similarity 100.
Matches 18; Conservative
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CRGANISM: Homo sapiens
US-10-661-798-11
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US-09-938-703-11
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US-09-725-285-2
                         RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/09939226
| Patent No. US20020110805A1
| GENERAL INFORMATION:
| APPLICANT: SAMSON, MICHEL
| PARMENTIER, MARC
| VASSART, GILBERT
| LIBERT, FREDERICK
| TITLE OF INVENTION: ACTIVE RD INACTIVE CC-CHEMOKINES RECEPTOR
| AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                      Gaps
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MEDIUM TYPE: FLORDY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRINT APPLICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                        Query Match 100.0%; Score 96; DB 9; Length 54; Best Local Similarity 100.0%; Pred. No. 8.7e-08; Matches 18; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
             REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: «Unknown»
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTR: 54 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <UNKnown>
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
                                                                                                                                                                   TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-939-226-11
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APPLICATION WUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INPORMATION:
NAME: Altman, Daniel E
                                                                                                                                                                                                                                                                                                                                                                        SQYQFWKNFQTLKIVILG 26
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Best Local Similarity 100.
Matches 18; Conservative
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US-09-939-226-11
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SQYQFWKNFQTLKIVILG 26

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| Sequence 2, Application US/09725285
| Patent No. US2001000241A1
| GENERAL INFORMATION:
| APPLICANT: Li, Yi
| APPLICANT: Li, Yi
| APPLICANT: Ruben, Steven, M.
| TILE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10
| TILE OF INVENTION: (CCR5 Receptor)
| FILE REFERENCE: 1488.1150003
| FILE REFERENCE: 1488.1150003
| CURRENT APPLICATION NUMBER: US/09/725,285
| PRIOR APPLICATION NUMBER: 09/339,912
| PRIOR FILING DATE: 1999-06-25
| PRIOR FILING DATE: 1998-11-18
| PRIOR FILING DATE: 1998-11-18
| PRIOR FILING DATE: 1995-06-06
| NUMBER OF SEQ ID NOS: 9
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                                                                               APPLICANT: SAWSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOXINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
FLING DATE: 24-Aug-2001
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 54;
                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 96; DB 9; I
100.0%; Pred. No. 8.7e-08;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <UNKnown>
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION UNDER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
Sequence 11, Application US/09938703
Patent No. US20020110870A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
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STRANDEDNESS: single
                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 18; Conservative
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General No. US20020061834A1

| Sequence 2. Application US/09779880A
| Patent No. US20020061834A1
| GENERAL INFORMATION:
| APPLICANT: Rosen, Craig A. |
| APPLICANT: Rosen, Steven, M. |
| APPLICANT: Ruben, Steven, M. |
| FILE REFERENCE: 1488.115000C |
| FILIS REFERENCE: 1200-0.02-09 |
| PRIOR FILING DATE: 2000-03-09 |
| PRIOR FILING DATE: 2000-03-08 |
| PRIOR FILING DATE: 2000-03-09 |
| PRIOR FILING DATE: 2000-03-09 |
| PRIOR FILING DATE: 2000-03-09 |
| PRIOR FILING DATE: 2000-03-08 |
| PRIOR FILING DATE: 2000-03-09 |
| PR
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Sequence 22, Application US/09779879A

Patent No. US2002004886A1

GENERAL INFORMATION:

APPLICANT: Rosen, Craig A.

APPLICANT: Rosen, Steven, M.

APPLICANT: Li, Yi

CURRENT APPLICANTON: Human G-protein Chemokine Receptor (CCR5) HDGNR10

FILE REFERENCE: 1488.115000A

CURRENT APPLICATION NUMBER: US 60/181,258

PRIOR FILING DATE: 2000-03-09

PRIOR APPLICATION NUMBER: US 60/187,999

PRIOR FILING DATE: 2000-03-09

PRIOR APPLICATION NUMBER: US 60/234,336

PRIOR PRILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 58

SOFFWARE: Patentin version 3.0
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Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
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100.0%; Score 96; DB 9; I
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0;
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; CRGANIEM: Homo sapiens
US-09-779-879A-2
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; ORGANISM: Homo sapiens
US-09-779-879A-22
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US-09-779-879A-22
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LENGTH: 352
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APPLICANT: Roschke, Viktor
APPLICANT: Roschke, Viktor
APPLICANT: Roschke, Viktor
APPLICANT: Rusen, Steven, M.
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
FILE REFERENCE: 1468.115.00A
CURRENT FILING DATE: 2001-02-09
PRIOR FILING DATE: 2000-02-09
PRIOR FILING DATE: 2000-03-09
PRIOR PLING DATE: 2000-03-09
PRIOR PLING DATE: 2000-03-09
PRIOR PLING DATE: 2000-03-09
PRIOR PLING DATE: 2000-03-09
PRIOR FILING DATE: 2000-03-09
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100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                    ; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-725-285-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09759841

Sequence 2, Application US/09759841

Sequence 2, Application US/09759841

Sequence 2, Application US/09759841

Septicant No. US20010039026A1

APPLICANT: Rickett, Graham A

APPLICANT: Rickett, Graham A

APPLICANT: Dobbs, Susan

APPLICANT: Dobbs, Susan

TILLE OF INVENTION: Assay Method

FILE REFERENCE: PC10348APME

CURRENT FILING DATE: 2001-01-12

PRIOR FILING DATE: 2000-01-12

PRIOR APPLICATION NUMBER: GB 0000663.5

PRIOR PILING DATE: 2000-01-12

PRIOR PILING DATE: 2000-01-12

PRIOR FILING DATE: 2000-01-12

PRIOR FILING DATE: 2000-01-12

PRIOR FILING DATE: 2000-01-12

SPIOR APPLICATION NUMBER: GB 0000659.3

FROM APPLICANT OF SEQ ID NOS: 6

SEQ ID NOS: 6

FROM APPLICANT OF SEQ ID NO
                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence: Genomic
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                        PatentIn version 3.0
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US-09-759-841-2
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US-09-779-879A-2
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                                                                     SEQ ID NO 2
LENGTH: 352
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US-09-759-841-2
                        SOFTWARE:
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Sequence 17, Application US/09813653

Sequence 17, Application US/09813653

Patent NO. US2020064770A1

GENERAL INFORMATION:

APPLICANT: Wilson, Carol

APPLICANT: See, Raymond

APPLICANT: See, Raymond

APPLICANT: Tan Hehir, Christina

TILB OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds

FILE REFERENCE: CNS-005

CURRENT FILING DATE: 2001-03-20

FRICK APPLICATION NUMBER: US 60/190,946

PRIOR FILING DATE: 2000-03-21

PRIOR SEQ ID NOS: 44

SOFTWARE: Patentin Version 3.0

SEQ DD NOS: 14

SOFTWARE: Patentin Version 3.0

SEQ DD NOS: 17
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; GENERAL INFORMATION:
; APPLICANT: Obson, William
; TILLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILLE REFERENCE: 2048/64010/DFW/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LEMSTH: 352
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     ; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-653-15
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Cordanism: Homo sapiens
US-09-813-653-17
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CRGANISM: human
US-09-796-202-1
                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-09-813-653-17
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US-09-796-202-1
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Patent No. US2002064770A1
GENERAL INFORMATION:
APPLICANT: Watson, Carol
APPLICANT: Walson, Carol
APPLICANT: Walson, Carol
APPLICANT: Walson, Carol
APPLICANT: Walson, Carol
APPLICANT: See, Raymond
APPLICANT: See, Raymond
APPLICANT: Tan Hehir, Christina
TITLE OF INVENTION: Binding Compounds
FILE REPERENCE: CNS-005
CURRENT APPLICATION NUMBER: US/09/813,653
CURRENT FILING DATE: 2001-03-20
PRIOR FILING DATE: 2000-03-21
PRIOR PAPLICATION NUMBER: US 60/190,96
PRIOR APPLICATION NUMBER: US 60/190,96
PRIOR APPLICATION NUMBER: US 60/191,299
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
SPRIOR PILING DATE: 2000-03-21
SUPTWARE: Patentin version 3.0
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| Sequence 22, Application US/09779880A
| Patent No. US20020066834A1
| Patent No. US20020066834A1
| APPLICANT: Rosen, Craig A.
| APPLICANT: Rosenke, Viktor
| APPLICANT: Ruben, Steven, M.
| APPLICANT: I. 1488.118000C
| TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
| TITLE REFERENCE: 1488.118000C
| TITLE REFERENCE: 1488.118000C
| CURRENT APPLICATION NUMBER: US 60/181,258
| PRIOR FILING DATE: 2000-02-09
| PRIOR FILING DATE: 2000-03-09
| PRIOR APPLICATION NUMBER: US 60/187,999
| PRIOR APPLICATION NUMBER: US 60/234,336
| PRIOR PILING DATE: 2000-09-22
| NUMBER OF SEQ ID NOS: 58
| SEQ ID NO 22
| LENGTH: 352
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                                                                                                                                                          Query Match
100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.Se-07;
Matches 18; Conservative 0; Mismatches 0; Indels
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; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-880A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
GORGANISM: Homo sapiens
US-09-779-880A-22
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US-09-813-653-15
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US-09-939-226-5
) Sequence 5, Application US/09939226
) Sequence 5, Application US/09939226
) Patent No. US20020110805A1
) GENERAL INFORMATION:
CARACTARIAN MACC
) VASSART, GILBERT

VASSART, GILBERT

LIBER, FREDERICK

TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR

AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                     APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Floppy disk
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,719
FILING DATE: 24-Aug-2001
CLASSIFTCATION: «Unknown»
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                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSES: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 96; DB 9; 1
100.0%; Pred. No. 5.5e-07;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Altman, Daniel E
REGIGTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <UNKnown>
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
PRIOR APPLICATION WUBER: 09/626,939
PILING DATE: 27-UULY-2000
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: Interaction MOLECTLE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 5: US-09-938-719-5
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COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
               Sequence 5, Application US/09938719
Patent No. US20020106742A1
GENERAL INFORMATION:
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Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
US-09-938-719-5
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Sequence 2, Application US/09339912A;
Patent No. US20020099176A1
GENERAL INFORMATION:
APPLICANT: Li, Yi,
APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: (CCR5 Receptor)
CURRENT APPLICATION NUMBER: US/09/339,912A
CURRENT PILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 352
                                                                                                                                                 Sequence 2, Application US/09195662A
Sequence 2, Application US/09195662A
Patent No. US20020076745A1
GENERAL INFORMATION:
APPLICANT: Li, Yi
APPLICANT: Li, NEGRO, Steven, M.
TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGNRIO (CCRS Receptor)
CURRENT APPLICATION NUMBER: US/09/195,662A
CURRENT FILING DATE: 1998-11-18
PRIOR PILING DATE: 1998-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 352
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100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 5.5e-07;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Deduced Amino Acid Sequence US-09-195-662A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Deduced Amino Acid Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence; Genomic FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence: Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 SOVOFWKNFOTLKIVILG 202
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                              185 SQYQFWKNFQTLKIVILG 202
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  1 SQYOFWKNFQTLKIVILG 18
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Matches 18; Conserv
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Gaps

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Query Match

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RESULT 19

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Gaps

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Query Match 100.0%; Score 96; DB 9; Length 352; Best Local Similarity 100.0%; Pred. No. 5.5e-07; Matches 18; Conservative 0; Mismatches 0; Indels
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US-09-938-703-5
                                                                                                                                                                                                                      185 SQYQFWKNFQTLKIVILG 202
                                                                                                                                                                                         1 SOYOFWKNFOTLKIVILG 18
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US-09-502-783A-2
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| Patent No. US20020110870A1
| GENERAL INFORMATION:
| APPLICANT: SAMSON, MICHEL
| PARMENTIER, MARC
| VASSART, GILBERT
| LIBERT, FREDERICK
| TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOXINES RECEPTOR
| TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: .....

ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DEADLE PC-DOS/MS-DOS
SOFFWARE: PATENTE PC-DOS/MS-DOS
SOFFWARE: PATENTE PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/9938,703
FILING DATE: 2001
CLASSIFICATION: ~UNKnown>
PRIOR APPLICATION: ~UNKnown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 34,115
REGISTRATION NUMBER: 34,115
REGISTRATION NUMBER: 34,115
REGISTRATION NUMBER: 34,115
REFERENCE/POCKET NUMBER: ~Unknown>
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acide
TYPE: amino acide
TYPE: amino acide
TYPE: protein
          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION: AURHORM:
PRIOR APPLICATION: DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-00-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGIGSTRATION NUMBER: 34,115
REGIGSTRATION NUMBER: 34,115
REGIGSTRATION NUMBER: «Unknown»
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTER/SILES:
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100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 352 amino acids TYPE: amino acid
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COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-939-226-5
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US-09-938-703-5
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Sequence 2, Application US/09502783A

Sequence 2, Application US/09502783A

Sequence 2, Application US/09502783A

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Li, Yi
APPLICANT: NUMBER: US/09/502,783A
TITLE OF INVENTION: HOGGRIO
FILE REFERENCE: 1488.115006
CURRENT APPLICATION NUMBER: US/09/502,783A
CURRENT PLING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DENG, HONGKUI
ELLANEIER, WILFRIED
LANDAU, NATHANIEL R.
LIU, RONG
TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
NAGROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esg.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RILING DATE: 11-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 96; DB 9; I
100.0%; Pred. No. 5.5e-07;
:ive 0; Mismatches 0;
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US-09-734-221A-14
i Sequence 14, Application US/09734221A
j Publication No. US20030096221A1
j GENERAL INPORMATION:
APPLICANT: LITTMAN, DAN R.
DENG, HONGKUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 SQYQFWKNFQTLKIVILG 202
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
US-09-502-783A-2
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APPLICANT: Littman, Dan R.
APPLICANT: Littman, Dan R.
APPLICANT: Exemples S.
APPLICANT: Town Kooyk, Tweete
APPLICANT: Van Kooyk, Tweete
APPLICANT: Geijtenbeck, Theo
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY
TITLE OF INVENTION: CELLS
FILE REFERENCE: 1049-1-017
CURRENT FILLING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US/09/517,605
PRIOR APPLICATION NUMBER: US/09/517,605
PRIOR FILLING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gray, Patrick W.

APPLICANT: Gray, Patrick W.
Schweickart, Vicky L.
Schweickart, Carol J.

TITLE OF INVENTION: Chemokine Receptor Materials and Methods
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 96; DB 12; Length 352; Best Local Similarity 100.0%; Pred. No. 5.5e-07; Matches 18; Conservative 0; Mismatches 0; Indels
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COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/106,623
FILING DATE: 26-Mar-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/771,276
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: No. US20020150888Aland, Greta E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33670
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/10106623 Publication No. US20020150888A1 GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 5
LENGTH: 352
TYPE: PRT
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Publication No. US20030204073A1

GENERAL INFORMATION:
APPLICANT: Lehmann-Bruinsma, Karin
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
TITLE OF INVENTION: NOWBER: US09/826,509
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 589
SOFTWARE: PatentIn Version 2.1
SEQ ID NO 477
LENGTH: 352
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100.0%; Score 96; DB 11; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
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                PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/666,020
APPLICATION NUMBER: US 08/227,319
FILING DATE: 19-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: JACKSON ESQ., David A.

REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-004 NZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) ORGANISM: Homo sapiens
) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-734-221A-14
                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 5, Application US/10151274
; Publication No. US20030064071A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 SQYQFWKNFQTLKIVILG 202
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; ORGANISM: Homo sapiens
US-09-826-509-477
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US-09-826-509-477
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US-10-151-274-5
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185 SQYQFWKNFQTLKIVILG 202

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; ORGANISM: Homo sapiens
US-10-067-800-2
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APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Li, Yi
TITLE OF INVENTION: Fuum G-Protein Chemokine Receptor (CCR5) HDGNR10
FILE REFERENCE: 1488.11500N
CURRENT PILING DATE: 10502-09-03
CURRENT APPLICATION NUMBER: 05/10/23,686
CURRENT APPLICATION NUMBER: 05/139,912
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-26
PRIOR FILING DATE: 1998-11-18
PRIOR FILING DATE: 1998-11-18
PRIOR FILING DATE: 1998-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
SOFTWARE: DATE OF THE O
                                                                                                                                                                                                                                                                                                                    Gaps
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US-10-086-814-1
; Sequence 1, Application US/10086814
; Fublication No. US20030092632A1
; GENERAL INFORMATION:
    APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William C.
; TITLE OF INVENTION: SULFATED CRS PEPTIDES FOR HIV-1 INFECTION
; FILE REFRENCE: 61010-AB-1
; CURRENT APPLICATION NUMBER: US/10/086,814
; CURRENT APPLICATION NUMBER: US/10/086,814
; CURRENT APPLICATION NUMBER: PATOM DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PATOM IN version 3.1
; SEQ ID NO 1
; LENGTH: 352
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Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                           Length 352;
NAME/KEY: misc_feature
OTHER INFORMATION: /= "88C amino acid sequence"
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0;
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; Publication No. US20030023044A1
; GENERAL INFORMATION:
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US-10-086-814-1
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ORGANISM: Homo sapiens
US-10-232-686-2
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US-10-106-623-2
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RESULT 29
US-10-067-800-2
; Sequence 2. Application US/10067800
; Publication No. US20030100058A1
; GENERAL INFORMATION:
; APPLICANT: Roselke, viktor
; APPLICANT: Roselke, viktor
; APPLICANT: Roselke, viktor
; APPLICANT: Roselke, Viktor
; TITE OF INVENTION: Human G-rotein Chemokine Receptor (CCR5) HDGNR10
; TITE OF INVENTION: Human G-rotein Chemokine Receptor
; CURRENT APPLICATION NUMBER: US/10/067,800
; CURRENT FILING DATE: 2001-02-08
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/297,257
; PRIOR APPLICATION NUMBER: 60/297,257
; PRIOR FILING DATE: 2001-06-12
; PRIOR PILING DATE: 2001-06-12
; PRIOR PILING DATE: 2001-06-08
; PRIOR PILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/328,447
; PRIOR APPLICATION NUMBER: 60/328,447
; PRIOR PILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; TANDER: DATE: 2001-12-21
; TANDER: DATE: 2001-12-21
; NUMBER: PATENTING DATE: 2001-12-21
; SEQ ID NO 2
; TANDER: DATE: 2001-12-21
; SEQ ID NO 2
; TANDER: DATE: 2001-12-21
; SEQ ID NO 2
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US-10-067-800-22
; Sequence 22, Application US/10067800
; Publication No. US2030100058A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craid A.
; APPLICANT: Rosen, Craid A.
; TILE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
; FILE REPRENCE: 1488.115001
; CURRENT APPLICATION NUMBER: US/10/067,800
; CURRENT APPLICATION NUMBER: PCT/US01/04153
; FRIOR APPLICATION NUMBER: 09/79,880
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-06-02
; PRIOR FILING DATE: 2001-06-03
; PRIOR FILING DATE: 2001-06-03
; PRIOR FILING DATE: 2001-10-12
; PRIOR FILING DATE: 2001-12-21
; TYPE: PRIOR FILING DATE: 2001-12-21
; TELE SACHWARE: PATENTIN VERSION 3.1
; SSOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Sequence 1, Application US/10072301
Publication No. US20030152913A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pauling, Michelle H.
APPLICANT: Zhu, Li
AITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNOBERJ
TITLE OF INVENTION: VIRUS
FILE REFERENCE: 25636-718
CURRENT FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin version 3.1
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Publication No. US20030162943A1
GENERAL INFORMATION:
TILL OF INVENTION:
NO. US20030162943A1el Molecules of the G Protein-Coupled NUMBER OF SEQUENCES: 56
CORRESPONDENCE - 56
CORRESPONDENCE ADDRESS:
STREET: 28 State Street
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                                                                                                                                                                       PEPTIDES FOR HIV-1 INFECTION
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100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                   Publication No. US20030139571A1
| Publication No. US20030139571A1
| GENERAL INFORMATION:
| APPLICANT: Dragic, Tatjana | APPLICANT: Dragic, Tatjana | APPLICANT: Olson, William | TITLE OF INVENTION: SULFATED CCRS PEPTIDES F | FILE EFFERENCE: 2048/61010-1/JFW/MAF/DJK | CURRENT APPLICATION NUMBER: US/10/323,314 | CURRENT FILING DATE: 2002-12-19 | NUMBER OF SEQ ID NOS: 17 | SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 SQYQFWKNFQTLKIVILG 202
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STATE: Massachusetts
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: human
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                                                                                                                                                                                                                                                                                                     SEQ ID NO 1
LENGTH: 352
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LENGTH: 352
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US-10-072-301-1
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Fortune 6, Application US/10290058A

Fublication No. US20030104455A1

GENERAL INFORMATION:
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Silos-Santiago, Inmaculada
TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Wethods and Compositions for Treating
TITLE OF INVENTION: WINDIA: US/10/290,058A

CURRENT APPLICATION NUMBER: 00/10/290,058A

CURRENT FILING DATE: 2002-11-07

PRIOR APPLICATION NUMBER: 60/344,552

PRIOR FILING DATE: 2001-11-07

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6
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100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                            Query Match 100.0%; Score 96; DB 14; Length 352; Best Local Similarity 100.0%; Pred. No. 5.5e-07; Matches 18; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                185 SQYQFWKNFQTLKIVILG 202
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Best Local Similarity 100.
Matches 18; Conservative
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CORGANISM: Homo sapiens
US-10-225-567A-352
; ORGANISM: Homo sapiens
US-10-067-800-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
; ORGANISM: Homo Sapien
US-10-290-058A-6
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i Sequence 22, Application US/10135839

publication No. US20030166024A1

j GENERAL INFORMATION:

APPLICANT: Rosen, Craig A.

APPLICANT: Rosen, Viktor

APPLICANT: Rosen, W.

TILE REFERENCE: 1488.11500A

TILE REFERENCE: 1488.11500A

CURRENT FILING DATE: 2002-05-01

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2000-03-09

PRIOR FILING DATE: 2000-03-09

PRIOR FILING DATE: 2000-03-09

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 58

SOFTWARE: Patentin version 3.0

SEQ ID NO 22

TAPP: DEN
                                 APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Steven, M.
APPLICANT: Li, Yi
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
FILE REPRENCE: 1488.11500A
CURRENT APPLICATION NUMBER: US/10/135,839
CURRENT FILING DATE: 2002-05-01
FRIOR PAPLICATION NUMBER: US 60/187,999
FRIOR PAPLICATION NUMBER: US 60/187,999
FRIOR PAPLICATION NUMBER: US 60/234,336
FRIOR APPLICATION NUMBER: US 60/234,336
FRIOR APPLICATION NUMBER: US 60/234,336
FRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LINGUILL SEQ ID NO 2
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Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tryes: PRT coganism: Homo sapiens US-10-135-839-22
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US-10-239-423-67
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Publication No. US20030165988A1
GENERAL INFORMATION:
APPLICANT: Hua, Shao-bing
APPLICANT: Pauling, Michelle H.
APPLICANT: Bulling, Michelle H.
APPLICANT: Pauling, Michelle H.
APPLICANT: Bulling, Michelle H.
APPLICANT: Diu, Li
TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST ITILE OF INVENTION: FRAGMENTS DERIVED FROM MEMBRANE PROTEINS
FILE REPERBENCE: 25636-717
CURRENT APPLICATION NUMBER: US/10/071,866
CURRENT APPLICATION NUMBER: US/10/071,866
CURRENT FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 54
SEQ ID NO 1
LENGTH: 352
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/164,649

FILING DATE: 07-Jun-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/990/045,583

FILING DATE: 20-MAR-1998

ATTORNEY/AGENT INFORMATION:

NAME: MANGE MANGEORIES: AMP E.

REGISTRATION NUMBER: 36,207

TELECAMUNICATION INFORMATION:

TELECAMUNICATION INFORMATION:

TELEFAX: (617)742-4214

INFORMATION: (617)742-4214

SEQUENCE CHARACTERISTICS:

LENGTH: 352 amino acids

TYPE: amino acids

TODOLOGY: 11-227

TYPE: amino acids

TODOLOGY: 11-227

TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 96; DB 14; Length 352; Best Local Similarity 100.0%; Pred. No. 5.5e-07; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 96; DB 14;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGWENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 37
US-10-135-839-2
Sequence 2, Application US/10135839
; Publication No. US20030166024A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 SÓYÓFWKNFÓTLKÍVÍLG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 SOYOFWKNFOTLKIVILG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SOYOFWKNFOTLKIVILG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-164-649-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 36
US-10-071-866-1
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APPLICANT: FORSSMANN, Wolf-Georg; FORSSMANN, Ulf; ADERMANN, Knut;
APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikola;
TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
TITLE OF INVENTION: Cell Surface Protecome of Tumor and Inflammation Cells and
TITLE OF INVENTION: For Treating Tumor Diseases and Inflammatory Diseases,
TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction
TITLE FEFRENCE: 022217us
CURRENT APPLICATION NUMBER: US/10/239,423
CURRENT FILING DATE: 2002-03-23
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PATENTION VOINS: 84
SOFTWARE: PATENTION VOINS: 84
SEQ ID NO 67
LENGTH: 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10439845
Sequence 2, Application US/10439845
Publication No. US20030195348A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
TITLE OF INVENTION: AND THERAPEUTIC AGENTS FOR HIV INFECTION
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 96; DB 14; Length 352; 100.0%; Pred. No. 5.5e-07; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DATE: DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/439,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/864,458
FILING DATE: May 28, 1997
APPLICATION NUMBER: Provisional 60/018,508
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Hails, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 06830/030001
TELECOMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEPHONE: 619/678-5099
INFORMATION FOR ERQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 SQYQFWKNFQTLKIVILG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SOYOFWKNFOTLKIVILG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-239-423-67
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US-10-439-845-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

6; Search time 9.675 Seconds (without alignments) 178.961 Million cell updates/sec 2004, 08:57:36 September 28, Run on:

US-10-084-813-13 Title: Perfect score:

1 SQYQFWKNFQTLKIVILG 18 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

283366 segs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	chemokine (C-C) re	am	ത		2-phosphoglycerate		hypothetical prote	hypothetical prote	probable 2-phospho	·H	ď	nitroreductase fam	NADPH-flavin oxido	oxidoreductase yhd	chemokine receptor	periplasmic sorbit	surfactin syntheta	UTR4 protein - yea	probable branched-	hypothetical prote	بد	hypothetical prote			0	ferric enterobacti	ferric enterobacti	NADH2 dehydrogenas	hypothetical prote
SUMMARIES	Ð	A43113	149339	T22609	S34499	A75203	G85575	G90724	867200	C71236	A81263	I64056	C95199	A98066	A86719	JC5942	G98183	I40486	S30843	E81303	D90528	AB2915	E97689	C84678	H81442	1629	8555	E90707	137047	H83734
	DB	2	~	7	7	N	N	~	~	~	~	н	~	~	Ŋ	N	N	N	N	0	N	~	N	N	~	7	~	~	~	N
	Length	352	355	196	177	302	314	314	1289	301	467	616	237	237	242	344	475	3587	241	350	383	421	421	496	159	334	334	334	46	
de	Query Match	. 0	49.0	7	46.9		46.9	ė.	ė.			45.8			44.8	4.	•	44.8	٠	ж.	ო	e,	'n	•			•		'n	42.7
	Score	96	47	46	4.5	45	4.5	45	45	44.5	44	44	43	43	43	43	43	43	42	42	42	42	42	4		•	41.5			41
	Result No.		2	n	4	ιΩ	φ	7	ထ	σ	10	11	12	13	14	15	16	17	18	19	20	21	17	23	24	25	26	27	28	53

A, Residues: 1-184, IXASHIGAGPAACHGHILLGNPKNSASVSK' c8AM3>
A, Cross-references: GB:X99393; NID:g1524062; PIDN:CAA67767.1; PID:g1524063
A, Cross-references: GB:X99393; NID:g1524062; PIDN:CAA67767.1; PID:g1524063
A, Note: this framesbift mutation results in a non-functional receptor but confers a degree of may have had a selective advantage by conferring resistance to Yersinia plague infect; I. Leukoc: Biol. 60, 147-152, 1996
A, Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine rect A, Reference number: A58832; MUID:96295970; PMID:8699119
A, Accession: A58832; MUID:96295970; PMID:8699119
A, Residues: 1-352 < COM1.
A, Residues: 1-352 < COM2.
A, Residues: 1-39. 'L', 91-352 < COM2.
A, Residues: 1-89. 'L', 91-352 < COM2.
A, Residues: 1-89. 'L', 91-352 < COM2.
A, Cross-references: EMBL:U57840
B, Residues: 1-89. 'L', 91-352 < COM2.
A, Cross-references: EMBL:U57840
B, Residues: 1-89. 'L', 91-352 < COM2.
A, Cross-references: EMBL:U57840
B, Ryaport, C.J.', Goraling, J.', Schweickart, V.L., Gray, P.W.; Charo, I.F.
A, Choss-references: EMBL:U5766, 1996
A, Risaport, C.J.', Goraling, and functional characterization of a novel human CC chemokine A, Reference number: AB8833; MUID:96291862; PMID:8663314

hypothetical prote envelope-like prot	oligopeptide ABC t hypothetical prote	hypothetical prote hymothetical prote	pre-mRNA splicing	related to TOMI pr DNA-damage-inducib	DNA-damage-inducib hypothetical prote		alcohol sulfotrans
S03215 A84494	140547 T22197 T11033	111033 D83385 E42594	S47920 T48016	T49799 H91193	A86041 G97365	G70827	138548
00	000	101	0 0	0 0	~ ~	<b>(1)</b>	٠,
244	303 316	0 6 4 1 6 7 1 6 7 1 6 7	629	3839	278 89	163	282
42.7	4. 4. 4. 2. 2. 4. 4. 7	42.7	42.7	42.7	42.2	41.7	41.7
441	4.4.4	4.4.	44	41	40.5	4. 4 0 C	4.
30	2 E L	9 P. P.	3.7	6 4 6 0	4142	43	42

## ALIGNMENTS

	RESULT 1 A43113
	chemokine (C-C) receptor 5 - human
	N/Alternate names: C-C CKR-5; CCR5
	C;Species: Homo sapiens (man)
	C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 20-Jun-2000
	C;Accession: A43113; S71808; A58834; A58832; G02653; A58833
	R;Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
	Biochemistry 35, 3362-3367, 1996
	A; Title: Molecular cloning and functional expression of a new human CC-chemokine receptor
	A; Reference number: A43113; MUID:96241590; PMID:8639485
	A; Accession: A43113
	A; Molecule type: mENA
_	A;Residues: 1-352 <sam1></sam1>
	A;Cross-references: GB:X91492; NID:q1262810; PIDN:CAA62796.1; PID:q1262811
	R; Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.: Farber, C.M.; Saradost;
	M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G. Pay
	Nature 382, 722-725, 1996
	A; Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of
	A;Reference number: S71808; MUID:96345670; PMID:8751444
	A; Accession: S71808
	A;Status: nucleic acid sequence not shown; not compared with conceptual translation
	A; Molecule type: DNA
	A;Residues: 182-206;207-230 <sam2></sam2>
	A/Accession: A58834
-	A; Status: nucleic acid sequence not shown; not compared with conceptual translation
	A; Molecule type: DNA
_	Dispositions 1-104 / TYDGUI CACOAAAACUCUITI TANDUNIAACUCU

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C;Species: Prococcus abyss: C;Decies: Prococcus abyss: C;Decies: Prococcus abyss: C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000 C;Accession: A75203 R;anonymous, Genoscope R;anonymous, Genoscope R;anonymous, Genoscope A;Pescription: Prococcus abyss: genome sequence: insights into archaeal chromosome struct A;Reference number: A75001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AJ248283; GB:AL096836; NID:G5457433; PIDN:CAB49072.1; PID:G5457583; A;Experimental source: strain Orsay
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein 177 (psbC 3' region) - Euglena gracilis chloroplast C;ppcies: chloroplast Euglena gracilis C;ppcies: chloroplast Euglena gracilis C;pace: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 11-Apr-1995 C;Accession: 334499; S34867 R;Hallick, R.B.; Hong, L.; Drager, R.G.; Favreau, M.; Monfort, A.; Orsat, B.; Spielmann, Submitted to the EMBL Data Library, January 1993 A;Bescription: The complete sequence of the Euglena gracilis chloroplast genome (tentative) A;Reference number: S34494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-177 <HAL1>
A;Cross-references: BmBL:X70810
B;Hallick, R.B.; Hong, L.; Drager, R.G.; Favreau, M.R.; Monfort, A.; Orsat, B.; Spielmanr
Nucleic Acids Res. 21, 3537-3544, 1993
A;Title: Complete sequence of Euglena gracilis chloroplast DNA.
A;Reference number: $34862; MUID:93347989; PMID:8346031
A;Accession: $34867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X70810
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
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                          A) Residues: 1-196 <WIL>
A) Residues: 1-196 <WIL>
A) Cross-references: EMBL:270208; PIDN:CAA94143.1; GSPDB:GN00028; CESP:F54B11.8
A) Experimental source: clone F54B11
C) Genetics:
A) Genetics:
A) Genetics:
A) Genetics:
A) An Desition: X
A) Introns: 26/1; 60/1; 94/3; 122/3
C) Superfamily: Caenorhabditis elegans hypothetical protein F54B11.8
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 177;
                                                                                                                                                                                                                                                                                                                                             Length 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                             47.9%; Score 46; DB 2;
66.7%; Pred. No. 4.5;
tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 QFW----KNFQTLKIVIL 17
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Best Local Similarity 55.6's
warches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 WKNFDSFKIAIL 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 WKNFQTLKIVIL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-177 <HAL2>
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C;Keywords: chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary A;Molecule type: DNA
A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                                                               A,Description: G protein-coupled receptor for chemokines MIP-lalpha, MIP-lbeta and RANTE A,Note: probably acts to control granulocyte proliferation and differentiation c, superfamily: vertebrate rhodopsin c, so seed that seed the status predicted c, superfamily: vertebrate from the status predicted c, superfamily: ransmembrane flatus predicted c, superfamily: ransmembrane flatus predicted c, superfamily: status superfamily: specific c, superfamily: specific c, superfamily: ransmembrane flatus predicted c, superfamily: specific c, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               macrophage inflammatory protein-1 alpha receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Uul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: 14939, P.M.
R;Gao, J.L.; Murphy, P.M.
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemoking A;Reference number: 149339; MUID:95340546; PMID:7542241
                                                                                                  A,Cross-references: GB:U54994; NID:g1457845; PIDN:AAC50598.1; PID:g1457946
C;Comment: This is a receptor for chemokines MIP-lalpha (see PIR:A30574), MIP-lbeta (see
C;Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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T22609
T22609
T22609
T22609
T22609
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C;Accession: T22609
Submitted to the EMBL Data Library, March 1996
A;Reference number: Z19588
A;Accession: T22609
A;Accession: T22609
A;Status: preliminary, translated from GB/EMBL/DDBJ
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: EMBL:U28404; NID:g881547; PIDN:AAA89153.1; PID:g881548
C;Superfamily: vertebrate rhodopsin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                       A;Gene: GDB:CMKBR5; CCR5; CKR-5; CC-CKR-5; CKR5; ChemR13
A;Cross-references: GDB:1230510; OMIM:601373
A;Map position: 3p21-3p21
C;Function:
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195 WKRFQALKLNILG 207
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Matches 8; Conserv
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                                                 A, Molecule type: mRNA
A, Residues: 1-352 <RAP>
                  A; Accession: A58833
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probable 2-phosphoglycerate kinase - Pyrococcus horikoshii

grobable 2-phosphoglycerate kinase - Pyrococcus horikoshii

C;Species: Pyrococcus horikoshii

C;Accession: C71236

R;Aswarabayasi, Y; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine

M;Ohlivu, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,

DNA Res. S; 55-76, 1998

A;Reference number: A71000, MUID:98344137; PMID:9679194

A;Reference number: A71000, MUID:98344137; PMID:9679194

A;Reference number: A71000, MUID:98344137; PMID:9679194

A;Residues: preliminary; nucleic acid sequence not shown; translation not shown

A;Rolecule type: DNA

A;Residues: 1-301 < KAM>

A;Residues: 1-301 < KAM>
A;Residues: 1-301 < KAM>
A;Residues: 1-301 < KAM>
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                                                                                                                                            Cyacession: S67200 Fraquence_Correspondence of Revision S67200 Fracession: S67200 Fracession: S67200 Fracession: S67200 Fracession: S67200 Fracession: S67194 Fracession: S67194 Fracession: S67194 Fracession: S67100 Fracess
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     Alternate names: hypothetical protein 05623
;Species: Saccharomyces cerevisiae
;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
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A,Map position: 15R
C;Superfamily: Saccharomyces cerevisiae hypothetical protein YOR296w
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46.4%; Score 44.5; DB 2; Length 301;
Best Local Similarity 40.0%; Pred. No. 12;
Matches 8; Conservative 6; Mismatches 3; Indels
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C;Superfamily: 2-phosphoglycerate kinase
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Best Local S
Matches 7
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G85575
hypothetical protein Z0898 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: 085575
R;Peranca, N.T.; Plunkett III, G; Burland, V; Mau, B; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L; Grocheck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, X.; Apodaca,
Nature 409, 529-533, 2001
A;Title Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Accession: G85575
A;Accession: G85575
A;Aclecule type: DNA
A;Scatus: preliminary
A;Molecule type: DNA
A;Residues: 1-314 <STO>
A;Cross_references: GB:AE005174; NID:g12513664; PIDN:AAG55067.1; GSPDB:GN00145; UMGP:208
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z0898
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G90724
G90724
C90724
C90724
Cypothetical protein ECs0767 [imported] - Escherichia coli (strain O157:H7, substrain RI
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: G90724
R;Haysshi, T; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res S 11-22, 2001
A;Reference number: A99629; MulD:21156231; PMID:111258796
A;Accession: G90724
A;Accession: G90724
A;Accession: G90724
A;Residues: 1-314 <HAY>
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC80767
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                                                                                                                                                      Length 302;
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56.2%; Pred. No. 11;
iive 3; Mismatches 4; Indels
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S67200
hypothetical protein YOR296w - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                4; Indels
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                                                                                                                                            Score 45; DB 2;
Pred. No. 10;
6; Mismatches
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                                                                                                                                            46.9%; Score 45; 37.5%; Pred. No. 1
A,Gene: PAB2253
C,Superfamily: 2-phosphoglycerate kinase
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SQYRFFKMFTNLALVI 304
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77 RYLFWRRFRKMKVPLL 92
                                                                                                                                                                                                                                                                                                                                2 QYQFWKNFQTLKIVIL 17
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                                                                                                                                                                                         Best Local Similarity 37.5%;
Matches 6; Conservative
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Best Local Similarity 56.27
Conservative 9; Conservative
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Matches 9; Conservative
                                                                                                                                            Query Match
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Genome Res. 11, 731-753, 2001
Affilie. The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. A,Reference number: A86625; MUID:21235186; PMID:11337471
A,Accession: A66719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: A99066
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Es R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Es R; LeBlanc, D.J.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; McAhren, S.; McAhren, S.; M.; J. Bacteriol. 183, S709-5717, 2001
J; Bacteriol. 183, S709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Accession: A98066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NADPH-flavin oxidoreductase (EC 1.6.99.-) homolog [imported] - Streptococcus pneumoniae C;Species: Streptococcus pneumoniae C;Species: 22-0ct-2001 #sequence_revision 22-0ct-2001 #text_change 02-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oxidoreductase yhgA [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
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A,Molecule type: DNA
A,Redidues: 1-242 <812
A,FRedidues: 1-242 <812
A,Cross-references: GB:Ab005176; PID:g12723669; PIDN:AAK04851.1; GSPDB:GN00146
A,Experimental source: strain IL1403
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A; Molecule type: DNA
A; Residues: 1-237 < KUR>
A; Cross_references: GB: AE007317; PIDN: AAL00358.1; PID: g15459219; GSPDB: GN00174
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                                                                             Length 237;
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41.7%; Pred. No. 17;
tive 5; Mismatches ;
                                                                      Score 43; DB 2;
Pred. No. 17;
5; Mismatches
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A;Gene: yhgA
C;Superfamily: NADPH-flavin oxidoreductase homolog
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C;Superfamily: NADPH-flavin oxidoreductase homolog
C;Keywords: oxidoreductase
       C, Superfamily: NADPH-flavin oxidoreductase homolog
                                                                             44.8%;
ilarity 41.7%;
Conservative
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Best Local Similarity
Matches 5; Conserv
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C95199

nitroreductase family protein [imported] - Streptococcus pneumoniae (strain TIGR4)

c;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C;Accession: C95199
E;Tettellin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
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A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP1710
A;Cross-references: GB:AL139079; GB:AL111168; NID:g6968971; PIDN:CAB73647.1; PID:g696907
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: Cj1660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, P. Gocynmann, R.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J. D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Authors: Gapcome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MuID:95350630; PMID:7542800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: GB:U32710; GB:L42023; NID:g1573200; PIDN:AAC21908.1; PID:g1573205;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                secretion protein secD - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-616 <TIGR>
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                                                                                                                                                                                                      DB 2; Length 467
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C; Superfamily: protein export membrane protein secD
                                                                                                                                                                                                      45.8%; Score 44; DB 37.5%; Pred. No. 23; tive 4; Mismatches
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77 FYFWKKIBILNFILLG 92
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Best Local Similarity
7; Conserv
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A;Molecule type: DNA
A;Residues: 1-237 <KUR>
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A; Accession: Solds and the complete type: DNA A; Alloni, G.; Azevedo, V.; Berterr A; Residues: 977-1104 cHAN-
A; Molecule type: DNA A; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berterr B; Kunst, F.; Ogaaswara, N.; Moszer, I.; Albertini, B.; Capuano, V.; Carter, N.M.; Choi A; Enrich, S.D.; Emmérson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, ich, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y.; Ogiwara, A.; Odiwara, A.; Odiega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, R.; Scohleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, A; Winters, Schleich, S.; Schroeter, R.; Terpstra, P.; Tosafo, J.; Saror, A; Winters, P.; Wipat, A.; Tanaka, T.; Yasumoto, H.; Yasumoto, K.; Yasua, K.; Yoshida, K.; A; Herence number: Asymbate genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Reference number: Asymbate acid sequence not shown; translation not shown
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A; Molecule type: DNA
A; Residues: 1-3537 < KUN>
A; Residues: 1-3537 < KUN>
A; Residues: 1-3537 < KUN>
A; Fabret; C: Quentin, Y: Guiseppi, A:; Busuttil, J:; Haiech, J:; Denizot, F.
A; Experimental seurce: strain 168
A; Residues: 1-35, Ventin, Y: Guiseppi, A:; Busuttil, J:; Haiech, J:; Denizot, F.
A; Reference number: $46967
A; Reference number: $46967
A; Reference number: $46967
A; Reference number: $46967
A; Residues: 1-32, FY; 34-41, G', 43-109, D', 111-114, G', 116-138, VV, 140-258, W', 260-308, A'
A; Residues: 1-32, FY; 1917-2138, SRL', 2142, 'OSLN', 2146-2444, 'Q', 2446-2712, H', 2714-2722, H', 2724
A; Residues: 1-32, FU; Shlima, Y:; Corbell, N:; D'Souza, C:; Nakano, M.M.; Zuber, P:; Yamane, K.
A; Fuma, S:; Fujishima, Y:; Corbell, N:; D'Souza, C:; Nakano, M.M.; Zuber, P:; Yamane, K.
Nucleic Acids Res. 21, 93-97, 1993
A; Title: Nucleotide sequence of 5' portion of srfA that contains the region required for A; Reference number: S35517; MUD: 93181186; PMID: 8441623
A; Accession: S3518
A; Status: significant sequence differences
A; Reference number: S35518
A; Status: significant sequence differences
A; Reference strain 168 trpC2
A; ENS Mccobert, S; Patil, S.S.; Marahiel, M.A.
FEMS Mccobert number: $25658
A; Title: Identification of putative multifunctional peptide synthetase genes using highly A; Reference number: $25658
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C;Superfamily: surfactin synthetase; acetate-CoA ligase homology; acyl carrier protein homology: antibiotic biosynthesis; carrier protein; duplication; ligase; phosphopanteth c;FsI1-951/Domain: acetate-CoA ligase homology <ACII->
F;968-1035/Domain: acetate-CoA ligase homology <ACII->
F;968-1035/Domain: repeat RRPI->
F;1035-1481/Domain: repeat RRPI->
F;1042-1995/Domain: acetate-CoA ligase homology <ACI2>
F;2013-2081/Domain: acetate-CoA ligase homology <ACI2>
F;2013-2081/Domain: acetate-CoA ligase homology <ACI3>
F;2013-2024/Domain: acetate-CoA ligase homology <ACI3>
F;2013-1036/Domain: acetate-CoA ligase homology <ACI3>
F;3041-3108/Domain: acyl carrier protein homology <ACI3>
F;3041-3108/Domain: acyl carrier protein homology <ACI3>
F;3041-3108/Domain: acyl carrier protein homology <ACI3>
F;999,2045,3073/Binding site: phosphopantetheine (Ser) (covalent) #status predicted
                     A;Title: A small gene, designated comS, located within the coding region of the fourth an A;Reference number: S60866; MUID:95272393; PMID:7752896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Title: Identification of putative multifunctional peptide synthetase genes using highly A,Reference number: $25658
A,Accession. $25658
A,Accession. $25658
A,Accession. $25658
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 168,'C',170-171,281-283;514-595,597-647,'R',649-679,'ETL',683-693,'DKR',697,'A,Cross-references: EMBL:X65835, NID:340202; PIDN:CAA46678.1; PID:340203
A,Experimental source: strain ATCC 21332
C,Comment: This procein contains several amino acid-activating domains for the synthesis the amino-terminal region of this protein, appear to be required for the development of c.Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 3587;
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Pred. No. 2.7e+02;
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33.3%;
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Best Local Similarity
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140486
surfactin synthetase component II - Bacillus subtilis
NiAlternate names: surfactin synthetase srfA2; surfactin synthetase/competence protein s
NiAlternate names: surfactin synthetase srfA2; surfactin synthetase/competence
NiAlternate names: surfactin synthetase srfA2; surfactin synthetase/competence protein s
NiAlternate names: surfactin synthetase srdA2; surfactin synthetase subtilis sub
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G198183
periplasmic sorbitol-binding protein, smoE (AF018073) [imported] - Agrobacterium tumefac
G198183
periplasmic sorbitol-binding protein, smoE (AF018073) [imported] - Agrobacterium tumefac
G198183
G198183
R198183
R198183
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Chemokine receptor - human
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: No. 2012-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
Cispecies: No. 2012-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
Cispecies: Commin. 243, 264-268, 1998
Biochem. Biophys. Res. Commun. 243, 264-268, 1998
Airtle: Cloning and characterization of a novel human chemokine receptor.
Airtle: Cloning and characterization of a novel human chemokine receptor.
Airtle: Cloning and characterization of a novel human chemokine receptor.
Aircleance number: JC5942; MUID:98139902; PMID:9473515
Aircleanle rype: DAN
Airclea
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Pred. No. 24;
2; Mismatches 2; Indels
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Pred. No. 34;
3; Mismatches 4; Indels
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ilarity 50.0%;
Conservative
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A;Map position: linear chromosome
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FWKHFLTLKMNI 206
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Best Local Similarity 66.7
Matches 8; Conservative
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Best Local Similarity
Matches 7; Conserv
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hypothetical protein MYPU_1320 [imported] - Mycoplasma pulmonis (strain UAB CTIF)
C;Species: Mycoplasma pulmonis
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
R;Accession: D90528
Nucleic Acids Res. 29, 2145-2153, 2001
A;Richambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Richer The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmc
A;Reference number: A99512; MUD::21267165; PMID::11353084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Riwood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClella farary, P.; Rang, S. Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - Agrobacterium tumefaciens (strain C58, Dupont)
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Ayîtile: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; WUID:21608550; PMID:11743193
A;Accession: AB2915
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A;Molecule type: DNA
A;Residues: 1-421 «KUR»
A;Cross-references: GB:AE008688; PIDN:AAL43736.1; PID:g17741269; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-383 «KUR»
A, Cross-references: GB: AL445566, PID: g14089545; PIDN: CAC13305.1; GSPDB: GN00153
A, Experimental source: strain UAB CTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FAD-dependent monooxygenase [imported] - Agrobacterium tumefaciens (strain (C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
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40;
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46.2%; Pred. No. 44;
tive 4; Mismatches
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Pred. No. 40;
3; Mismatches
Best Local Similarity 44.4%; Pred. No. 36;
Matches 8; Conservative 4; Mismatches
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246 TQFDFLLTFQLLIIIVLG 263
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                                                                                                           1 SOYOFWKNFOTLKIVILG 18
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349 RYQSWRRFDTLRM 361
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Matches 7; Conservative
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Matches 6, Conserv
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E97689
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A, Molecule type: DNA
A, Molecule type: DNA
A, Residues: 1-350 < PAR.
A, Cross-references: GB: AL139077, GB: AL111168; NID: g6968444; PIDN: CAB73272.1; PID: g696845
A, Experimental source: serotype O2, strain NCTC 11168
C, Genetics:
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C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: E81303
R;Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A;Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: 1-21 - 210.

A;Cross-references: GB:U18779; EMBL:L10830; NID:g603625; PIDN:AAB65004.1; PID:g603641

R;Dietrich, F.S.
submitted to the EMBL Data Library, December 1994

A;Description: The sequence of S. cerevisiae cosmids 8199, 8334, and 9871.

A;Reference number: S50491

A;Accession: S50506

A;Accession: S20506

A;Accession
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                                                                                                                                                                                                                                                                                                                                      UTR4 protein - yeast (Saccharomyces cerevisiae)
N/Alternate names: protein YEL038w
C.pacies: Saccharomyces cerevisiae
C.pacies: Saccharomyces cerevisiae
C.pace: 28-May-1993 #sequence revision 28-May-1993 #text_change 18-Aug-2000
C.Accession: 830843; S50506; S38544
R.Mulligan, J.T.; Dietrich, F.S.; Hennessey, K.M.; Sehl, P.; Komp, C.; Wei, Y.; Taylor, Submitted to the EMBL Data Library, Pebruary 1993
A; Reference number: 830812
A; Accession: S30843
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Residues: 1-69,'MH',72-152,'GMIRWI' <MEL>
Cross-references: EMBL:S66121; NID:g430827; PIDN:AAB28443.1; PID:g430828
           Gaps
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C,Superfamily: Klebsiella oxytoca methionine salvage pathway enzyme
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           Indels
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Pred. No. 25;
3; Mismatches
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           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 42;
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1751 ASFAFDANFESLRLIVLG 1768
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                                                                                   1 SOYOFWKNFOTLKIVILG 18
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Best Local Similarity 63.6
Matches 7; Conservative
           Conservative
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KYQVYKNFETL 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: DNA
Residues: 1-241 <MUL>
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               Matches
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A;Cross-references: GB:ALl139074; GB:ALL11168; NID:g6967505; PIDN:CAB72717.1; PID:g6967726
A;Experimental source: serotype O2, strain NCTC 11168
A;Genetical source: Serotype O2, strain NCTC 11168
C;Superfamily: Campylobacter jejuni hypothetical protein Cj0249
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33 YKFWKNAEIGRYQGTRIIFL 52
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Best Local Similarity 40.0%;
Matches 8; Conservative
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hypothetical protein AGR C 4995 [imported] - Agrobacterium tumefaciens (strain C58, Cere C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 C; Accession: E9768  
C; Accession: E9768  
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001  
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Recence number: A97359; MUD:21608551; PMID:11743194  
A; Accession: E97689  
A; Status: preliminary A; Residues: 1-421  
A; Mollam, A; Residues: 1-421  
A; Mollam, A; Residues: 1-421  
A; Mollam, A; Molam, A; Mollam, A; Mollam, A; Mollam, A; Mollam, A; Mollam, A; Mol
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C84678
hypothetical protein At2g27900 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: C84678
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A64420; MUID:20083487; PMID:10617197
A;Accession: C84678
A;Status: preliminary
A;Accession: C94678
A;Status: preliminary
A;Accession: C94678
A;Cossareferences: GB:AE002093; NID:94510426; PIDN:AAD21512.1; GSPDB:GN00139
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H8142
H81442
H81442
Cypothetical protein Cj0249 [imported] - Campylobacter jejuni (strain NCTC 11168)
C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: H81442
R;Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp. A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: H81442
A;Accession: H81442
A;Accession: L99482
A;Reteure DNA
A;Residues: 1-159 <-PAR>
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44;
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Pred. No. 44;
4; Mismatches
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100 SIHQFLKNYEDLSIFIL 116
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Best Local Similarity 52.9
Matches 9; Conservative
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Best Local Similarity
Matches 6; Conserve
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A,Map position: 2
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Nylternate names: Extracterobactin permease tepD

(Species: Escherichia coli

(Species: Escherichia coli

(C)Date: 04-0e-1992 #sequence revision 04-De-1992 #text_change 01-Mar-2002

(C)Accession: S16296; Mid.A.

Mol. Microbiol. 5, 1415-1428, 1991

A;Title: Nucleotide sequence and genetic organization of the ferric enterobactin transpon

A;Reference number: S16295; MUD:92157868; PMID:1838574

A;Accession: S16296

A;Molecule type: DNA

A;Reference number: S16295; MUD:92157868; PMID:1838574

A;Accession: S16296

A;Accession: S16296

A;Accession: S16296

A;Atle: Organization of genes encoding membrane proteins of the Escherichia coli ferrier

A;Accession: S16305

A;Accession: 
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N/Alternate names: ferrienterobactin permease fepD
                                                                                                      Gaps
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     DB 2; Length 159;
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                                                                                                      3; Indels
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C.Superfamily: vitamin B12 transport protein btuC
C.Superfamily: vitamin B12 transport protein btuC
C.Keywords: transmembrane #status predicted <TM1>
F.16-32/Domain: transmembrane #status predicted <TM2>
F.54-110/Domain: transmembrane #status predicted <TM2>
F.121-137/Domain: transmembrane #status predicted <TM4>
F.121-137/Domain: transmembrane #status predicted <TM4>
F.188-214/Domain: transmembrane #status predicted <TM6>
F.198-214/Domain: transmembrane #status predicted <TM6>
F.240-256/Domain: transmembrane #status predicted <TM6>
F.284-300/Domain: transmembrane #status predicted <TM6>
F.310-326/Domain: transmembrane #status predicted <TM6>
Score 41.5; DE Fred. No. 20; 4; Mismatches
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Best Local Similarity 34.8%; Pred. No. 42;
Matches 8; Conservative 5; Mismatches
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envelope-like protein [imported] - Arabidopsis thaliana
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Local Similarity 40.0%;
les 6; Conservative 6
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Best Local Similarity 41.2%;
Matches 7; Conservative
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70 QYEYWKHTQLIIDVVDG
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                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 7; Conserv
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A;Gene: BH0680
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Best Local S:
Matches 6
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                   C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002
R;Perna, N.T.; Plunket III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Axtute, Ganome sequence of enterchemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 28
137047
NADLE dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - siamang mitochondrion (fragment)
C;Species: mitochondrion Hylobates syndactylus (siamang)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 03-Jun-2002
C;Accession: 137047
R;Horal, S: Satta, Y:; Hayasaka, K.; Kondo, R.; Inoue, T.; Ishida, T.; Hayashi, S.; Tak J. Mol. Evol. 35, 32-43, 1992
A;Title: Man's place in Hominoidea revealed by mitochondrial DNA genealogy.
A;Reference number: 137047; MulD:92389366; PMID:1518083
                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-334 <STO>
A;Cross-references: GB:AE005174; NID:g12513480; PIDN:AAG54925.1; GSPDB:GN00145; UWGP:207
A;Experimental source: strain O157:H7, substrain EDL933
erric enterobactin (enterochelin) transport [imported] - Escherichia coli (strain 0157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
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A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-334 cHAV>
A;Cross-references: GB:BA000007; PIDN:BAB34052.1; PID:gl3360087; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
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A,Molecule type: DNA
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C,Superfamily: vitamin B12 transport protein btuC
                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: fepD
C;Superfamily: vitamin B12 transport protein btuC
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43.2%; Score 41.5; Dest Local Similarity 34.8%; Pred. No. 42;
Matches 8; Conservative 5; Mismatches
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Local Similarity 34.8%;
les 8; Conservative 5
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hypothetical protein BH0680 (imported) - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 0.1-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: H83734
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran
R;Takami, E.; Masone, M.; Takaki, Z.; Hiran
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and c;
A;Reference number: A83550; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1118 <STO>
A;Cross-references: GB:AP001509; GB:BA000004; NID:g10173176; PIDN:BAB04399.1; GSPDB:GN001
A;Experimental source: strain C-125
A;Residues: 1-46 cHOR>
A;Cross-references: GB:D38484; NID:g558513; PIDN:BAA07494.1; PID:g558514
C;Genetics:
A;Genome: ND1
A;Genome: mitochondrion
A;Genome: mitochondrion
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 1
C;Superfamily: NADH dehydrogenase (complex; mitochondrion; NAD; oxidative phosphorylation; C;Reywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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C; Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Apr-2000
C; Palling, B.; Zillig, W.; Yeats, S.; McWilliams, P.; Reiter, W.D.
S; Palling, B.; Zillig, W.; Yeats, S.; McWilliams, P.; Reiter, W.D.
A; Reference number: S03211
A; A; Accession: S03215
A; Molecule type: DNA
A; Residues: 1-244
A; Cross-references: EVBL: X07234; NID:946703; FIDN:CAA30214.1; PID:946708
C; Superfamily: Sulfolobus particle SSV1 hypothetical protein D-244
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Pred. No. 37;
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                                                                                                                                                                                                                                                                                                               Score 41; DB 2;
Pred. No. 6.7;
2; Mismatches (
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Pred. No.
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NADIZ dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - common gibbon mitochondrion C.Species: mitochondrion Hylobates lar (common gibbon, white-handed gibbon) (C.Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002 C.Accession: T1833
R.Arnason, U.; Gullberg, A.; Xu, X.
Hereditas 124, 185-189, 1996
A.ittle: A complete mitochondrial DNA molecule of the white-handed gibbon, Hylobates lar, A.Reference number: Z17353
A.Accession: T1833
A.Accession: T1833
A.Accession: T1833
A.Accession: T1834
A.Reference number: Z17355
A.Accession: T1834
A.Reference number: Z17355
A.Accession: T1831
A.Reference number: Z17355
A.Accession: T1834
A.Reference number: Z17353
A.Accession: T1834
A.Reference nu
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                                                                                                                                                                                                                                                                     hypothetical protein F44G3.5 - Caenorhabditis elegans
CjSpecies: Caenorhabditis elegans
CjSpecies: Caenorhabditis elegans
CjDate: 120ct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
CjDate: 1722.97
RjmCMmurray, A.
RimMmurray, A.
RimMitted to the EMBL Data Library, November 1996
A;Reference number: 2195.9
A;Reference number: 2195.9
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-316
A;Genetics: CGP-F44G3
C;Genetics: CGP-F44G3
C;Genetics: CGP-F44G3
C;Genetics: CGP-F44G3
C;Genetics: CGP-F44G3
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Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas,
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C;Superfamily: NADH dehydrogenase (ubiquinone) chain 1
C;Keywords: membrane-associated complex; mitochondrion; NAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41; DB 2;
Pred. No. 48;
3; Mismatches 3
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Pred. No. 48;
2; Mismatches
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Best Local Similarity 57.1%;
Matches 8; Conservative
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Best Local Similarity 46.7%;
Matches 7; Conservative
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                           ||: | |: |||
29 FWEKFSKNKLAILG 42
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A;Introns: 142/3; 185/3; 256/3
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    C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001
C;Accession: A84494
N; Kaul, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R;Lin, X.; Kaul, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
N; Kaul, Moffat, X.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Mierman, W.C.; Wnite, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84424
A;Reference number: A84420; MUD:20083487; PMID:10617197
A;Molecule type: DNA
A;Residues: 1-285 <STO>
A;Cross-references: GB:AE002093; NID:g4733967; PIDN:AAD28650.1; GSPDB:GN00139
C;Genetics:
A;Gene: AtJg10850
A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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|Species: Arabidopsis thaliana (mouse-ear cress)
|Pate: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
|Accession: A84494
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Pred. No. 46;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Length 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41; DB 2
Pred. No. 43;
4; Mismatches
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Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 41.7%;
Matches 5; Conservative
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Gaps

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P.; Hickey, M.J.; Bri A.; Larbig, K.; Lim,

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Gaps

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Divolable zinc-finger protein - Arabidopsis thaliana
NyAlternate names: protein T17013.200
CySpecies: Arabidopsis thaliana (mouse-ear cress)
CySpecies: Arabidopsis thaliana (mouse-ear cress)
CyBate: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
CyAccession: T48016
RyRieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer, is ubmitted to the Protein Sequence Database, February 2000
A;Referse number: Z24482
A;Recession: T48016
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Description: pre-mRNA splicing A; Note: necessary for the stable interaction of mRNA precursors with the snRNP components C; Keywords: nucleus; pre-mRNA splicing; transmembrane protein F; 429-445/ Domain: transmembrane #status predicted < TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T4979
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A;Reference number: 225022
                                       A;Cross-references: EmBi:L29224; NID:g460045; PIDN:AAA20131.1; PID:g460046
A;Note: the authors translated the codon GAC for residue 29 as Ala
R;Odell, C:; Bowman, S.
Bubmitted to the EMBL Data Library, January 1995
A;Reference number: S50941
                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:Z47816; NID:g642303; PID:g642309; MIPS:YML046w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-812 <RIE>
A;Cross-references: EMBL:AL138651
A;Experimental source: cultivar Columbia; BAC clone T17J13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               related to TOM1 protein [imported] - Neurospora crassa N;Alternate names: protein B11B22.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 2; ; Pred. No. 1.2e+02; 5; Mismatches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41; DB 2;
Pred. No. 96;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 3
A;Introns: 56/3; 159/3; 229/2; 245/3; 275/3; 296/3
A;Note: T17J13.200
                                                                                                                                                                                                                                                                                                                                                                   A,Gene: SGD:PRP39
A,Cross-references: SGD:S0004509; MIPS:YML046w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 42.7%; Sci
Best Local Similarity 37.5%; Pri
Matches 6; Conservative 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 FGFWKRFATIEYOLFG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18
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Local Similarity 46.2%;
Les 6; Conservative :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 YOFWKNFOTLKIVILG
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A; Molecule type: DNA
A; Residues: 1-629 < LOC>
                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-629 <ODE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 13L
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Species: Pseudomonas sp.
C; Species: Pseudomonas sp.
C; Spaces: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C; Accession: E42594; A4189
B; Watebe, K.; Ishikawa, T.; Mukohara, Y.; Nakamura, H.
J; Bacteriol: 174, 962-969, 1992
J; Bacteriol: 174, 962-969, 1992
A; Title: Cloning and sequencing of the genes involved in the conversion of 5-substituted A; Reference number: A42594; MUID:92121137; PMID:1732229
                                                                                                                                                                                   A;Residues: 1-359 <STO>
A;Cross-references: GB:AE004636; GB:AE004091; NID:g9948093; PIDN:AAG05478.1; GSPDB:GN001
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA2090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pre-mRNA splicing factor PRD39 - yeast (Saccharomyces cerevisiae)

NiAlternate names: protein YMB27.06; protein YML046w
C;Species accharomyces cerevisiae
C;Species accharomyces cerevisiae
C;Species: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
C;Accession: S4720; S50946
R;Lockhart, S.R.; Rymond, B.C.
Mol. Cell. Biol. 14, 3623-3633, 1994
A;Title: Commitment of yeast pre-mRNA to the splicing pathway requires a novel U1 small A;Reference number: S47920; MUID:94254621; PMID:8196608
A;Accession: S47920
      .; Lory, S.; Olson, M.V.
Mature 406, 959-964, 200.
Asture 406, 959-964, 200.
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: D83385
A;Accession: D83385
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-245 <WA2>
A; Residues: 1-245 <WA2>
A; Residues: 1-245 <WA2>
A; Residues: 1-245 <WA2>
A; Cross-references: GB:D90469; NID:g216829; PIDN:BAA01380.1; PID:g216834
A; Cross-references: GB:D90469; NID:g216829; PIDN:BAA01380.1; PID:g216834
A; Note: sequence extracted from NCBI backbone (NCBIN:77753, NCBIP:77764)
B; Watabe, K.; Ishikawa, T.; Mukohara, Y.; Nakamura, H.
J; Bacteriol. 174, 3461-3466, 1992
A; Title: Identification and sequencing of a gene encoding a hydantoin racemase from the A; Reference number: A41895; MUID:92276321; PMID:1339422
A; Accession: A41895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein ORF5 hyuC 3'-region, hyuE 5'-region - Pseudomonas sp. plasmid pHN6
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;Experimental source: strain NS671
;Note: sequence extracted from NCBI backbone (NCBIN:104597, NCBIP:104598)
;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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C,Superfamily: Escherichia coli probable transport protein b0511
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Pred. No. 69;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       42.7%; Score 41; DB 2;
60.0%; Pred. No. 54;
iive 2; Mismatches
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Best Local Similarity 42.9%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 KFWKHFQ----VILG 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Best Local Similarity
9, Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
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S47920
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Gaps

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A;Residues: 1-3839 <SCH>
A;Cross-references: EMBL:AL356834; GSPDB:GN00116; NCSP:B11B22.10
A;Experiental source: BAC clone B11B22; strain OR74A
C;Genetics:
A;Gene: NCSP:B11B22.10
A;Map position: 6
A;Introns: 16/3; 2607/1; 2658/1; 2845/1; 2987/2; 3204/3; 3694/1; 3809/1
Ouery Match
Best Local Similarity 54.5%; Pred. No. 6e+02;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
CQ 6 WKNPQTLXIVI 16
: || || || || ::::
Db 1219 YKNPQTLXIL 1229
```

RESULT 40
H91193
DNA-damage-inducible protein [imported] - Escherichia coli (strain O157:H7, substrain RI C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 18-Jul-2001
C;Accession: H91193
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA, Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genchyterence number: A99629; MUID:21156231; PMID:11258796
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Residues: 1-278 <AX>
A;Molecule type: DNA
A;Residues: 1-278 <AX>
A;Cross-references: GB:BA000007; PIDN:BAB37943.1; PID:G13363995; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:

ï

23; Gaps

Query Match (42.2%; Score 40.5; DB 2; Length 278; Best Local Similarity 25.6%; Pred. No. 50; Matches 10; Conservative 4; Mismatches 2; Indels 23

3 YOFWKNFQ-----TLKIVILG 18

8

Search completed: September 28, 2004, 09:07:09 Job time : 11.925 secs

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us-10-084-813-13.rsp

GenCore version 5.1.6 . Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

September 28, 2004, 08:55:11; Search time 5.625 Seconds (without alignments) 166.624 Million cell updates/sec Run on:

Title: US-10-084-813-13
Perfect score: 96
Sequence: 1 SQYQFWRNFQTLKIVILG 18

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

iption	P56493 cerconithed	O9tv42 cercopithec	~	•	homo sar	hylob		Q95nc5 hylobates s	P56440 pan troglod	P56441 papio hamad	O97881 pongo pygma	097880 pygathrix b	097882 pygathrix n	097878 trachypithe		-	P51682 mus musculu	ratt	P51675 mus musculu	mus	P56482 macaca mula		homo sar	haemo				Q983uB chromobacte	747	P32626 saccharomyc		213 s	2063 bacillus
SUMMARIES	CKR5 CERAE	CKR5 CERPY	CKR5_CERTO	CKR5 GORGO	CKR5 HUMAN	CKRS_HYLLE	CKR5 HYLML	CKR5 HYLSY		CKR5_PAPHA	CKR5_PONPY	CKR5_PYGBI	CKR5_PYGNE	CKR5_TRAFR	CKR5_TRAPH	CKR5_MACMU	CKR5_MOUSE	CKR5_RAT	CKR1_MOUSE	CKR2_MOUSE	CKR1_MACMU	YCX3_EUGGR	DYHB_HUMAN		PYRB_MYCPE	CKR3_CERAE	CKR3 MACMU	VIOD_CHRVO	SRF2_BACSU	UTR4_YEAST	FEPD_ECOLI	Y28K_SSV1	APPC_BACSU
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Length	352	352	352	352	352	352	352	352	352	352	352	352	352	352	352	352	354	354	355	373	355	634	4523	616	300	355	355	373	3587	241	334	244	303
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Score	6	96	96	96	96	9	9	96	96	96	96	96	96	96	96	93	74	74	47		45						43	43	43	4	41.5	41	41
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Q96126 hylobates 1 Q92213 cartus norre O55193 rattus norv P81910 droscophila O75072 homo sapien P39682 saccharomyc Q06520 homo sapien P44298 heemophilus P32246 homo sapien Q04354 clostridium Q97ke5 clostridium Q97ke5 clostridium
NUIM HYLLA CKR3_CAVPO CKR2_RAT O22B DROME PCMD_HUMAN PR39_YEAST SUIA_HUMAN SUIA_HUMAN X18C_CLOAB ARLY_CLOAB ARLY_CLOAB
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318 3373 3373 3303 4461 3309 3309 531 531
444444444 00000001111111 
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## ALIGNMENTS

(POTENTIAL)

FRANSMEM

us-10-084-813-13.rsp

EMBL, AF035222; AAD44015.1; -. Interpro, IPR000276; GPCR\_Rhodpsn. Pfam, PF00001; 7tm\_1; 1.

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- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                15-WAR-2004 (Rel. 43, Created)
115-WAR-2004 (Rel. 43, Last sequence update)
115-WAR-2004 (Rel. 43, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCRS OR CWKBRS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cercopithecus pygerythrus (Vervet monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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                                                                                                                                                                                                                                                 Score 96; DB 1; Length 352;
Pred. No. 6.6e-08;
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                                                                                                                                     7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
                                                                4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                             6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
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                    2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                            3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                        5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
        (POTENTIAL)
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MEDLINE=99335215; PubMed=10408730;
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                                                                                                                                                                                                                                                                                                              Cercopithecinae, Cercopithecus.
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                                                                                                                                                                                                                                40561 MW;
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Best Local Similarity 100.
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352 AA;
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ID CKR5 CERPY
AC Q9TV42;
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VARIANT
VARIANT
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=1801ate 079, 085, 087, and 089;
MEDLINE=9832115; PubWed=965699;
Chen Z., Gettie A., Ho D.D., Marx P.A.;
Chen Z., Gettie A., Ho D.D., Marx P.A.;
The solution isolates use the CRS coreceptor from sooty mangabeys
naturally infected in west Africa: a comparison of coreceptor usage
of primary SIVsm, HIV-2, and SIVmac.";
Virology 246:113-124(1598).

-I. FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANIES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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CKRS CERTO STANDARD; PRT; 352 AA.

AC 062743; 062744; 062746;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR-5)

GN CCRS OR CMKBRS.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
DOMAIN
TRANSMEM 31 58 1 (POTENTIAL).

    -!- SUBCELLULAR LOCATION: Integral membrane protein.
    -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
3 (POTENTIAL).
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SULFATION (BY SIMILARITY)
SULFATION (BY SIMILARITY)
EF17D67CBCCCG3DB0 CRC64;
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                                                                                      1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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100.0%; Pred. No. 6.6e-08;
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18; Conservative
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352 AA;
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R EMBL; AF051902; AAC39830.1; -.
R RMBL; AF051903; AAC39831.1; -.
R RMBL; AF051905; AAC39831.1; -.
R MRBL; AF051905; AAC39833.1; -.
R InterPro; IPR000276; GPCR_Rhodpsn.
R PRINTS; PR00021; 7tm_1; 1.
R PRINTS; PS000237; GPCRHODOPSN.
R PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
R PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
R PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
TRANSMEM 31 58 (CYTORIALMILAR).
T TRANSMEM 31 59 68 CYTORIALMILAL).
T DOMAIN 59 68 CYTORIALMILAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97268687; PubMed=9108095;

MEDLINE=97268687; PubMed=9108095;

Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;

"Differential utilization of CCR5 by macrophage and T cell tropic
simian immunodeficiency virus strains.",
Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).

-I- FUNCTION: Receptor for a C-C type chemoxine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C-C chemokine recepture.

CCRS OR CMKBRS.

GOTILLB gorilla (Lowland gorilla).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Gorilla.

NCBI_TAXID=9595;
                                                                                                                                                                                                                                                                                                                                                    SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
D -> E (IN ISOLATE 087).
V -> G (IN ISOLATE 087).
V -> G (IN ISOLATE 087).
L -> V (IN ISOLATE 087).
L -> V (IN ISOLATE 089).
V -> G (IN ISOLATE 089).
V -> G (IN ISOLATE 089).
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EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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SULFATION (BY SIMILARITY
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CYTOPLASMIC (POTENTIAL)
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146
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352 AA;
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tes 18; Conserv
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CKR5_GORGO
ID CKR5_GORGO
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CONTRES HUMAN STANDARD; 014695; 014696; 014699; 014699; 014708; 014708; 014708; 014708; 014708; 014709; 014709; 014708; 014708; 014709; 014709; 014708; 015538; Q9UPA4; 014704; 014708; 014707; 014708; 015538; Q9UPA4; 01-0CT-1996 (Rel. 34, Created)

TO 1-0CT-1996 (Rel. 34, Last sequence update)

TO 15-MAR-2004 (Rel. 34, Last sequence update)

CC chemokine receptor type 5 (CC CRR-5) (CC-CKR-5) (CCRS)

CC Chemokine receptor) (CHEMRI3) (CD195 antigen).

CHIV-1 fusion co-receptor) (CHEMRI3) (CD195 antigen).

CHIV-1 fusion Co-receptor) (CHEMRI3) (CD195 antigen).

CHIV-1 fusion Co-receptor) (CHEMRI3) (CD195 antigen).

CM CMRS OR CMRESS.

CMS OR CMRESS.

CMS OR CMRESS.
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PIGETER, PRODOST6; GPCR_Rhodpsn.

PERMITS; PR00237; GPCRHODOPSN.

PRINTS; PR00237; GFCRHODOPSN.

PROSTITE; PS00247; G PROTEIN RECEP. F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

G-protein 1 30 EXTRACELULAR (POTENTIAL).

TRANSEM 1 59 CYTOPLASMIC (POTENTIAL).
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MEDLINE=S6241590; PubMed=8639485;
Samson M., Labbe O., Mollereau C., Vassart G., Parmentier M.;
"Molecular cloning and functional expression of a new human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 96; DB 1; Length 352;
Pred. No. 6.6e-08;
Mismatches 0; Indels
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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TATRACELLUIAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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Best Local Similarity
Matches 18; Conserv
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increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or

increases...
in the control of gramulouy...
differentiation.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
SIMILARITY: Belongs to family 1 it is produced through a collab

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AAB65731.1
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SEQUENCE FROM N.A.
MEDLINE=56291862; PubMed=86633114;
Rappir C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F.;
"Molecular cloning and functional characterization of a novel human CC chemokine receptor (CCRS) for RANTES, MIP-1beta, and MIP-1alpha.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND POLYMORPHISMS.
MEDLINE=98022612; PubMed=9359654;
Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDANED 5388201, MEDILIE=89694523; PubMed=9388201, MEDILIE=98049523; PubMed=9388201, Mummidi S., Ahuja S.K.; McDaniel B.L., Ahuja S.K.; "The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts with 5'-end heterogeneity, dual promoter usage, and evidence for polymorphisms within the regulatory regions and noncoding exons."; J. Biol. Chem. 272:30662-30671(1997).
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"Polymorphisms in the CCR5 genes of African green monkeys and mic implicate specific amino acids in infections by simian and human immunodeficiency viruses.", J. Virol. 71:8642-8656(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  type 1 subtypes, coreceptor usage, and CCR5 polymorphism."; Res. Hum. Retroviruses 13:1357-1366(1997).
                                                                                                                                                                                                                         MEDLINE=96295970; PubMed=8699119;
Combadiere C., Ahuja S.K., Tifffany H.L., Murphy P.M.;
"Cloning and functional expression of CC CKR5, a human monocyte
chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and
                                                                                                                                                                                                                                                                                                                                                                                  McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., Mhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K., Ghoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D., Sagripanti J.L., Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kopatz S.A., Aronstam R.S., Sharma S.V.; "cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org)."; submitted (JAN-2003) to the EMBL/GenBank/DDEJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
MEDLINE=96260017; PubMed=8649511;
Deng H., Liu R., Ellmeier W., Choe S., Unutmaz D., Burkhart M.,
di Marzio P., Marmon S., Sutton R.E., Hill C.M., Davis C.B.,
Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;
"Identification of a major co-receptor for primary isolates of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Magierowska M., Barre-Sinoussi F., Issafras H., Theodorou
Debre P.,
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND VARIANT ARG-178.
                                                                                                                                                               Biol. Chem. 271:17161-17166(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=98001387; PubMed=9343222;
                                                                                                                                                                                                                                                                                                                            J. Leukoc. Biol. 60:147-152(1996)
  CC-chemokine receptor gene.";
Biochemistry 35:3362-3367(1996).
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or send an email to license@isb-sib.ch).
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REQUENCE FROM N.A.

X MEDLINE=99416438, PubMed=10486970;

X A Zhang Y.-W., Ryder O.A., Zhang Y.-P.;

RI "Sequence evolution of the CCR5 chemokine receptor gene in primates.";

RI "Sequence evolution of the CR5 chemokine. Binds to MIP-1-alpha,

CC "FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

CC "Increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.

CC differentiation.

CC -: SUBCELLULAR LOCATION: Integral membrane protein.

CC -: SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                               15-WAR-2004 (Rel. 43, Created)
15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
C-C chemokine receptor type 5 (C-C CRR-5) (CC-CRR-5) (CCRS OR CWKBRS.
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Hylobates moloch (Silvery gibbon).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hylobatidae, Hylobates.
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4F8E4F344CEB7C91 CRC64;
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100.0%; Pred. No. 6.6e-08;
ive 0; Mismatches 0;
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352 AA;
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Best Local Similarity
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MEDLINE=99416438; PubMed=10486970;

Zhang Y.-W., Ryder O.A., Zhang Y.-P.;

Zhang Y.-W., Ryder O.A., Zhang Y.-P.;

Sequence evolution of the CCR5 chemokine receptor gene in primates.";

MOl. Biol. Evol. 16:1145-1154 (1999).

-! FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

MIP-1-beta and RANTES and subsequently transduces a signal by

increasing the intracellular calcium ions level. May play a role

in the control of granulocytic lineage proliferation or
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR5)
CCR5 OR CMKRR5.
Hylobates leucogenys (White-cheeked gibbon)
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Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
NCBI TaxID=61853;
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
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E EMBL, AF011534; AAB65734.1; ...
E EMBL, AF011535; AAB65735.1; ...
EMBL, AF011537; AAB65736.1; ...
EMBL, AF011537; AAB65737.1; ...
EMBL, AF01237, AAB94735.1; ...
EMBL, AY221093; AAD18131.1; ...
Genew, HGNC.1606; CGRS.
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CCRS OR CMKBRS.
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-! FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.
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15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
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                                                                                                                                           InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODDPSN.
PROSITE; PS00237; GPOTEIN RECEP_F1 1; 1.
PROSITE; PS50262; G_PROTEIN RECEP_F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
DOMAIN
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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les 18; Conservative (
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SEQUENCE FROM N.A.
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MEDLINE=98022612; PubMed=9359654;
Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
Ho D.D.;
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P56440; 002778;
15-JTL-1998 (Rel. 36, Last sequence update)
16-JTL-1998 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR5).
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  as its content is in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.
NCBL_TaxID=9598;
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100.0%; Pred. No. 6.6e-08;
.ive 0; Mismatches 0; Indels
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Zimmerman P.A., Buckler-White A., Alkhatib G.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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SULPATION (BY SIMILARITY)
SULFATION (BY SIMILARITY)
P4F64B3AD5AF65BA CRC64;
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
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Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@isb-sib.ch).
                                                                                                                              EMBL, AF177884, AAK43367.1; -.
InterPro, IPR000276; GPCR_Rhodpsn.
Pfam, PF00001; 7rm 1; 1.
PRINTS; PR000237; GFRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phylogeny.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RAWTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
                                                          SEQUENCE FROM N.A.
MEDLINE=97426118; PubMed=9282822;
Zacharova V., Zachar V., Goustin A.S.;
"Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Galiferinication:
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
"HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism."; AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDILINE=98090115; PubMed=9430250;
MEDILINE=98090115; PubMed=9430250;
Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.;
"Chimpanzee CKR4 and CKR5 act as coreceptors for HIV type 1.";
AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
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N-LINKED (GLCNAC. . . ) (POT
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                        HIV type 1 host.";
AIDS Res. Hum. Retroviruses 13:1159-1161(1997).
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-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or
                                                                        Gaps
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR-5) (CCR-5)
CCR5 OR CMCRRS.
Papio hamadryas (Hamadryas baboon), and
Papio anubis (Olive baboon),
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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MEDLINE 97268687; PubMed-9108095;
Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
Piper S.C., Parmentier M., Broder C.C., Doms R.W.;
simian immunodeficiency virus strains.";
Froc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
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MEDLINE=99210133; PubMed=10195758;
Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., I "Species-specific changes in the CCR5 gene from African and inonhuman primates."; https://doi.org/10.1016/j.j.
       Length 352;
Query Match 100.0%; Score 96; DB 1; Length 35
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels
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EMBL; AF10528; AAD20556.1; --
EMBL; AF105288; AAD20557.1; --
EMBL; AF105289; AAD20558.1; --
EMBL; AF105290; AAD20559.1; --
EMBL; AF03452; AAC63830.1; --
InterPro; IPR000276; GPCR.Rhodpsn.
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                                                                                                                                      1 SOYOFWKNFOTLKIVILG 18
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NCBI_TaxID=9557, 9555;
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EMBL; AF075445; AAD19857.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
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NCBI_TaxID=61621;
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MEDLINE=99416438; PubMed=10486970;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Saquence evolution of the CRR5 chemokine receptor gene in primates.";
Mol. Biol. Evol. 16:1145-1154(1999).
-! FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
-! FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
in Increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
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28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         differentiation.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pongo pygmaeus (Orangutan).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
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Pred. No. 6.6e-08;
                                                                              EXTRACELLULAR

3 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

4 (POTENTIAL).

5 (POTENTIAL).

5 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
SULFATION (BY SIMILARITY).
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SULFATION (BY SIMILARITY).
NILRATION (BY SIMILARITY).
NILRATION (BY SIMILARITY).
NILRATION (BY SIMILARITY).
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SE1504A9BA1FE8B2 CRC64;
                                                 1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                185 SQYQFWKNFQTLKIVILG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                CKRS PONPY STANDARD; 1097881; 30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                    1 SOYOFWKNFOTLKIVILG 18
                                                                                                                                                                                                                                                                                  40489 MW;
                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                            18; Conservative
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                  352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCRS OR CMKBR5.
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DOMAIN
TRANSMEM
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DOMAIN
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TRANSMEM
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CKR5_PONPY
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Matches
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MEDLINE=99416438; PubMed=10486970;
Mand Y.-W., Ryder O.A., Zhang Y.-P.;
Mand Y.-W., Ryder O.A., Zhang Y.-P.;
Mol. Biol. Evol. 16:1145-1154(1999).
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
-!- FUNCTION: Receptor for a c-C type chemokine. Binds to MIP-1-alpha,
-!- FUNCTION: Receptor for a c-C type chemokine. Binds to MIP-1-alpha,
-!- FUNCTION: Receptor for a c-C type chemokine. Binds to MIP-1-alpha,
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-!- FUNCTION: Receptor for a c-C type chemokine. Binds to MIP-1-alpha,
-!- FUNCTION: Receptor for a c-C type chemokine. Binds to MIP-1-alpha,
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-!- FUNCTION: Receptor for a c-C type chemokine. Binds to MIP-1-alpha,
-!- FUNCTION: Receptor for a c-C type chemokine. Binds to MIP-1-alpha,
-!- FUNCTION: Receptor for a c-C type chemokine.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CRR-5) (CC-CRR-5) (CC-CRR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  differentiation.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS0237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

DOWAIN

TRANSMEM

31 58 1 (POTENTIAL).
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SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).

**, F4E2F47135AF658A CRC64;
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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SULFATION (BY SIMILARITY)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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Best Local Similarity luc..
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nterPro; IPR000276; GPCR_Rhodpsn.
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DOMAIN
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99416438; PubMed=10486970; Zhang Y.-F.; Zhang Y.-W., Ryder O.A., Zhang Y.-F.; Zhang Y.-P.; Zhang Y.-P.; Sequence evolution of the CCR5 chemokine receptor gene in primates."; Mol. Biol. Evol. 16:1145-1154(1999).
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordatā; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C.C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCRS).
Pfam, PF00001, 7tm 1, 1.

PRINTS; PR00237; GPCRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50362; G_PROTEIN_RECEP_F1_2; 1.

G_PROSITE; PS50362; G_PROTEIN_RECEP_F1_2; 1.

G_PROSITE; PS50362; G_PROTEIN_RECEP_F1_2; 1.

G_PROSITE; PS50362; G_PROTEIN_RECEP_F1_2; 1.

G_PROSITE; PS50362; G_PROTEIN_RECEP_F1_2; 1.

G_PROSITE RECEP_F1_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
4366F142730F938F CRC64;
                                                                                                                                    1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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SULFATION (BY SIMILARITY
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Pred. No. 6.6e-08;
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100.0%;
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Les 18; Conservative
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Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Sequence evolution of the CCRs chemokine receptor gene in primates.";
Mol. Biol. Evol. 16:1145-1154(1999).
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
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Bukaryota, Metazoa; Chordata; Craniata; Verrebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
Trachypithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR5)
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SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
SULFATION (BY SIMILARITY).
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SULFATION (BY SIMILARITY).
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SULFATION (BY SIMILARITY).
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EXTRACELLULAR (POTENTIAL)
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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100.0%; Pred. No. 6.6e-08;
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es 18; Conserv
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097878;
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us-10-084-813-13.rsp

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EMBL; AF075443; AAD19855.1; -.

Interpro; IPR000276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRHODDPSN.

PROSITE; PS00237; G PROTEIN RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G_PROTEIN COUpled receptor; Transmembrane; Glycoprotein; Sulfation.

G_Protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=M.mulatta; STRAIN=Indian macaque;
MEDLINE=97213934; PubMed=9060623;
Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
Genetically divergent strains of simian immunodeficiency virus use CCRS as a coreceptor for entry.";
J. Virol. 71:2705-2714(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRRS MACMU STANDARD; PRT; 352 AA.
P79436; 002746;
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
CCC chemokina receptor type 5 (C-C CRR-5) (CC-CRR-5) (CC-CRS).
Macaca mulatta (Rhesus macaque),
Macaca mulatta (Crab eating macaque) (Cynomolgus monkey), and
Macaca nemestrina (Pig-tailed macaque).
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SPECIES=M.mulatia;
SPECIES=M.mulatia;
MEDILINE=9718452;
PubMed=9032394;
Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,
Newman W., Gerard N., Gerard C., Sodroski J.;
Mutilization of C-C chemokine receptor 5 by the envelope
glycoproteins of a pathogenic simian immunodeficiency virus,
SIVMac239.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 352;
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2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
5 XTRACELLULA.
5 (POTENTIAL).
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6 (POTENTIAL).
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6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
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100.0%; Pred. No. 6.6e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cercopithecinae; Macaca.
NCBI_TaxID=9544, 9541, 9545;
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"Sequence evolution of the CCRS chemokine receptor gene in primates.";

"Sequence evolution of the CCRS chemokine. Binds to MIP-1-alpha,

Mol. Biol. Bvol. 16:1145-1154(1999).

-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

MIP-1-beta and RANTES and subsequently transduces a signal by

increasing the intracellular calcium ions level. May play a role

in the control of granulocytic lineage proliferation or

differentiation.

-!- SUBCELIULAR LOCATION: Integral membrane protein.

-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
90-MAY-2000 (Rel. 39, Last sequence update)
28-FBB-2003 (Rel. 41, Last amnotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5)
EMBL; AP075442; AAD19854.1; -.

InterPro; IPR000276; GPCR_Rhodpsn.

PEAM; PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRHODDPSN.

PROSITE; PS00237; GPROTEIN RECEP_F1 1; 1.

PROSITE; PS00262; G_PROTEIN_RECEP_F1 2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation. I 30 EXTRACELLULAR (POTENTIAL).

TRANSMEM 31 S I (POTENTIAL).

DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
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Pred. No. 6.6e-08;
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4366F148C255938F CRC64;
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CYTOPLASMIC (POTENTIAL).
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MEDLINE=99416438; PubMed=10486970;
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Best Local Similarity 100.
Matches 18; Conservative
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352 AA;
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                                                                                                                                    SPECIES—M. mulatta, M. fascicularis, and M.nemestrina;
X. MEDINES—100095;
A. Beinger A.J., Amedee A., Miller, K., Doranz B.J., Endres M.,
Edinger A.L., Amedee M., Miller, C., Doranz B.J., Endres M.,
Sharron M., Samson M., iu Z.H., Clements J.E., Murphey-Corb M.,
A. Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
T. Differential utilization of CCR5 by macrophage and T cell tropic
T. Simian immunodeficiatory virus strains.",
L. Proc. NMLI. Acad. Sci. U.S.A. 94:4005-4010(1997)
L. Proc. NMLI. Acad. Sci. U.S.A. 94:4005-4010(1997)
C. I. FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and Subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
C. I. SUMCERLULAR LOCATION: Integral membrane protein.
C. I. SUMLARITY: Belongs to family 1 of G-protein coupled receptors.
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R EMBL; U73739; AAC51158-1; -
R EMBL; U73739; AAC51158-1; -
R EMBL; AF005660; AAB6255-1; -
R EMBL; AF005661; AAB62555-1; -
R EMBL; AF005662; AAB62555-1; -
R EMBL; AF005662; AAB62555-1; -
R EMBL; AF005662; AB62555-1; -
R EMBL; AF005662; AB62555-1; -
R EMBL; AF005662; AB62555-1; -
R PRINTS; PR00237; GPCRHODOPSN.
R PROSTTE; PS00237; GPCRHODOPSN.
R PROSTTE; PS00237; GPCRHODOPSN.
R PROSTTE; PS00237; GPCRHODOPSN.
M G-procein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
T DOMAIN.
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SULFATION (BY SIMILARITY).
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SULFATION (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-Y (IN REF. 3).
I -> M (IN REF. 3).
W, 58B96C85909FACB2 CRC64;
                                                      Margulies B.J., Hauer D.A., Clements J.E.; "Identification and comparison of eleven rhesus macaque chemokine
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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SULFATION (BY SULFATION (BY
                      SPECIES=M.mulatta;
MEDLINE=21354176; PubMed=11461684;
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352 AA;
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Length 352;

Score 93; DB 1; Pred. No. 2e-07;

96.9%;

Query Match Best Local Similarity

28 15:49:57 2004

Tue Sep

008556;

Gaps . 0 Length 354; 77.1%; Score 74; DB 1; Length 354 76.5%; Pred. No. 0.0002; ive 3; Mismatches 1; Indels 1 SOYOFWKNFOTLKIVIL 17 Conservative Local Similarity es 13; Conserv Query Match **fatches** 

40863 MW;

CONFLICT CONFLICT SEQUENCE

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RESULT 18 CKR5\_RAT ID \_CKR5\_RAT

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354 AA.

PRT;

STANDARD;

EXPUNENCE FROM N.A.

RECORDINE=9818173; PubMed=9555467;

RA Diang Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K., Diang Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K., Diang Y. Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K., Diang P. C., Pennell N.A., Streit W.J., Harrison J.K.;

RT "Chemokine receptor expression in cultured glia and rat experimental RT "lergic encephalomyelltis.";

RT "Isragic encephalomyelltis.";

RJ J. Neuroimmunol. 86:1-12(1988).

C. I. FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, In J. Neuroimmunol. 86:1-12(1988).

C. I. FUNCTION: Receptor for a C-C type chemokine signal by Increasing the intracellular calcium ions level.

C. I. SUBCELLULAR LOCATION: Integral membrane protein.

C. I. SUBCELLULAR LOCATION: Integral Rattus norvegicus (Rat). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 01-NOV-1997 (Rel. 35, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (MIP-1 STRAIN=Wistar; TISSUE=Brain;
BEDIINE=9834064; Pubmed=9670989;
Spleiss O., Gourmala N., Boddeke H.W.G.M., Sauter A., Fiebich B.L.,
Berger M., Gebicke-Haerter P.J.;
"Cloning of rat HIV-1-chemokine coreceptor CKR5 from microglia and
upregulation of its mRNA in ischemic and endotoxinemic rat brain.";
J. Neurosci. Res. 53:16-28(1998). -LINKED (GLCNAC. . .) (POTENTIAL) 77EDB368A4C868D CRC64; EMBL, V12009; CAA72737.1; -.
EMBL, V17350; AAC0343.1; -.
InterPro; IPRO00276; GPCR\_Rhodpsn.
Pfam; PF00001; 7tm\_1; 1.
PRINTS; PR00237; GPCRHODPSN.
PROSITE; PS00237; GPROTEIN RECEP\_F1\_2; 1.
PROSITE; PS0262; G\_PROTEIN RECEP\_F1\_2; 1.
PROSITE: PS0262; G\_PROTEIN RECEP\_F1\_2; 1. 3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLUGAR (POTENTIAL).
EXTRACELLUGAR (POTENTIAL).
7 (POTENTIAL). 2 (POTENTIAL). EXTRACELLULAR (POTENTIAL) CYTOPLASMIC (POTENTIAL). 7 (POTENTIAL). CYTOPLASMIC (POTENTIAL). BY SIMILARITY. 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last seq 30-MAY-2000 (Rel. 39, Last ann 41030 MW; 354 AA; SEQUENCE FROM N.A. SEQUENCE FROM N.A. NCBI\_TaxID=10116; alpha receptor). CCR5 OR CMKBR5. DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN DISULFID CARBOHYD SEQUENCE DOMAIN TRANSMEM DOMAIN 

ö Score 74; DB 1; Length 354; Pred. No. 0.0002; 3; Mismatches 0; Indels ch 77.1%; 1 Similarity 81.2%; 13; Conservative 3 Query Match Best Local Similarity Matches 13; Conserv

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Gaps

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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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R EMBL; U28404; AAA86119.1; -
R EMBL; U28404; AAA89153.1; -
R EMBL; BOURD2; AAH11092.1; -
R EMBL; BOURD2; AAH11092.1; -
R EMBL; GO COURT CALL
R GO; GO: 0005515; F: protein binding; IPI.
GO; GO: 0005515; F: protein binding; IPI.
GO; GO: 0005515; F: protein binding; IPI.
GO; GO: 000599; P: inflammatory response; IMP.
GO; GO: 000599; P: inflammatory response; IMP.
R Ffam; PF0001; 7tm 1; 1.
R PRINTS; PRO027; GPCRENDODPSN.
R PROSITE; PS00237; G PROTEIN RECEP FI 1; 1.
R G-Protein coupled receptor; Transmembrane.
M G-Protein Coupled receptor; Transmembrane.
TRANSMEM 35 60 1 (POTENTIAL).
TRANSMEM 36 60 1 (COMPANTIAL).
THENNING COUPLESSILE (POTENTIAL).
THENNING COUPLESSILE (POTENTIAL).
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EXTRACELLUAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
M -> V (IN REF. 3).
H -> Q (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
5 (POTENTIAL).
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FCE9FFF70E6F38B1 CRC64;
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CYTOPLASMIC (POTENTIAL).
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Conservative
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195 WKRFQALKINLLG 207
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CKR2 MOUSE
CKR2 MOUSE
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DT 01-NOV-DT 28-FEB-DE (-C-CAPRO)
DF CCC CAPRO
OC BUKBTY,
OC BUKBTY,
OC MARMABI.
OC MARMABI.
OC BUKBTY,
OC MARMABI.
OC MAR
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**A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

**A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

**A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

**A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

**A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

**A Altschul S.F., Zeeberg B., Bonaldo M.F., Carainot P., Haieh F.,

**Brownstein M.J., Usdin T.B., Toshiyuki S., Carninot P., Prange C.,

**Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

**Roback S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

**Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

**Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

**Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

**Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

**Richards S., Worley K.C., Schards S.J., In X., Gibbs R.A.,

**A Haley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

**A Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

**A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

**A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

**A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

**A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

**Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)

**Proc. Mall D.ESS EFFICISHLY. TOWLELLER FOR AFFECTING STEM CELL

**PROC. PROC. P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=129/SvJ;
MEDINE=59540546, PubMed=7542241;
MEDINE=59540546, PubMed=7542241;
"Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor-";
J. Biol. Chem. 270:17494-17501(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gerard C.; "Molecular characterization of two murine eosinophil beta chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELUIAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Detected in the heart, spleen, lung, peritoneal exudate cells and leukocytes.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Wakaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                               CKRI_MOUSE STANDARD; PRT; 355 AA.
P51675; Q91VP9;
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2003 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
(Macrophage inflammatory protein-1 alpha receptor) (MIP-1alpha-R) (RANTES-R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=129/Sv; TISSUE=Peritoneal macrophage;
MEDLINE=96072806; PubMed=7594543;
Post T.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptors.";
J. Immunol. 155:5299-5305(1995).
                                                        ||:|||:|||:||| ||:||| QYRFWKHFQTLKMVIL 203
                                 2 OYOFWKNEOTLKIVIL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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CKR2 MOUSE STANDARD; PRT; 373 AA.

CKR2 MOUSE STANDARD;

01-0CT-1996 (Rel. 34, Created)

01-NOV-1997 (Rel. 35, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

CC chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2)

CJE/FIC receptor) (MCP-1 receptor).

CCR2 OR CMKBR2. SEQUENCE FROM N.A. MEDLINE=96205938; PubMed=8631787; Boring L., Gosling J., Monteclaro F.S., Lusis A.J., Tsou C.-L., Charo I.F.;

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CKR1 MACMU
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                                                                                                                                                                                                                                      MGD; MGI:106185; CCT2.

R GO; GO:0016493; F:C-C chemokine receptor activity; IDA.

R GO; GO:0019955; P:C-C chemokine binding; IPI.

GO; GO:0019955; P:C-C chemokine binding; IPI.

R GO; GO:0010995; P:C-C chemokine response (sensu Vertebrata); IMP.

R GO; GO:0006959; P:Nemopoiesis; IMP.

R GO; GO:0006959; P:Nemopoiesis; IMP.

R GO; GO:0006954; P:Inflammatory response; IMP.

R GO; GO:0010334; P:regulation of cell migration; IMP.

R FO; GO:001037; GPCRRHODOPSN.

R PRINTS; PRO0201; Tem 1; 1.

R PROSITE; PS00237; GPCRHODOPSN.

R PROSITE; PS00262; GPROTEIN RECEP FI 1; 1.

R PROSITE; PS00262; GPROTEIN RECEP FI 2; 1.

M GO:DOCCOMPANIAN CONTRIBER FI 2; 1.
"Molecular cloning and functional expression of murine JE (monocyte chemoattractant protein 1) and murine macrophage inflammatory protein laipha receptors: evidence for two closely linked C-C chemokine receptors on chromosome 9.";
J. Biol. Chem. 271:7551-7558(1996).
                                                                                                                                                              Kurihara T., Bravo R.; "Cloning and functional expression of mCCR2, a murine receptor for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

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CYTOPLASMIC (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

BY SIMILARITY.

Y -> H (IN REF. 1).

A -> G (IN REF. 1).
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                                                                                                                                                                                               the C-C chemokines JE and FIC.";
J. Biol. Chem. 271:11603-11606(1996).
                                                                                                                            STRAIN=BALB/c;
MEDLINE=96216064; PubMed=8662823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U47035; AAC52453.1; -. EMBL; U51717; AAC52557.1; -. EMBL; U56819; AAC52784.1; -. MQD; MGI:106185; CCr2.
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SEQUENCE FROM N.A.
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                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptors.";
AIDS Res. Hum. Retroviruses 17:981-986(2001).
-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOXINE. BINDS TO MIP-1-ALPHA, RANTES, MCP-3 AND, LESS BFFICIENTLY, TO MIP-1-BETA OR MCP-1 AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING STEM CELL
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
18-EBB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 1 (C-C CKR-1) (CC-CKR-1) (CCR.1).
CCR1 CR CWKBR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

**BEDLINE=21354176, PubMed=11461684;

**Marguline=21354176, Hauer D.A., Clements J.E.;

**Marguline=8 B.J., Hauer D.A., Clements J.E.;

**Identification and comparison of eleven rhesus macaque chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae;
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CYTOPLASMIC (FOTENTIAL).
N-LINKED (GLCNAC. ..) (FOTENTIAL).
BY SIMILARITY.
                                                                                                                                                ..
                                                                                  Length 373;
                                                                                                                                                4; Indels
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001, 7tml; 1.
PRINTS; PR00237; GPCRHODDSN.
PROSITE; PS00237; GPCRHODPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
DOMAIN

EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
264 264 V -> G (IN REF. 1).
373 AA; 42782 MW; FA012C10F4C9325A CRC64;
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CYTOPLASMIC (POTENTIAL).
                                                                                  Ouery Match
Best Local Similarity 64.3%; Pred. No. 5.8;
Matches 9; Conservative 1; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                               355 AA
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                                                                                                                                                                                                          4 QFWKNFQTLKIVIL 17
                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                               CKR1_MACMU
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                                                                                                                       Gaps
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ciliary dynein heavy chain 11 (Axonemal beta dynein heavy chain 11).
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ARG-639; CYS-654; ALA-1023; THR-1038; GLY-1640; ASN-2641; THR-3474;
VAL-3715; PRO-3765 AND ILE-4177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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STRAIN=Z / UNIX 753;
STRAIN=Z / UNIX 753;
Hallick R.B., Hong L., Drager R.G., Favreau M.R., Monfort A., Orsat B., Spielmann A., Stutz B.;
"Complete sequence of Euglena gracilis chloroplast DNA.";
Nucleic Acids Res. 21:3537-3544(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.9%; Score 45; DB 1; Length 634; 55.6%; Pred. No. 14; 2; Indels iive 2; Indels
                                                        Score 45; DB 1; Length 355;
Pred. No. 8;
                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                              YCX3_EUGGR STANDARD; PRT; 634 AA.
P31916; P31917;
01-JUL-1993 (Rel. 2)
01-FBE-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 78.0 kDa protein in PSBC intron 2 (ORF635).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z11874; -; NOT ANNOTATED_CDS.

EMBL; X70810; CAA50080.1; -.

PIR; S34499; S34499.

PIR; S34500; S34500.

Chloroplast; Hypothetical protein.

SEQUENCE 634 AA; 78049 NW; D966B8864519E334 CRC64;
355 AA; 41198 MW; 41CAEA7CC19D23D4 CRC64;
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NCBI_TaxID=3039;
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                                                                                                              3; Mismatches
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                      Ouery Match
Best Local Similarity 55.0
Best Local 10; Conservative
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Chloroplast.
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AC 0960F2; 090H2
DT 28-FEB-2003
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RETISGUE-Assal spithalium and Testis;

RETISGUE-Assal spithalium and Testis;

RETISGUE-ASSA STANDAG-1214446;

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RETISGUE-ASSA STANDAG-1214446;

RETISGUE-ASSA STANDAG-1214446;

RETISGUE-ASSA STANDAG-1214446;

RETISGUE-ASSA STANDAG-1214446;

RETISGUE-ASSA STANDAG-121446;

RETISGUE-ASSA STANDAG-121466;

RETISGUE-ASSA STANDAG-12146;

RETISGUE-ASSA STANDAG-12146;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K., Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
"The complete genomic sequence of Mycoplasma penetrans, an intracellular bacterial pathogen in humans.";
Nucleic Acids Res. 30:5293-5300(2002).
-!- CATALWITY: Carbamoyl phosphate + L-aspartate = phosphate + N-carbamoyl-L-aspartability biosynthesis; second step.
-!- PATHWAX: Pyrimidine biosynthesis; second step.
-!- SIMILARITY: Belongs to the ATCase/OTCase family.
                                     -!- FUNCTION: Involved in protein export (By similarity).
-!- SUBUNIT: Part of the prokaryotic protein translocation apparatus which comprise secA, secB, secB, secE, secF, secG and secY (By
                                                                                                                    similarity).
SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
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Complete proteome. 31 POTENTIAL.
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                                                                                                                                                            (By similarity).
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Pred. No. 20;
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15-MAR-2004 (Rel. 43, Last annotation update)
Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate
transcarbamylase) (ATCase).
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7DE1E4B085065F8F CRC64;
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STRAIN=HF-2;
MEDLINE=22354719; PubMed=12466555;
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InterPro; IPR003335; SecD_SecF.
Pfam; PF02355; SecD_SecF; I.
PRINTS; PR01755; SEĞFTRNLCASE.
TIGRRAMS; TIGR00916; ZA0604801; I.
TIGRRAMS; TIGR01129; SecD; I.
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                      Science 269:496-512(1995).
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Best Local Similarity 38.5.
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PYRB OR MYPE7890.
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PYRB_MYCPE
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STRAIN=Rd / KW20 / ATCC 51907;

MEDLIXE=95550630; PubMed=7542800;

Relischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fitchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Venter J.C., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.,
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Pasteurellaceae; Haemophilus.
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Pred. No. 97;
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/FTIA=VAR 013863.
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FTId=VAR_013860.
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(Rel. 32, Last sequence update)
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                                                                       (POTENTIAL).
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substitutions)
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  COILED COILED COILED COILED ATP (PO)
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                                                                                                                                                                             EMBL, APPO4173; BAC44582.1; -.

R HAMAP; MF 00001; -; 1.

R InterPro; IPR006131; ASp/orn COtranf.

R InterPro; IPR006131; OTGace_O.

R InterPro; IPR006132; OTGace_O.

R Pfam; PF00185; OTCace_P.

R Pfam; PF02729; OTGace, 1.

R Pfam; PF02729; OTGace, 1.

R Pfam; PF02729; OTGace, 1.

R PF1075; PR00100; AOTGĀSE.

R PROSITE; PS00907; CARBAMOYITRĀNSFERĀSE; 1.

W PYLINIGHE ÞIOSYT, CARBAMOYITRĀNSFERĀSE; 1.

W PYLINIGHE ÞIOSYT, CARBAMOYITRĀNSFERĀSE; 1.

W PYLINIGHE ÞIOSYT, CARBAMOYITRĀNSFERĀSE; 1.
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44.8%; Score 43; DB 1; Length 300; 50.0%; Pred. No. 14; 1. Indels ive 5; Mismatches 3; Indels 3 YQFWKNFQTLKIVILG 18 | : : | : | | | : | 143 YEKFKSFEGLKIAIVG 158 Query Match
Best Local Similarity 50.0°
Matches 8; Conservative g

15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3) (CCR-3) (CCR3) STANDARD; CCR3 OR CMKBR3. CKR3 CERAE P56492; 

SEQUENCE FROM N.A.

Sol N., Treboute C., Gomas E., Ferchal F., Alizon M.;

Sul N., Treboute C., Gomas E., Ferchal F., Alizon M.;

Submitted (Un1-1997) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,

MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors. Cercopithecus aethiops (Green monkey) (Grivet).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.

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EMBL; Y1375; CAA74106.1; -...
InterPro; IRRO00276; GPCR\_Rhodpsn.
PRINTS; PRO0037; GPCRFADOPSN.
PROSITE; PSO0237; GPROTEIN RECEP\_F1\_2; I.
PROSITE; PSSO262; G\_PROTEIN\_RECEP\_F1\_2; I.
G\_PROTEIN\_RASSEMENT (POTEINIAL).
TRANSMEM 35 62 I (POTENTIAL).

6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
4) 44F7ASEFEEB978FF CRC64; 3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL). 2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL) (POTENTIAL). (POTENTIAL) MW. 40830 306 106 355 AA; DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN DISULFID SEQUENCE 

ô Score 43; DB 1; Length 355; Pred. No. 17; 3; Mismatches 2; Indels 44.88; 58.3%; Query Match
Query Match
Best Local Similarity 58.3%,
Best Local Similarity 58.3%,

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6 WXNFQTLKIVIL 17 |::|||:|| 195 WRHFHTLKMTIL 206

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Gaps

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STANDARD; MACMU RESULT 27 CKR3\_MACMU ID CKR3\_MACM AC P56483;

15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 41, Last annotation update)
C-C chemokine receptor type 3 (C-C CKR-3) (CCR3) (CKR3).

Macaca mulatta (Rhesus macaque).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Butheria, Primates, Catarrhini, Cercopithecidae;
Cercopithecinae, Macaca. SEQUENCE FROM N.A.
MEDLINE=21354176; PubMed=11461684;
Margulies B.J., Hauer D.A., Clements J.E.;
"Identification and comparison of eleven rhesus macaque chemokine

receptors."; AIDS Res. Hum. Retroviruses 17:981-986(2001) 

NOTIONAL PROM N.A.

PEQUENCE FROM N.A.

RA SIGNEME=98118416; PubMed=9454694;

RA SOL N., Treboute C., Gomas E., Ferchal F., Shacklett B., Alizon M.;

RT for HIV-2, but not for HIV-1.";

RT for HIV-2, but not for HIV-1.";

RU Virology 240.213-220(1998).

CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to ectaxin,

CC --- FUNCTION: Receptor for a C-C type chemokine a signal by

INCREASING HE INTERCEILULAR and subsequently transduces a signal by

CC --- SUBCELLULAR LOCATION: Integral membrane protein.

CC --- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

CC --- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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EMBL; AF017283; AAB70527.1; -. EMBL; Y13776; CAA74107.1; -. InterPro; IPR000276; GPCR\_Rhodpsn. Pfam; PF00001; 7tm 1; 1. — PRINTS; PR00237; GPCRRHODOPSN

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Fartinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
RA Grattapaglia D., Grisard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA Madeira H.M.F., Manfilo G.P., Maranhao A.C., Martins W.S.,
A immuro S.M.Z., de Wedeiros R.R.B., Meissner R.V., Moreira M.A.,
RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Pereira J.C.,
RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
RA Santos B.B.P., Santos F.R., Schneider M.P.C., Seuanez H.N.,
Souza R.C., Steffens M.B.R., Schneider M.P.C., Seuanez H.N.,
R. Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Souza K.R.L.,
RA Santos B.B., Sonzes C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
RA Silva A.M.R., Soares R.B.A., Simpson A.J.G.,
R.Y. The complete genome sequence of Chromobacterium violaceum reveals
RT Tremarkable and exploitable bacterial adaptability.",
RT Tryptophan + O(2) = 5-hydroxytryptophan.
C. CATALYTIC ACTIVITY: Tryptophan + O(2) = 5-hydroxytryptophan.
C. CATALYTIC ACTIVITY: Tryptophan + O(2) = 5-hydroxytryptophan.
C. I. DNDUCTION: By N-acylhomoserine lactone (AHL).
C. I. NDUCTION: By N-acylhomoserine lactone (AHL).
C. I. BUTCHONCY: Violacein biosynthesis, branch 2; first step.
C. I. INDUCTION: By N-acylhomoserine lactone (AHL).
C. I. BUTCHONCY: Violacein production is used as a biosensor for the artibacterial, antiviral, antitumoral activities.
C. C. Trypanocidal and potential antitumoral activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01360; Monooxygēnase; Ĩ.
PRINTS; PR00420; RNGMNOXGNASE.
Oxidoreductase; Flavoprotein; FAD; Antibiotic biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 373;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        373 AA; 41622 MW; 64205F8BCED4BC25 CRC64;
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V -> I (IN REF. 1).
V -> A (IN REF. 1).
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15-UL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Surfactin synthetase subunit 2.
SRFAB OR SRFA2 OR COML OR BSU03490.
Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
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EMBL, AB012799; BAA84785.1; -.
EMBL, AE016921, AAQ60935.1; -.
INTERPO; IPR000733; Flav monooxygnse.
InterPro; IPR0003042; Rng_mnoxygenase.
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SEQUENCE OF 1-3077 FROM N.A.
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Q04747;
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CONFLICT
SEQUENCE
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C 001-FEB
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NO ROSE
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August P.R., Grossman T.H., Minor C., Draper M.P., MacNeil I.A.,
Pemberton J.M., Call K.M., Holt D., Osburne M.S.;
Sequence analysis and functional tharacterization of the violacein
biosynthetic pathway from Chromobacterium violaceum.";
J. Mol. Microbiol. Biotechnol. 2:513-519(2000).
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STRAIN=ATCC 12472 / DSM 30191;
MEDLINE-25828280. PubMed=14500782;
MEDLINE-25828280. PubMed=14500782;
Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
Alves-Gomes J.A., Andrade E. M., Araripe V., de Araujo M.F.F.,
Astoli-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burity H.A.,
Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,
Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Chromobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43; DB 1; Length 355; Pred. No. 17;
                             PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G_-protein coupled receptor; Transmembrane.

DOWAIN 35 62 1 (POTENTIAL).

DOWAIN 73 93 2 (POTENTIAL).

TRANSMEM 73 93 2 (POTENTIAL).

DOMAIN 94 107 EXTRACELLULAR (POTENTIAL).

DOMAIN 94 107 EXTRACELLULAR (POTENTIAL).

TRANSMEM 130 146 CYTOPLASMIC (POTENTIAL).

TRANSMEM 147 171 4 (POTENTIAL).

TRANSMEM 147 171 4 (POTENTIAL).

DOMAIN 172 203 EXTRACELLULAR.

TRANSMEM 204 223 5 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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"Biosynthetic gene cluster for violacein pigment.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K -> E (IN REF. 2).
K -> R (IN REF. 2).
E271F1E694970D9F CRC64;
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15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Probable tryptophan hydroxylase vioD (EC 1.-.-.).
VIOD OR CV3271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
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195 WRHFHTLKMTIL 206
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Matches 7; Conserv
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DOMAIN
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Gaps

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MEDINE-98044033; PubMed-9384377; Albertini A.M., Alloni G.,

KURDINE-98044033; PubMed-9384377; Albertini A.M., Alloni G.,

KUNDEL R., Ogasawara N., Moszer I., Bloctin A., Borchert S.,

Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

Brouillet S., Bruschi C.V., Caldwell B., Captano V., Carter N.M.,

Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

Britz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Daniel R.A.,

Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

Britz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,

Chim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

Anibert H., Holsappel S., Haga K., Haiech J., Harwood C.R., Henaut A.,

Anibert H., Holsappel S., Haga K., Haiech J., Harwood C.R., Medin G.,

Anibert H., Holsappel S., Haga K., Haiech J., Lazarevic N.,

Anibert H., Holsappel S., Hondon S., Hullo M.F., Itaya M., Jones I.,

Anibert H., Holsappel S., Hondon S., Mauel C., Medigue C.,

Anita K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

Anita K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

An Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

Persecan E., Pujic P., Purnelle B., Rapport G., Rey M., Reynolds S.,

Anto T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

Sato T., Scanlan E., Schleich S., Schroeter R., Takeuchi M., Tamakoshi H., Takamani H., Takeman K.,

Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,

Tosato V., Uchiyama S., Vandenbol M., Vanier R., Vasaumoto K., Yata K.,

Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,

Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,

Winters P., Wipat A., Yamamoto G. the Gram-positive bacterium Bacillus

Harris M., Waller S., Waller B., Schole S., Sch STRAIN=168 / JE642;
MEDLINE=9316081; Pubmed=8355609;
MEDLINE=9316081; Pubmed=8355609;
Cosmina P., Rodriguez F., de Ferra F., Grandi G., Perego M.,
Venema G., van Sinderen D.;
"Sequence and analysis of the genetic locus responsible for surfactin Synthesis in Bacillus subfalls.";
Mol. Microbiol. 8:821-831(1993). "Nucleotide sequence of 5' portion of srfA that contains the region required for competence establishment in Bacillus subtilis."; Nucleic Acids Res. 21:93-97(1993). Yamane K., Kumano M., Kurita K., "The 25 degrees 36 degrees region of the Bacillus subtilis Chromosome: determination of the sequence of a 146 kb segment and identification of 113 genes."; Microbiology 142:3047-3056(1996). ., Fujishima Y., Corbell N., D'Souza C., Nakano M.M., WEDLINE=93181186; PubMed=8441623; MEDLINE=97124189; PubMed=8969502; Yamane K.; SEQUENCE FROM N.A. SEQUENCE FROM N.A. [2] SEQUENCE FROM N.A. STRAIN=168 Fuma S zuber 

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PATHWAY: Cyclic peptide antibiotic surfactin biosynthesis. SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme

-1- SIMILARITY: Contains 3 acyl carrier domains

S -> FOUR REF. 1).
A -> G (IN REF. 1).
A -> G (IN REF. 1).
C -> D (IN REF. 1).
C -> D (IN REF. 1).
C -> W (IN REF. 1).
C -> M (IN REF. 1).
C -> L (IN REF. 1).
C -> C (IN REF. 1). EMBL; D13222; BAA02553.1; 
BRBL; D5043; BAA02553.1; 
BRBL; D5043; BAA02593.1; 
BRBL; X70356; CAA49817.1; 
BRBL; X65835; CAA46678.1; 
BRSP, P140486; LA40486.

BR HSSP; P140681; AMP-bind.

BR InterPro; IPR006163; Pp bind.

InterPro; IPR006163; Pp bind.

BR InterPro; IPR006163; Pp bind.

BR InterPro; IPR006163; Pp bind.

BR FROSTIE; PR006163; Pp bind.

BR FROSTIE; PR00154; AMP-binding; 3.

BR PROSTIE; PR001654; AMP-BINDING; 3.

BR PROSTIE; PS00015; ACP\_DOMAIN; 3.

BROSTIE; PS00015; ACP\_DOMAIN; 3.

BROMAIN 2015 2082 ACYL CARRIER (ACP) 1.

BOWAIN 3043 3109 ACYL CARRIER (ACP) 3.

BINDING 2045 2045 PHOSPHOPANTETHEINE (POTENTIAL).

BINDING 2045 2045 PHOSPHOPANTETHEINE (POTENTIAL).

BRINDING 2045 2045 PHOSPHOPANTETHEINE (POTENTIAL).

BRINDING 2045 2045 PHOSPHOPANTETHEINE (POTENTIAL).

BRINDING 2045 2045 PHOSPHOPANTETHEINE (POTENTIAL). 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 101010 10 11133 1310 1333 1384 1582 648 680 788 788 11038 11133 11333 11333 2075 2079 2141 1915 CONFLICT
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STRAIN=ATCC 21332;
MEDLINE=22290255; PubMed=1601288;
Borchert S., Patil S.S., Marahiel M.A.;
"Identification of putative multifunctional peptide synthetase genes using highly conserved oligonucleotide sequences derived from known

SEQUENCE OF 514-800 FROM N.A. Nature 390:249-256(1997).

synthetases.";
FEMS Microbiol. Lett. 71:175-180(1992).
-!- FUNCTION: THIS PROTEIN IS A MULTIFUNCTIONAL ENZYME ABLE TO
-!- FUNCTION: THIS PROTEIN IS A MULTIFUNCTIONAL ENZYME ABLE TO
ACTIVATE AND POLYMERIZE THE AMINO ACIDS LEU, GLU, ASP AND VAL.
ACTIVATION SITES FOR THESE AA CONSIST OF INDIVIDUAL DOMAINS.
-!- COFACTOR: Contains 3 covalently bound phosphopantetheines.

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Gaps

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Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Federspiel N., Hyman R., Roberts D., Schramm S., Davis R.W.; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM FOR FERRIC ENTEROBACHTIN. PROBABLY RESPONSIBLE FOR THE TRANSLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE.
-!- SUBCELLIARA LOCATION: Integral membrane protein. Inner membrane.
-!- INDUCTION: Controlled in part by the amount of available iron.
-!- SIMILARITY: Belongs to the binding-protein-dependent transport system permease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shea C.M., McIntosh M.A.;
"Nucleotide sequence and genetic organization of the ferric
enterobactin transport system; homology to other periplasmic binding
protein-dependent systems in Bscherichia coli.";
Mol. Microbiol, 5:1415-1428(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chenault S.S., Earhart C.F.; "Organization of genes encoding membrane proteins of the Escherichia coli ferrienterobactin permease."; Mol. Microbiol. 5:1405-1413(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=K12 / MG1655,
STRAIN=K12 / MG1669 J., Plunkett G. III, Bloch C.A., Perna N.T., Buxland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                  FEPD_ECOLI STANDARD; PRT; 334 AA.
P21876; P77097;
01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ferric enterobactin transport system permease protein fepD.
                              ID -> MH (IN REF. 2).
AHDSLD -> GMIRWI (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                 Length 241;
                                                                          241 AA; 26735 MW; BF6FBBC7FB14B5AD CRC64;
                                                                                                                 43.8%; Score 42; DB 1;
63.6%; Pred. No. 16;
iive 3; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                334 AA
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InterPro; IPR005834; Hydrolase.
                   Pfam; PF00702; Hydrolase; 1.
CONFLICT 70 71
                                                                                                                                                               7; Conservative
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231 KYQVYKNFETL 241
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli.
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Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=562;
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                                                          CONFLICT
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ID FEPD E(
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      E -> Q (IN REF. 1).
ATDLF -> RQICS (IN REF. 1).
TVHQLFEETVQRHKDRPAVTY -> DGCISYSKRLSSATKT
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MEDILINE=9731264; PubMed=9169868;
MEDILINE=9731264; PubMed=9169868;
MEDILINE=9731264; PubMed=9169868;
Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M., Garman E., Hartzell G.,
Hunicke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H.,
Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P.,
Oh C., Petell F.X., Roberts D., Sehl P., Schramm S., Shogren T.,
Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
I'the nucleotide sequence of Saccharomyces cerevisiae chromosome V.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIINE=94016558; PubMed=8411151;
Melnick L., Sherman F.;
"The gene clusters ARC and COR on chromosomes 5 and 10, respectively,
of Saccharomyces cerevisiae share a common ancestry.";
J. Mol. Biol. 233:372-388(1993).
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                          ARLSHT (IN REF. 1).

MSAAVLGV -> KCPPRCSAS (IN REF. 1).

KL -> NV (IN REF. 1).

D -> H (IN REF. 1).

GELCVA -> RALNG (IN REF. 1).

GELCVA -> RALNG (IN REF. 1).

EDR -> COA (IN REF. 1).

EDR -> L (IN REF. 1).

EDR -> A (IN REF. 1).

EDR -> A (IN REF. 1).
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                         Score 43; DB 1; Length 3587;
Pred. No. 1.6e+02;
8; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1993 (Rel. 27, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
UTR4 protein (Unknown transcript 4 protein).
UTR4 OR YELO38W OR SYGP-ORF20.
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1751 ASFAFDANFESLRLIVLG 1768
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EMBL; S6564; AAD13973.1; -.
EMBL; S66121; AAB28443.1; -.
EMBL; U18779; AAB6504.1; -.
PIR, S30843; S30843.
Germonline; 139042; -.
GGTD. S00007764. UTR4.
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Local Similarity 33.3%;
es 6; Conservation
                                                                                                                                                                                                                                                        AA; 401248
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SEQUENCE OF 1-158 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 387:78-81(1997).
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2645
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                                                                                         25608
27113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 30
UTR4 YEAST

DU TR4 YEAST

DO 10-OCT-1993

DT 10-OCT-1993

DE SACCHATOMYCE

RO SACCHATOMYCE

RO SACCHATOMYCE

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RO STRAIN=2919

RA Araujo R., A

RA Araujo R., A

RA Araujo R., A

RA HUNICKE-5MIL

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RA HUNICKE-5MIL

RA DIELINE=944

RA MEDLINE=944

RA MEDLINE SSOR43

DR EMBL; SSOR43
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and for commercial
          (See http://www.isb-sib.ch/announce/
                                                        EMBL; AE000164; AAC73691.r; --
EMBL; U82599; AAA90789.1; ALT_INIT.
EMBL; U82596; SLOSON
ECGENA; EGIO236; fepb.
InterPro; IPR000515; BPD transp.
InterPro; IPR000522; RecD.
ProDom; PF01032; PecCD; 1.
ProDom; PF01035; TecCD; 1.
Iron transport; Transport; Inner membrane; Transmembrane;
                                                                                                                                                                                                                                                   V -> AL (IN REF. 2).
BB5C5E939A96951B CRC64;
dified and this statement is not removed. titles requires a license agreement (See Feend an email to license@isb-sib.ch).
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                                        EMBL; X57471; CAA40707.1; -. EMBL; X59402; CAA42043.1; -.
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Gaps

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3; Indels

5; Mismatches

/ Match Local Similarity 34.8%; les 8; Conservative

Query Match Matches

Score 41.5; DB 1; Length 334; Pred. No. 27;

MEDLINE-92024080; PubMed=1926776; Palm P., Schleper C., Grampp B., Yeats S., McWilliam P., Reiter W.-D., Zillig W.; 01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
Hypothetical 28.5 kba protein (ORF D-244).
Sulfolobus virus-like particle SSV1.
Viruses, dsDNA viruses, no RNA stage; Fuselloviridae; Fusellovirus. "Complete nucleotide sequence of the virus SSV1 of the archaebacterium Sulfolobus shibatae."; Virology 185:242-250(1991). 244 AA. STANDARD; NCBI\_TaxID=244589; SEQUENCE FROM N.A. Y28K SSV1 P20213; 

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EMBL; X07234; CAA30214.1; -.

42.7%; Score 41; DB 1; Length 244; 40.0%; Pred. No. 24; tive 4; Mismatches 5; Indels PIR; S03215, S03215. Hypothetical protein. SEQUENCE 244 AA; 28515 MW; 9326209BC3B9DD86 CRC64; Query Match Best Local Similarity Matches 6; Conservat

Conservative

216 OYWKNLTDLRVSLKG 230 OFWKNFOTLKIVILG 18

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Koide A., Hoch J.A.;
 "Identification of a second oligopeptide transport system in Bacillus
 subtilis and determination of its role in sporulation.";
Mol. Microbiol. 13:417-426(1994). Bacillus subtilis. Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus. NCBI\_TaxID=1423; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) 01igopeptide transport system permease protein appC. APPC OR BSUI1400. 303 AA. PRT; MEDLINE=95089678; PubMed=7997159; STANDARD; SEQUENCE FROM N.A. SEQUENCE FROM N.A. RESULT 33 APPC\_BACSU ID \_APPC\_BACSU AC P42063; 

RAGAINELES BO044033; PubMed=9304377;

Runst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

Runst F., Ogasawara N., Moszer I., Albertini A.M., Barchert S.,

Racvedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

Racvillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

Rachis S.K., Codani J.J., Connerton I.F., Cummings N.J., Emmerson P.T.,

Rachis C., Pujita M., Pujita Y., Funa S., Galizzi A., Galleron N.,

Rachis S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

Runia K., Lapidua P., Kasahara Y., Klaerr-Blanchard M., Yones L.,

Robayashi Y., Koetter P., Koningstein G., Kroch S., Kunno M.,

Runia K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

Runia K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

Runia W., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

Robayashi Y., Cortetelle D., Porvollik S., Perscott A.M.,

Racon D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

Racon E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,

Rieger M., Rivolta C., Rohleich S., Schroeter R., Scoffone F.,

Sekiguchi J., Scanlan E., Schleich S., Schroeter R., Rose M., Sacrot S.J., Serror P., Shin B.S., Soldo B.,

Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,

Tosato V., Uchiyama S., Vandenbol M., Vanlier F., Vasarctti A.,

Winters P., Wambutt R., Wedler E., Wedler H., Weitzenegger T., A.,

Wander B., Winters P., Wammone B., Sonniager B., Yoshikaw H., Sandhila B.,

Normalse A., Yoshikawa H., Sandhila B., Sandhila B., Ryohida K., Yoshikawa H., Sandhila B., Sa

"The complete genome sequence of the Gram-positive bacterium Bacillus subtilis."; Nature 390:249-256(1997)

Nature 390:249-230(1997).

-!- FUNCTION: This protein is a component of an oligopeptide permease, a binding protein-dependent transport system. This APP system can completely substitute for the OPP system in both sporulation and genetic competence, though, unlike OPP, is incapable of transporting tripeptides. Probably responsible for the translocation of the substrate across the membrane (By

Similarity).
SUBCELLULAR LOCATION: Integral membrane protein (Potential).
SIMILARITY: Belongs to the binding-protein-dependent transport system permease family. OppBC subfamily.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sabroe I., Conroy D.M., Gerard N.P., Li Y., Collins P.D., Post T.W., Jose P.J., Williams T.J., Gerard C.J., Ponath P.D.;
Jose P.J., Williams T.J., Gerard C.J., Ponath P.D.;
"Cloning and Characterization of the guinea pig eosinophil eotaxin receptor, C-C chemokine receptor-3: blockade using a monoclonal antibody in vivo."; J. file139-6147(1998).
J. Immunol. 161:6139-6147(1998).
MCP-3, MCP-4 and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level (By similarity).
Increasing the intracellular calcium ions level (By similarity).
SUBCELULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3) (CCR-3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cavia porcellus (Guinea pig).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Cavidae, Cavia.
                                                     42.7%; Score 41; DB 1; Length 318; ilarity 46.7%; Pred. No. 31; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
EXTRACELLULAR (POTENTIAL)
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7B73FAB7A3BC3670 CRC64;
318 AA; 35814 MW; 3988A4B0EFE13711 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF060698; AAC80428.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99049845; PubMed=9834099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41623 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFINTS; PRO0237; GPCRRHODOPSN
                                                                                                                                                                                                                                   287 YLLWKNFLPLTLTLL 301
                                                                                                                                                                                 3 YOFWKNPOTLKIVIL 17
                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                  Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1] _
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCR3 OR CMKBR3
                                                                                                                                                                                                                                                                                                                                                                                               CKR3 CAVPO
Q9Z2I3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                     CKR3_CAVPO
                                                                                                                                                                                                                                                                                                                                         RESULT 35
                                                                                                                                                                                                                                                                                                                                                                                                                           SOLUTION OF THE STANDARD BRANCH BRANC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
               between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                             EMBL; U20909; AAA62360.1; -.
EMBL; Z99110; CAB12997.1; -.
PIR; 140547; 140547.
Subtilist; BG11089; appC.
Interpro; IPR000515; BPD_transp.
Pfam; PF00528; BPD_transp; 1.
PROSITE; PS50928; ABC TM1; 1.
Competence; Sporulation; Transport; Peptide transport; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arnason U., Gullberg A., Xu X.;
"A complete mitochondrial DNA molecule of the white-handed gibbon, Hylobates lar, and comparison among individual mitochondrial genes of all hominoid genera.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hylobatidae, Hylobates.
NCBI_TaxID=9580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hereditas 124:185-189(1996).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-!- SIMILARITY: Belongs to the complex I subunit 1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
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PROSITE; PSC0667; COMPLEXI_NDI_1; 1.
PROSITE; PSC0668; COMPLEXI_NDI_2; 1.
Oxidoreductase; NAD; UbiquInone; Mitochondrion; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41; DB 1; Length 303;
Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33420 MW; B9CD2CD936C46DC5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NADH-ubjquinone oxidoreductase chain 1 (EC 1.6.5.3)
MTND1 OR ND1 OR NADH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IR; T11833; T11833.
InterPro; IPR001694; Resp_NADH_dhl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hylobates lar (Common gibbon). Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X99256; CAA67628.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 FWKNFQTLKIVILG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 FWEKFSKNKLAILG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            303 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome.
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NUIM HYLLA 096126;

RESULT 34

NULM HYLLA

IN HYLLA

NULM AC

096126

DT 01-NOV

DT 01-NOV

DT 15-JUL

OS Hyloba

OG MAMMAI

OO MAMAI

7;

Matches

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TRANSMEM TRANSMEM

SEQUENCE

TRANSMEM TRANSMEM

TRANSMEM

42.7%; Score 41; DB 1; Length 358;

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Length 373;

42.78;

us-10-084-813-13.rsp

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Query Match
Best Local Similarity 66.7
Matches 8, Conservative
                                                                                                                                    DROME
                                                                                                                       RESULT 37
022B_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
               ö
                                                                                                                                                                                                                                                                                                            MEDLINE-Sprague-Dawley,
MEDLINE-Sprague-Dawley,
MEDLINE-Sprague-Dawley,
MEDLINE-Sprague-Dawley,
MEDLINE-Sprague-Dawley,
MEDLINE-Sprague-Dawley,
MEDLINE-Sprague-Dawley,
MEDLINE-Sprague-Dawley,
M.N., Adhikati S., Xia Y., Feng L., Sonntag M.K.,
deFiebre C.M., Pennell N.N., Streat W.J., Harrison J.K.,
"Chemokine receptor expression in cultured glia and rat experimental
allergic enceptor expression in cultured glia and rat experimental
allergic enceptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5
Chemokines. Transduces a signal by increasing the intracellular
calcium ions level (By similarity)
-: SUBCELLULAR LOCATION: Integral membrane protein.
-: TISSUE SPECIFICITY: Expressed in lung, spleen, kidney, thymus and
                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 2 (C-C CKR-2) (CC-CXR-2) (CCR-2) (CCR2 OR CMKBR2.
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TAXID=10116;
              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             macrophages.
-!- INDUCTION: In animals in which experimental allergic encephalomyelitis (EAE) has been induced.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ent...

R EMBL; U77349; AAC03242.1;

R EMBL; U77349; AAC03242.1;

R InterPro; IPR000276; GPCR.Rhodpsn.

DR Pf00001; Trm 1; 1.

DR PROSITE; P850262; GPROTEIN RECEP F1 1; 1.

DR PROSITE; P850262; GPROTEIN RECEP F1 2; 1.

TAMAIN 61 81 POTENTIAL.

61 81 POTENTIAL.

CYTOPLASMIC (POTENTIAL).
              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUTENILAL
EXTRACELULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
1; 2578B012F5D6FD09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
EXTRACELLULAR (POTENTIAL)
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
               4,
                                                                                                                                    373 AA
Pred. No. 35;
2; Mismatches
                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42763 MW;
53.8%;
                                                        || || |:: | |
199 WKRFQALRMNIFG 211
                                        6 WKNFQTLKIVILG 18
              7; Conservative
                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
982
982
1139
1129
1150
1150
2242
2257
2257
3303
313
343,
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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055193;
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DOMAIN
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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REGUENCE FROM N.A.

SEQUENCE FROM N.A.

RADINE_20196006, PubMed=10731132,

RADINE_20196006, PubMed=107, Blazej R.G., Champe M., Henderson S.N.,

RADINED R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RADINED R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RADINED R.C., Basun A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RADINED R.W., Cawley P., Berman B.P., Bhandari D., Bolshakov S.,

RADINED R.C., Busam D.A., Butler H., Cadieu E., Center P., Bolshakov S.,

RADINE R.C., Busam D.A., Butler H., Cadieu E., Center P., Davises P.,

RADINE R.C., Busam D.A., Butler M., Dawen S., Dunkov B.C., Dunn P.,

RADINE R.C., Busam D.A., Butler M., Dagan-Rocha S., Dunkov B.C., Dunn P.,

RADINE R.C., Evangelieta C.C., Ferraz C., Ferraz S., Fleischmann W.,

RADINE R.C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser R.,

RADINE R., Kodira C.C., Rerraz C., Remison J.A., Harris M.,

RADINE R., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,

RADINE R., Kodira C.D., Kraft C., Kravitz S., Kull D., Lai Z.,

Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mosherson D.,

RADINE R.M. Moy M., Murphy B., Murphy L., Murzhy D.M., Nelson D.L.,

RADINE R.M. Moy M., Murphy B., Murshy L., Murshy D.M., Persee M.G.,

RADINE R.M. Pelson K.M., Mixphy B., Palazolo M., Pittman G.S., Pollard J., Pull V., Reese M.G.,

RADINE R.M. Pelson K.M., Mixphy B., Reese M.G.,

RADINE R.M. Pelson K.M., Mixphy B., Reese M.G., Pollard J., Pull V., Reese M.G.,

RADINE R.M. Pelson K.M., Pelson K., Mixon R., Pelson D., Pullard J., Pullard 
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEOURNCE FROM N.A., AND TISSUE SPECIFICITY.
STRAIN-Oregon-R. TISSUE-Antenna,
MEDLINE=99189757; PubMed=10089887;
Vosshall L.B., Amrein H., Morozov P.S., Rzhetsky A., Axel R.;
A Spatial map of olfactory receptor expression in the Drosophila
                                                                                                                                                                                                                                                           DECORAGE STANDARD, PRT, 397 AA.

PR1910; O9U6X6; Q9VQ19;

T 16-OCT-2001 (Rel. 40, Created)

T 16-OCT-2001 (Rel. 42, Last sequence update)

T 00-OCT-2003 (Rel. 42, Last annotation update)

E 00crant receptor 22b.

E 00crant receptor 22b.

D 0R22B OR OR22A.2 OR DOR2A.2 OR DOR67 OR AN12 OR CG4231.

S Drosophila melanogaster (Fruit fly).

C EDKATYOTA; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

C Ephydroidea; Drosophilidae; Drosophila.

K NCPL TAXID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDILINE-99389733; PubMed=10458908;
Gao Q., Chess A.;
"Identification of candidate Drosophila olfactory receptors from
                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REVISION TO 58. Vosshall L.B., Amrein H., Morozov P.S., Rzhetsky A., Axel Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                 3; Indels
Score 41; DB 1;
Pred. No. 36;
1; Mismatches
                                                                                                                                |||||||
211 WKNFQTIMRNIL 222
                                                                                                6 WKNEOTLKIVIL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genomic DNA sequence.";
Genomics 60:31-39(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell 96:725-736(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO:0016021; C:integral to membrane; NAS.
GO:0004984; F:olfactory receptor activity; NAS.
GO:0007186; P:G-protein coupled receptor protein signalin. . .; NAS.
GO:0007608; P:olfaction; NAS.
                                                                                                                                                                                                                                                           TISSUE=Antenna;
MEDLINE=99166868; PubMed=10069338;
Clyne P.J., Warr C.G., Freeman M.R., Lessing D., Kim J., Carlson J.R.;
Clyne P.J., Warr C.G., Freeman M.R., Lessing D., Kim J., Carlson J.R.;
A novel family of divergent seven-transmembrane proteins: candidate odorant receptors in Drosophila.";
Neuron 22:227-338(1999).
-! FUNCTION: Probable role in the odorant response, being an odorant
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier B., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Yelliams S.M., Zhong W., Zhou K., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu S., Shu X., Smith H.O. Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Integral membrane protein (Potential).
TISSUE SPECIFICITY: EXPRESSED IN 20-22 SENSORY NEURONS ON THE
MEDIAL-PROXIMAL EDGE OF THE ANTENNA. THIS EXPRESSION PATTERN
MATCHES THE DISTRIBUTION OF THE LARGE SENSTILA BASICONICA.
EXPRESSION IS FIRST SEEN AT 60 HOURS APF IN A SUBSET OF CELLS
RESTRICTED TO A SUBREGION OF THE DEVELOPING ANTENNA. EXPRESSION
CONTINUES THROUGHOUT ANTENNAL DEVELOPMENT.
SIMILARITY: Belongs to family Dr-or of G-protein coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D -> TICFDKFFYLPYFFS (IN REF. 3).
MYKLAFTVVTIVKQFNLAEKFQ -> VSINQYEL (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -> L (IN REF. 3, 4 AND 5).
-> TICFDKFFYLPYFFS (IN REF. 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB 1; Length 397; Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0016021; C:integral to membrane; NAS.
GO; GO:0004984; F:olfactory receptor activity; NAS.
GO; GO:0007186; P:olfactory receptor protein s
GO; GO:0007186; P:olfaction; NAS.
InterPro; IPR004117; 7tm_6.
PF02949; 7tm_6; 1.
Transmembrane; G-protein coupled receptor; Olfaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EB7816E9D0A13E50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                               "The genome sequence of Drosophila mela
Science 287:2185-2195(2000).
[5]
IDENTIFICATION, AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF127924; AAD26359.2; -.
EMBL; AE003586; AAF51363.1; -.
FlyBase; FBgn0026397; Or22b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46387 MW;
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DOMAIN 1
TRANSMEM 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptors.
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TRANSMEM
DOMAIN
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Best Local Similarity

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MEDLINE=983157-86; PubMed=9690476;
MEDLINE=983157-86; PubMed=9690476;
MEDLINE=983157-86; PubMed=9690476;
Momura Y., Nakahori Y., Mayake M., Saito K., Osawa M., Hamano K., Sakakhara Y., Nonaka I., Nakagome Y., Kanazawa I., Nakamura Y., Tokunaga K., Toda T.;
"An ancient retrotransposal insertion causes Fukuyama-type congenital
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encompassing the outside and inside of muscle membranes. May also be involved in brain development.

-!- FUNCTION: May interact with and reinforce a large complex. Bay also be involved in brain development.
-!- SUBCELLUIAR LOCATION: Secreted (Probable). May be located in the
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-21099876; PubMed=11165248;
Kobayashi K., Sasaki J., Kondo-Iida E., Fukuda Y., Kinoshita M.,
Sunada Y., Nakamura Y., Toda T.;
"Structural organization, complete genomic sequences and mutational analyses of the Fukuyama-type congenital muscular dystrophy gene,
                                                                                                                                                                                                                                                                                       Euteleostomi;
;
                                                                                                                                             PCMD HUMAN STANDARD; PRT; 461 AA.
075072, 2096F11, 209295;
16-OCT-2001 (Rel. 40, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Fukutin precursor (Fukuyama-type congenital muscular dystrophy protein).
                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Babbage A.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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9
   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEBS Lett. 489:192-196(2001).
                                  3 YOFWKNEQTLKIVIL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     muscular dystrophy.";
Nature 394:388-392(1998).
 Conservative
                                                                48 YKLWSTFVTLVIFIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genew, HGNC:3622, FCMD.
MIM, 607440, -.
MIM, 253800, -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
   8
                                                                                                                                 FCMD_HUMAN
   Matches
                                                                                                                RESULT 38
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STRAIN-S288C / AB972;
MEDLINE=9713268; PubMed=9169872;
Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
Withe nucleotide sequence of Saccharomyces cerevisiae chromosome XIII.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "identification of the proteins of the yeast UI small nuclear ribonucleoprotein complex by mass spectrometry.";

ribonucleoprotein complex by mass spectrometry.";

-1. FUNCTION STAN 94:385-390(1997).

UI SNRNP PARTICLE TO FACILITATE OR STABILIZE THE UI SNRNP/5'

SPLICE SITE INTERACTION. HAS A DIRECT ROLE IN THE ASSEMBLY OR FUNCTION OF A CATALYTICALLY ACTIVE SPLICEOSOME.

-1. SUBCELLULAR LOCATION: Nuclear.

-1. SIMILARITY: Contains 7 HAT repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97165029; PubMed=9012791;
Neubauer G., Gottschalk A., Fabrizio P., Seraphin B., Luehrmann R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=GRF88;
MEDLINE=94254821; PubMed=8196608;
Lockhart S.R., Rymond B.C.;
"Commitment of yeast pre-mRNA to the splicing pathway requires a novel U1 small nuclear ribonucleoprotein polypeptide, Prp39p.";
Mol. Cell. Biol. 14:3623-3633(1994).
                                                                                                                                                                                  . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                               12;
                                                                                                                                                                                                                                                                                                                DB 1; Length 461;
                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                        FUKUTIN,
N-LINKED (GLCNAC. . .) (PC
R -> Q (IN REF. 1).
2D11F28E4BCCD858 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
PRP39 OR YML046W OR YM9827.06.
                                                                                                                                                                                                                                                                                                                Score 41; DB 1
Pred. No. 44;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              629 AA
GO; GO:0005615; C:extracellular space; TAS. GO; GO:0007517; P:muscle development; TAS. GO; GO:0007399; P:meurogenesis; TAS. Glycoprotein; Signal. 21 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OYHLWKNEEGWFRIAENMGFQCLKI 140
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                                                                                                                       1 21 PO
22 461 FU
92 8-1
203 203 N-1
461 AA, 53724 MW;
                                                                                                                                                                                                                                                                                                                42.7%;
ilarity 40.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 387:90-93(1997).
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 39
PR39 YEAST
D PR39 YEAST
D PR39 YEAST
D O L-EB-1995
DT O1-FEB-1995
DT O1-FEB-1995
DT O1-FEB-1995
DE PRESS OR YMI
CS SACCHARONYCE
CS CARLYOLA;
FOC SACCHARONYCE
FRC
RC STRAIN-GREBE
RA ICCCKHART 9.73
RA ICCCKHART 9.73
RA MEDLINE-973;
RA COMMON R., 1
RA RICE P., SK
RT "The MALLINE-973;
RA GORDOR R., 1
RA RICE P., SK
RT "The MALLINE-973;
RA MEDLINE-973;
RA MEDLINE-971
RA MEDRING-971
RA MED
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CARBOHYD
CONFLICT
SEQUENCE
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      RARXFFFFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Otterness D.M., Wieben E.D., Wood T.C., Watson R.W.G., Madden B.J., McCormick D.J., Weinshilboum R.M.; "Human liver dehydroeplandrosterone sulfotransferase: molecular cloning and expression of CDNA."; Mol. Pharmacol. 41:865-872(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q06520;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
Alcohol sulfortansferase (EC 2.8.2.2) (Hydroxysteroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria, Primates, Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE = 3143674; PubMed=7678732; Comer K.A., Falany J.L., Falany C.N.; "Cloning and expression of human liver dehydroepiandrosterone sulphotransferase.";
EMBL; L29224; AAA20131.1; -.

EMBL; Z47816; CAA87828.1; -.

PIR; 247816; CAA87828.1; -.

Remontine; 142575; -.

SGD; S0004509; PRR39.

GO; GO:0005243; C:scommitment complex; IPI.

GO; GO:0005325; C:snRNN UJ; IDA.

GO; GO:0005317; P:RNA binding; IPI.

RGO; GO:0003107; HRNA splicing; IMP.

InterPro; IPRO03107; HAT; 2.

NARR; SM0386; HAT; 2.

REPEAT 102 114 HAT 1.
                                                                                                                                                                                                                                                                                                                                                                                                                   ore 41; DB 1; Length 629;
ed. No. 60;
Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND SEQUENCE OF 80-107 AND 176-198
                                                                                                                                                                                                                                                                                                                                                                                     67480ED01347B6AB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expressed enzyme.";
Mol. Cell. Endocrinol. 112:53-60(1995)
                                                                                                                                                                                                                                          HAT 2.
HAT 3.
HAT 4.
HAT 5.
HAT 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                            42.7%; Scor.
37.5%; Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Liver;
MEDLINE=92269778; PubMed=1588921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. J. 289:233-240(1993).
                                                                                                                                                                                                                                                                                                                                                                                       74748 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : | | | | | : : | | FGFWKRFATIEYQLFG 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                  134
173
208
265
480
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SULT2A1 OR STD OR HST.
                                                                                                                                                                                                                                                                                   138
175
233
270
446
629 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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9
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Matches
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EWEL; X84816; CAA59274.1; -.

DR EWEL; L36196; AAA75491.1; -.

DR EWEL; L36191; AAA75491.1; JOINED.

BREL; L36192; AAA75491.1; JOINED.

DR EWEL; L36193; AAA75491.1; JOINED.

DR EWEL; L36193; AAA75491.1; JOINED.

DR EWEL; L36194; AAA75491.1; JOINED.

DR EWEL; L36195; AAA75491.1; JOINED.

DR EWEL; U31056; AAA75491.1; JOINED.

DR EWEL; U31056; AAA75133.1; JOINED.

DR EWEL; U31058; AAA75133.1; JOINED.

DR EWEL; U31059; AAA75135.1; JOINED.

DR EWEL; U31059; AAA75155.1; -.

DR EWEL; U31059; BAE23169.2; -.

DR EWEL; U31059; BAE23169.2; -.

DR EWEL; BAND11458; SULT2A1.

DR GONOWALS; P: steroid metabolism; TAS.

DR CO; GO:000830; Sulfortansferase. 1.

DR Fordom; PRO0685; Sulfortansferase. 1.

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FOWER: TOWER: TOWER: TOWER.

DR SINDING SIRE POTENTIAL.

DR PRINDING SIRE POTENTIAL.

DR PRINDING SIRE POTENTIAL.

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                                                                                                                                "Human dehydroepiandrosterone sulfotransferase gene: molecular
SEQUENCE FROM N.A.
MEDLINE=95322029; PubMed=7598806;
Luu-The V., Dufort I., Faquet N., Reimnitz G., Labrie F.;
"Structural characterization and expression of the human dehydroepiandrosterone sulfotransferase gene.";
DNA Cell Biol. 14:511-518(1995).
                                                                    [5]
SEQUENCE FROM N.A.
MEDILINE=5525880; PubMed=7710689;
Otterness D.M. Her C., Aksoy S., Kimura S., Wieben E.D.,
Weinshilboum R.M.;
                                                                                                                                            cloning and structural characterization.";
DNA Cell Biol. 14:331-341(1995).
                                                                                                                                                                                                    MEDLINE=92392364; PubMed=1520333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, L20000, AAA35758.1, -.
EMBL, X70222, CAA49755.1, -.
EMBL, U08024, AAA17749.1, -.
EMBL, U08025, AAA17750.1, -.
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Kong A.-N.T., Yang L., Ma M., Tao D., Bjornsson T.D.; "Molecular cloning of the alcohol/hydroxysteroid form (hSTa) of sulfotransferase from human liver."; Blochem. Blophys. Res. Commun. 187:448-454(1992).
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Search completed: September 28, 2004, 09:04:06 Job time : 6.625 secs

128 SGYFFWKNMKFIK 140 1 SOYOFWKNFOTLK 13 Conservative

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Gaps

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41.7%; Score 40; DB 1; Length 284; 53.8%; Pred. No. 40; Arive 2; Mismatches 4; Indels

Best Local Similarity

Query Match Matches

3C89C7597833EBA1 CRC64;

BY SIMILARITY.

PAPS BINDING SITE (POTENTIAL).

A -> P (IN REF. 1; AA SEQUENCE)

I -> D (IN REF. 1).

L -> U (IN REF. 6).

62 62 A 89 89 T 118 118 L 158 L 284 AA, 33648 MW,

CONFLICT CONFLICT CONFLICT CONFLICT SEQUENCE

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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	TT. T.  TS. QPPITS, PRELIMINARY QPPITS, OPPLY COTT-2000 (TEMBLEE). 01-OCT-2000 (TEMBLEE). 01-OCT-2000 (TEMBLEE). 01-UN-2003 (TEMBLEE). Mitant chemokine recept CCRS. Homo sapiens (Human). Eukaryota, Metazca, Cho Mammalia, Butheria, Pri NCHT TaxID=9606, [1] SEQUENCE FROM N.A. MEDILINE=99392755, PubMe ARDINES=99392755, PubMe Bond V.C.; (Chinchare Cerization of a heteroxygous HIV-1-infe AIDS 13:1585-1586(1999) EMBL, APO56019, AAF6557 GO, GO.0004872; F:recept Receptor. 1 VARTANT 1 SEQUENCE 52 AA; 5962 ery Match st Local Similarity 10 tches 18; CONSERVATIVI
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2 Anng L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
A D.D.D.,
A D.D.D.,
A LIV-1 subtypes, co-receptor usage, and CCR5 polymorphism.";
A LIDS Res. Hum. Retroviruses 0:0-0(1997).
B EMBL, AF011504, AAB5704.1, ...
B GO, GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; F:receptor activity; IEA.
GO; GO:0016021; F:receptor activity; IEA.
GO; GO:00186; P:G-protein coupled receptor protein signalin. ..; IEA.
InterPro; IPR000276; GPCR_Rhodopsn.
B Ffam; PF00001; 7tm 1, 1.
B RINTS; PR000217; GPCRRHODOPSN.
B ROSITE; PS00237; GPCRRHODOPSN.
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heterozygous HIV-1-infected individuals.
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heterozygous HIV-1-infected individuals.
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MEDLINE=99392755; PubMed=10465086;
Aikhionbare F.O., Newman C., Womack C., Roth W.W., Stringer H.G. Jr.,
Bond V.C.;
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                      Oppir4;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
Chemokine receptor CCR5 (Fragment).
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0004872; F:receptor activity; IEA.
GO; GO:000184; F:rhodopsin-like receptor activity; IEA.
GO; GO:000186; F:receptor activity; IEA.
GO; GO:000186; P:receptor activity; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
PFGm; PF00001; Tum 1. 1.
PRINTS; PR00237; G_PROTEIN_RECEP_F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1 1; 1.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Brythrocebus.
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K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCR5 genes from diverse simian and prosimian
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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100.0%; Score 96; DB 4; Length 333; 100.0%; Pred. No. 1.9e-07; cive 0; Mismatches 0; Indels
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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334 AA; 38460 MW; B19D0CEC667B69F0 CRC64;
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01-WAY-2000 (TrEMBLrel. 13, Created)
1-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).

Homo sapiens (Human)

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI\_TaxID=9606;

species.";
Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161919; AAD47676.1;
GO; GO:0016201; C:integral to membrane; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001884; F:rhodopsin-like receptor protein signalin. .; IEA.
InterPro; IPR000276; GPCR\_Rhodopsn.
FRAM; PR00037; GPCRRHODOPSN.
PROSITE; PS00037; GPRRHODOPSN.
PROSITE; PS50262; GPROTEIN\_RECEP\_FI\_1; 1.

.. 0 Query Match 100.0%; Score 96; DB 4; Length 339; Best Local Similarity 100.0%; Pred. No. 2e-07; Matches 18; Conservative 0; Mismatches 0; Indels

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PRELIMINARY; Q9UN26 RESULT 6
COUNZ6

OUNZ6, 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) C-C chemokine receptor 5 (Fragment). PRT; 339 AA.

Homo sapiens (Human)

Kinstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Sinbata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; Sinbata R., Yoder CRS genes from diverse simian and prosimian species."; Sequences of the CCRS genes from diverse simian and prosimian species."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, ARIE1916; AADA/733.1; -. GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:000186; F:receptor activity; IEA.

GO; GO:000186; F:receptor activity; IEA.

GO; GO:000186; P:G-protein coupled receptor activity; IEA.

InterPro., IPRO00276; GPCR\_Rhodpsn. Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. NCBI\_TaxID=9606;

1 339 339 339 AA; 39162 MW; A56369FE0529F4AB CRC64; PEAM; PF00001; Ttm 1; 1.
PRINTS; PR00237; GFCRRHODOPSN.
PROSITE; PS00237; GFRRHODOPSN.
Receptor.
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SEQÜENCE 339 AA; 39162 MW; A56369FE0529

Query Match
100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels

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RESULT 7 Q9UN23 ID Q9UN23

PRELIMINARY;

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Anistman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; Sequences of the CCRS genes from diverse simian and prosimian species."; Sequences of the CRS genes from diverse simian and prosimian species."; Part 1990; Lo the EMBL/GenBank/DDBJ databases.

Submitted (JUL-1999) to the EMBL/GenBank/GenBank/DDBJ databases.

Submitted (JUL-1999) to the EMBL/GenBank/Ge 100.0%; Score 96; DB 4; Length 339; 100.0%; Pred. No. 2e-07; Live 0; Mismatches 0; Indels 1 339 339 339 AA, 39115 MW, 3C6369F922C91AA7 CRC64; Receptor. NON TER NON TER SEQUENCE 

178 SQYQFWKNFQTLKIVILG 195 1 SOYOFWKNFOTLKIVILG 18 Query Match
Best Local Similarity 100.
Matches 18; Conservative 셤 ઠે

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RESULT 8 Q9UBJ7

090BJ7; 090BJ7; 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAY-2003 (TrEMBLrel. 24, Last annotation update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) C-C chemokine receptor 5 (Fragment). 339 AA PRT; PRELIMINARY; **09UBJ7** 

Homo sapiens (Human). Sukaryora, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. NCBI\_TaxID=9606;

EQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibara R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
Shibara R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
Sequences of the CCR5 genes from diverse simian and prosimian

RT "Sequences of the EMBL/GenBank/DDBJ databases.

EMBL; APIG1921; AAD47678.1; -.

EMBL; AF161921; AAD47678.1; -.

EMBL; AF161917; AAD47678.1; -.

EMBL; AAD476778.1; -.

EMBL; AAD476778.1; -.

EMBL; AAD476778.1; -.

EMBL; AAD476778.1;

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EMBL; AFIG1914; AAD47671.1; ...
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:000184; F:rhodopsin-like receptor activity; IEA.
GO; GO:000186; P:rhodopsin-like receptor protein signalin. . .; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
PRIMIS; PR00017 7tm 1.
PRIMIS; PR00037; GFRRHODPSN.
PROSITE; PS00237; GFRRHODPSN.
PROSITE; PS00237; GFRRHODPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_1; 1.
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EMBL; AF161909; AAD47667.1; -
EMBL; AF161910; AAD47667.1; -
EMBL; AF161911; AAD47668.1; -
EMBL; AF161911; AAD47668.1; -
EMBL; AF161912; AAD47669.1; -
EMBL; AF161912; Cintegral to membrane; IEA.
GO; GO:000487; F: receptor activity; IEA.
GO; GO:000188; F: rhodopsin-like receptor activity; IEA.
GO; GO:000186; P:G-protein coupled receptor protein signalin. .; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCRS genes from diverse simian and prosimian
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCRS genes from diverse simian and prosimian
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                            species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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339 AA; 39086 MW; 88AD8B44E2CB4ECZ CRC64;
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339 AA; 39114 MW; 3C6369F92C29F4A7 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UMY-2003 (TrEMBLrel. 24, Last annotation update)
01-UTW-2003 (TrEMBLrel. 26, Last annotation update)
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nes 18; Conservative
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004812; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. ..; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
COST. TaxID=9606;
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
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                                                                                                                 100.0%; Score 96; DB 4; Length 339; 100.0%; Pred. No. 2e-07; tive 0; Mismatches 0; Indels
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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339 339
339 AA, 39128 MW, 9C3369FFF1F2F27A CRC64;
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339 339
339 AA, 39146 MW, 10FE05FE5371D4B3 CRC64;
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemckine receptor 5 (Fragment).
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100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels

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178 SQYQFWKNFQTLKIVILG 195

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SEQUENCE 339 AA; 39036 MW; 5555FEAF2614D35C CRC64;
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHODOPSN.
PROSITS; PS00237; G PROTEIN RECEP F1 1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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Best Local Similarity 100.0
Matches 18, Conservative
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Anibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
Anibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
T. Sequences of the CCR5 genes from diverse simian and prosimian
Expecies.";
Sequences of the CCR5 genes from diverse simian and prosimian
Expecies.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

B. Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

CO GO:00016021;
Cintegral to membrane; IEA.

CO; GO:00016021;
Cintegral to membrane; IEA.

CO; GO:0001884;
F:receptor activity; IEA.

CO; GO:0001884;
F:receptor activity; IEA.

CO; GO:000188;
F:receptor protein signalin...; IEA.

InterPro; IRR00276; GPCR_Rhodpsn.

PEGNI PRO0217;
CFCRENDOPSN.

PROSITE; PSG0237; GPRRHODPSN.

PROSITE; PSG0237; GPRCTEIN_RECEP_FI_1; 1.
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EMBL, AF162024; AAD47779.1; -.

EMBL, AF161889; AAD47779.1; -.

EMBL, AF161889; AAD4779.1; -.

EMBL, Frieceptor in embrane, IEA.

GO, GO:00016221, C:integral to membrane, IEA.

GO, GO:0001887; F:receptor activity, IEA.

GO, GO:0001887; F:receptor activity, IEA.

GO, GO:000186; P:G-protein coupled receptor protein signalin. ., IEA.
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Welleyarota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hylobatidae, Hylobates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryofa, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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339 339
339 AA, 39183 MW, 56C819F92D6DB1A6 CRC64;
                                                                                                                                                                                                                                                                                                         0.1-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last amnotation update)
C-C_chemokine receptor 5 (Fragment).
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Best Local Similarity 100.0
----hes 18; Conservative
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Q9UN28;
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF161887; AAD47644.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:001584; P:rhodopsin-like receptor activity; IEA.
GO; GO:0001584; P:rhodopsin-like receptor protein signalin. . .; IEA.
InterPro; IPR000276; GPCR_Rhodopsn.
FRAM; PP00001; Trul 1,
PRINTS; PR00237; GPCRRHODOSN.
PROSITE; PS00237; GPRRHODOSN.
PROSITE; PS50262; GPROTEIN_RECEP_F1_1; 1.
                                                             Gaps
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CCRs.

Hylobates concolor (crested gibbon);

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCRS genes from diverse simian and prosimian
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100.0%; Score 96; DB 6; Length 339; 100.0%; Pred. No. 2e-07; ive 0; Mismatches 0; Indels
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NON TER 1 1 1
NON TER 319 339 SEQÜENCE 339 AA, 39075 MW, 09257FBFB834C4AE CRC64;
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O9TUX1;
O9TUX1;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 24, Last annotation update)
01-UTM-2003 (TrEMBLrel. 24, Last annotation update)
CC Chemokine receptor 5 (Fragment).
CCRS.
Cercopithecus diana (Diana monkey).
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                                                                                                                     1 SOYOFWKNFOTLKIVILG 18
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Best Local Similarity 100.
Matches 18; Conservative
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18

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178 SOYOFWKNFOTLKIVILG 195
                   1 SQYQFWKNFQTLKIVILG
                                                                                                                                                                                PRELIMINARY;
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NON TER
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                                                                                                                                                                                                                                            EMBL; AF161948; AAD47704.1; ..., COORDINGS AF161948; AAD47704.1; ..., COORDINGS AF161948; AAD47704.1; ..., COORDINGS AF161948.2; Exceptor activity; IEA.

GO; GO:0001584; F:rcecptor activity; IEA.

GO; GO:0001584; F:rcecptor activity; IEA.

GO; GO:0001584; F:rcecptor coupled receptor protein signalin. ..; IEA.

FARMES FROUGAT; GPROTEAN COUPLED FILE.

PROSTE: PROOF AF1 1. 1.

PROSTE: PROOF AF1 1. 1.

PROSTE: PROOF AF1 1. 1.

PROSTE: PROOF AF1 1. 1.
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GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.

InterPro; IPR00276; GPCR_Rhodopsin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                            SEQUENCE FROM N.A. Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinksy S.; "Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCR5 genes from diverse simian and prosimian
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 96; DB 6; Length 339;
100.0%; Pred. No. 2e-07;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                            species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             339 AA; 39015 MW; 6D1A91546270F70D CRC64;
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339 339
339 AA; 39024 MW; EC4CE48DEEEF107E CRC64;
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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PROUNTS, PRO0237, GPCRHODOPSN.

PROSITE, PS00237, G PROTEIN RECEP F1 1, 1.

PROSITE; PS00262, G PROTEIN RECEP F1 2, 1.
                                        Cercopithecinae, Cercopithecus,
NCBI TaxID=36224;
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Matches 18; Conserva
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SEQUENCE
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;

T. Sequences of the CGK5 genes from diverse simian and prosimian

T. Species.";

Embl. AF162023; AAD47778.1; -.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:001681; F:indodopain-like receptor activity; IEA.

GO; GO:0001584; F:indodopain-like receptor activity; IEA.

GO; GO:0001586; P:G-protein coupled receptor protein signalin. ..; IE

R Interpro; IPR00276; GPCR.Hoopsn.

R PRINTS; PR00217; GPCR.HOOPSN.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalla; Butheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Cercopithecus.
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Submitred (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161949; AAD41705.1; -.
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OSTUUB;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-UN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                        01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
01-C chemokine receptor 5 (Fragment).
   339 AA
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PROSITE; PS50262; G PROTEIN RECEP_F1_2; 1.
PRT;
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Matches 18; Conservative
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EQUENCE FROM N.A.

Kunstnan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Kunstnan K., Chen Z., Fullai S., Kuiken C., Marx P., Wolinksy S.;
Whibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CRS genes from diverse simian and prosimian
"Sequences of the CRS genes from diverse simian and prosimian
"Sequences",
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF161903; AAD47660.1; -.
EMBL; AF161903; GPCREN cactivity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor protein signalin. .; IEA.
InterPro; IPRO00076; GPCR.Rhodopsn.
PEam; PF00001; 7tm 1; 1.

PROSITE; PS00237; GPCRRHODOPSN.
PROSITE; PS00227; GPCRHODOPSN.
PROSITE; PS00223; GPROTEIN_RECEP_F1_2; 1.
                      01-MAY-2000 (TYEMBLrel. 13, Created)
01-MAY-2000 (TYEMBLrel. 13, Last sequence update)
01-MAY-2003 (TYEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
CCR5.
CCR5.
End troglodytes (Chimpanzee).
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
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339 339
339 AA, 39159 MW; 8E699E882BAC0E84 CRC64;
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NON TER
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Q9TQU7
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R GO; GO:0016021; C:integral to membrane; IEA.
R GO; GO:0014872; F:receptor activity; IEA.
R GO; GO:001844; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001844; F:rhodopsin-like receptor protein signalin. ..;
R GO; GO:000186; P:G-protein coupled receptor protein signalin. ..;
R InterPro; IRR000276; GPCR_Rhodopsn.
R PROSITE; PRO0021; GPCRHODOPSN.
R PROSITE; PRO0237; G PROTEIN RECEP_F1_1; 1.
R Receptor.
R R Receptor.
I NON_TER 339 339
C SEQUENCE 339 AA; 39049 MW; GDIA93F66270F3ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pan troglodytes (Chimpanzee).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.
NCBI_TaxID=9598;
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                                                                                                                                                                                                                                                                                                                                                                     / Match
Local Similarity 100.0%; Pred. No. 2e-07;
les 18; Conservative 0; Mismatches 0; Indels
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NON TER 139 339 339 SEQÜENCE 339 AA, 39129 MW; 4A88F9BBG01D46A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         339 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SOYOFWKNFOTLKIVILG 18
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Q9TUW4
ID Q9TUW4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 19
COTOWA
AC COTOWA
AC COTOWA
DT 01-MA
DE CC-C C
GN REMA
RA RANSUR
DR RABL;
DR EMBL;
DR FETT,
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Gaps

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EQUENCE FROM N.A.

Xunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

Xunstman K., Chen Z., Fallai S., Kuiken C., Marx P., Wolinksy S.;

Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;

XI "Gequences of the CCR5 genes from diverse simian and prosimian

RT species.";

RML: Alto2041; AAD47802.1; -.

BRML: AP162044; AAD47799.1; -.

BRML: AP162044; AAD47799.1; -.

BRML: AP162044; AAD47799.1; -.

BRML: AP162044; AAD47799.1; -.

BR GO: GO: 00016021; C: Integral to membrane; IEA.

GO: GO: 00016021; F: receptor activity; IEA.

GO: GO: 0001684; F: rhodopsin-like receptor activity; IEA.

GO: GO: 0001184; F: rhodopsin-like receptor activity; IEA.

GO: GO: 0001184; F: rhodopsin-like receptor activity; IEA.

BR GO: GO: 0001184; F: Rhodopsin-like receptor protein signalin. ..; IEA.

BR RINTS; PRO0021; GPCRRHODOPSN.

BR RINTS; PRO0221; GPCRRHODOPSN.

BR RINTS; PRO0221; GPCRRHODOPSN.

BR RINTS; PRO0221; GPCRRHODOPSN.
                                                                                                                                              Cercopithecus nictitans (white-nosed guenon).
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Cararrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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339 AA.

PRELIMINARY;

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EMBL; AF162005; AAD47760.1; --
EMBL; AF162005; AAD47760.1; --
EMBL; AF162001; AAD47760.1; --
EMBL; AF162000; AAD47760.1; --
EMBL; AF162002; AAD47760.1; --
EMBL; AF162003; AAD47750.1; --
EMBL; AF162004; AAD47750.1; --
EMBL; AF162004; AAD47750.1; --
EMBL; AF162003; AAD47750.1; --
EMBL; AF16200376; GPCR_Rhodpsn.
                                                                  Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 96; DB 6; Length 339; 100.0%; Pred. No. 2e-07; Live 0; Mismatches 0; Indels
                                                                                                                                        species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                339 339
339 AA; 39168 MW; 6A4BF72FEBFF566F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE, PS00237, G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
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PRINTS; PR00237; GPCRRHODOPSN
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339 AA;
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                                             SEQUENCE FROM N.A.
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  NCBI_TaxID=33548;
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NON TER
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    OX REPRESENTATION OF THE PROPERTY OF THE PROPE
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Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF162026; AAD47781.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001886; F:G-protein coupled receptor protein signalin. . ; IEA.
InterPro; IRR000276; GFCR_Rhodopsn.
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Colbus guereza (Black-and-white colobus monkey).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
Colobus.
                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria; Primates; Catarrhini, Cercopithecidae,
Cercopithecinae, Cercopithecus.
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                                                                                                                              Query Match 100.0%; Score 96; DB 6; Length 339; Best Local Similarity 100.0%; Pred. No. 2e-07; Matches 18; Conservative 0; Mismatches 0; Indels
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                                        1 1
339 339
339 AA; 39150 MW; 847D5F92BB03E6E2 CRC64;
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339 339
339 AA, 39178 MW; 9DF2A6F446C55AED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS0237; GPROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-C chemokine receptor 5 (Fragment).
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                                                                                                                                                                                                                                                   178 SQYQFWKNFQTLKIVILG 195
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                                                                                                                                                                                                                           1 SOYOFWKNFOTLKIVILG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SOYOFWKNFOTLKIVILG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cercopithecus aethiops vervet.
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nes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                           NON TER
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                          Receptor.
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Q9TUR6
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Q9TQV6
ID Q9TQV
AC Q9TQV
DT 01-MA
DT 01-MA
DT 01-JU
DE CCR C
GN CCR C
OC BUKAT
OC BUKAT
OC COLOD
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF161900; AAD47657.1; -

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0004842; F:receptor activity; IEA.

GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001886; P:G-protein coupled receptor protein signalin. .

Interpro; IPR00027; GPCR.Rhodpsn.

PRINTS; PR00237; GPCR.Rhodpsn.

PROSITE; PS00237; GPCREIN RECEP F1 1; 1.

PROSITE; PS50262; G-PROTEIN RECEP F1 2; 1.
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                                                                                                                                                                                                                                                         01-WAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6;
                                                                                                                                                                                               339 AA
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                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                  C-C chemokine receptor 5 (Fragment)
178 SQYQFWKNFQTLKIVILG 195
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Receptor.
NON_TER
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                                              Gaps
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bamanla; Eutheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Cercopithecus.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mamaalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Erythrocebus.
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCR5 genes from diverse simian and prosimian species.";
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Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemoxine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                 339 AA.
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF162034; AAD47789.1; -..

EMBL; AF162034; AAD47789.1; -..

EMBL; AF162034; AAD47789.1; -..

EMBL; AF162034; AAD47789.1; -..

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0001284; F:receptor activity; IEA.

GO; GO:0001188; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001188; F:rhodopsin-like receptor protein signalin. . ; IEA.

InterPro; IPR000276; GPRR. Rhodpsn.

PROMINS; PR00227; GFRR. PROPENN. EECEP FI.1; 1.

PROSITE; PS50262; G-PROTEIN_RECEP FI.1; 1.
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCR5 genes from diverse simian and prosimian
species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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                                                                                                                                                                                                                                                                                                                                       339 AA; 39138 MW; AD31455EBBC69499 CRC64;
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339 339
339 AA, 39113 MW, 7F9803EAOEOAF9ED CRC64,
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UJN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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Best Local Similarity 100...
Best Local Similarity 100...
18; Conservative
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Best Local Similarity 100.
Matches 18; Conservative
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NCBI_TaxID=100937;
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Gaps

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species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161908; AAA4665.1; -.
GO; GO:0004812; F:receptor activity; IEA.
GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:d-protein coupled receptor protein signalin. . .; IEA.
InterPro; IFR000276; GFCR_Rhodopsin.
PRINTS; FR00237; GFCR_Rhodopsin.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Papio.
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
NCBI_TaxID=9600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M
Shibata R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinksy S
Shibata R., Yoder A., Fillai S., Kuiken C., Marx D., Wolinksy S
"Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                         Match 100.0%; Score 96; DB 6; Length 339; Local Similarity 100.0%; Pred. No. 2e-07; les 18; Conservative 0; Mismatches 0; Indels
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339 339 WW, 84EB018085DC0A62 CRC64;
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09TUSS,
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                            339 AA
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PS50262; G PROTEIN RECEP_F1_2;
                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                178 SQYQFWKNFQTLKIVILG 195
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es 18; Conserv
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 PROSITE;
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Matches
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Submitteed (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161995; AAD47750.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin.like receptor activity; IEA.
GO; GO:0001584; F:rhodopsin.like receptor protein signalin. .; IEA.
InterPro; IPR000276; GPCR_Rhodopsn.
Pfam; PF00001; 77m 1; GPCRRHODOPSN.
                                                                                          Cercopithecus nictitans (white-nosed guenon).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
mamalia; Butheria, Primates; Catarrhini, Cercopithecidae;
Cercopithecinae; Papio.
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                                                                                                                                                                                                                                 Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; "Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                              EMBL; AF162046; AAD47801.1; EMBL; AF162046; AAD47801.1; EMBL; AF162043; AAD477801.1; EMBL; AF162043; AAD47798.1; C. EMBL; AF162043; AAD47798.1; C. EMBL; AF162043; AAD47798.1; C. EMBL; AF162043; C. CO.0016472; F. Ereceptor activity; IEA. GO; GO:0001584; F. Erhodopsin-like receptor activity; IEA. GO; GO:0001584; F. Erhodopsin-like receptor protein signalin. InterPro; IPR00274; GPCR_Rhodpsn.
PRINTS; PR00237; GPCRADOPSN.
PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M
Kunstman K., Chen Z., Kollai S., Kuiken C., Marx P., Wolinksy S
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
"Sequences of the CCRS genes from diverse simian and prosimian
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                                                                                                                                                                                                                                                                                      species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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339 339 339 MW; 847F8F936B00E6E2 CRC64;
                   Q9TQU5;
1-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
     339 AA.
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     PRT;
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     PRELIMINARY;
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                                                             178 SQYQFWKNFQTLKIVILG 195
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Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                   RESULT 33
Q9TQV3
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Kunstman K., Chen Z., Korber B., Chibatea R., Wolinksy S.;
Subjatea R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCRS genes from diverse simian and prosimian
"Sequences of the CCRS genes from diverse simian and prosimian
"Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF161993; AAD47742.1; -.

EMBL; AF161991; AAD47742.1; -.

EMBL; AF161991; AAD47745.1; -.

EMBL; AAD47745.1; -.

EMBL;
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                          SEQUENCE FROM N.A.

K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinkey S., "Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Papio.
MCBI_TaxID=100937;
                                                                                                                                                                    species.";
Submitted (ULL-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (ULL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161997; ALINEGYAL to membrane; IEA.
GO; GO:001681; E:neceptor activity; IEA.
GO; GO:001786; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001786; F:rhodopsin-like receptor protein signalin.
InterPro; IPR00276; GPCR.Rhodopsn.
PRINTS; PR00237; GPRCHHODOSN.
PROSITE; PS00237; GPRCHHODOSN.
PROSITE; PS00237; GPRCHHODOSN.
PROSITE; PS00237; GPRCHHODOSN.
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100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
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339 339
339 AA, 39079 MW; 7176E3EAOE00F3ED CRC64;
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01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UMY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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Papio papio (Guinea baboon)
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Best Local Similarity
Matches 18; Conserv
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NON TER
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EMBL; AF162040; AAD47795.1; -...
GO; GO:0016021; C:integral ac membrane; IEA.
GO; GO:0016021; E:receptor activity; IEA.
GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001884; F:rhodopsin-like receptor protein signalin. .; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRNINTS; PR00237; GCRRHODPSN.
PROSITE; PS00237; GFRPTEIN_RECEP_FI_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_FI_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Kunstman K., Chen Z., Korber B., Oprondek J., Marx P., Wolinksy S., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CGR5 genes from diverse simian and prosimian species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Cercopithecus.
                                                                                                                                                                                                                                         Cercopithecus mona.
Cercopithecus mona.
Cercopithecus, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
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100.0%; Pred. No. 2e-07;
cive 0; Mismatches 0; Indels
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                              Q9TQV3;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-TUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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Submitted (UTL-1999) to the EMBL/GenBank/DDBJ databases.

Submitted (UTL-1999) to the EMBL/GenBank/DDBJ databases.

Refig. Ap161907; Ap4047664.1; ...

Refig. Ap161907; Ap4047664.1; ...

Refig. Ap161906; Ap4047663.1; ...

Refig. Ap161906; Ap404663.1; ...

Refig. Ap161906; Ap404663.1; ...

Refig. Ap161906; Ap404663.1; ...

Refig. Ap161906; Ap404876.1; ...

Refig. Ap161907; Refig. Refig.
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GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001586; P:chodopsin-like receptor protein signalin. . .; IEA.
InterPro; IPR000276; GCR_Rhodopsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                           Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Pongo.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Erythrocebus.
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K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy P. Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S. Sequences of the CCRS genes from diverse simian and prosimian
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
      01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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EMBL; AF162035; AAD47790.1; --
EMBL; AF162036; AAD47791.1; --
EMBL; AF162050; AAD47803.1; --
EMBL; AF162050; AAD47805.1; --
EMBL; AF162052; AAD47805.1; --
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                                                                                                                                                              Pongo pygmaeus (Orangutan).
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18; Conservative
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submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF162031; AAD47788.1;
GO; GO:001621; C:integral to membrane; IEA.
GO; GO:001584; F:receptor activity; IEA.
GO; GO:0001584; F:receptor activity; IEA.
GO; GO:0007186; P:chotoein coupled receptor protein signalin. .; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
InterPro: IPR00027; GPCR_Rhodpsn.
Pfan; PF0001; 7fm.1; 1.
PRINTS; PR00237; GPRTEIN_RECEP_F1.1; 1.
PROSITE; PS00237; GPROTEIN_RECEP_F1.2; 1.
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Erythrocebus patas (Red guenon) (Hussar).
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Erythrocebus.
EMBL, AF162045, AAD47800.1; -. GCG; GO.001601; C.integral to membrane; IEA. GC; GO.0016012; C.integral to membrane; IEA. GC; GO.0016842; F.receptor activity; IEA. GC; GO.001584; F.rhodopsin-like receptor activity; IEA. GC; GO.0011884; F.rhodopsin-like receptor protein signalin. InterPro; IPR000275; GFG_Rhodpsn. FRINTS; FR00027; GFG_Rhodpsn. FRINTS; FR00027; GFRATEIN RECEP FI 1; 1. PROSITE; PS500262; G_PROTEIN_RECEP_FI 2; 1.
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Pred. No. 2e-07;
Mismatches 0; Indels
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339 339
339 AA; 39148 MW; 0CA289CDDEEDE831 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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Q9TQW2 Q9TQW2;

RESULT 36 Q9TQW2

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EMBL, AFL2006; AAD47761.1; -- EMBL/GenBank/DDBJ databases.

EMBL, AFL2006; Cintegral to membrane; IEA.

GO; GO:0004884; Friedeptor activity; IEA.

GO; GO:0001864; Friedeptor activity; IEA.

GO; GO:0001864; Friedeptor activity; IEA.

R GO; GO:000186; P:G-protein coupled receptor protein signalin. . .; II PRINTS; PRO0237; GPCRRHODOFSN.

R PROSITE; PS00237; GPCRRHODOFSN.

R PROSITE; PS00237; GPCRRHODOFSN.

R PROSITE; PS00237; GPRRHODOFSN.

R PROSITE; PS00237; GPRRHODOFSN.

R PROSITE; PS00262; GPROTEIN_RECEP_FI_2; 1.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUA-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
CGCs.
Gorilla gorilla (Lowland gorilla).
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cercopithecus aethlops (Green monkey) (Grivet).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
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100.0%; Pred. No. 2e-07;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 96; DB 6; Length 339; Best Local Similarity 100.0%; Pred. No. 2e-07; Matches 18; Conservative 0; Mismatches 0; Indels
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339 339
339 AA; 39154 MW; 09715882A6074884 CRC64;
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339 339
339 AA; 39164 MW; 85CF8E22DB00E6E3 CRC64;
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U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN RECEP_F1_1; 1.
RECEPTOR.
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NON TER 339 339
SEQÜENCE 339 AA; 39154 MW; 09715882A60
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Best Local Similarity 100.
Matches 18; Conservative
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Q9TQR
C09TQR
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10 10-MA
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REMBL; AF161897; AAA476481;

REMBL; AF161897; AAA476481;

REMBL; AF161891; AAA476491;

REMBL; AF161891; AAA476491;

REMBL; AF161895; AAA476521;

REMBL; AF161895; AAA476521;

REMBL; AF161895; AAA476521;

REMBL; AF161895; AAA476521;

REMBL; AF161895; AAA476531;

REMBL; AF161896; AAA476531;

ROG; GO:00104872; F:receptor activity; IEA.

GO; GO:001884; F:rhodopsin-like receptor activity; IEA.

ROG; GO:0001884; F:rhodopsin-like receptor protein signalin. .;

RICHERPRO 1 PROUGOST; GERRRHODDSN.

REMINTS; PRO0237; GERRHODDSN.

REMINTS; PRO0237; GERRHODDSN.
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A KUNSERMAN K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., A SLibbata R., Yoder A., Pillai S., Kulken C., Marx P., Wolinksy S.; A "Sequence of the CCRS genes from diverse simian and prosimian repecies.";

I "Sequence of the EMELY Genes from diverse simian and prosimian of submitted (JUL-1999) to the EMELYGENBANK/DDBJ databases.

E MEMBL, AFL62007; AAD4762.1; -.

R GO; GO:00016021; C:integral to membrane; IEA.

GO; GO:00018872; F:receptor activity; IEA.

R GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.

R GO; GO:000188; F:rhodopsin-like receptor activity; IEA.

R InterPro; IPR00027; GPCR_Rhodopsin.

R PFIMTS; PR00027; GPCR_RHODOPSN.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Cercopithecus.
                                                                                                                          SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M. Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S. Sequences of the CCR5 genes from diverse simian and prosimian species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Gorilla.
NCBI_TaxID=9595;
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339 339
339 AA; 39219 MW; BFFE9138E82933D0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 SQYQFWKNFQTLKIVILG 195
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10 097503
10 01-MA
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0; Gaps Query Match
100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels

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Search completed: September 28, 2004, 09:06:19 Job time: 29.8 secs

us-10-084-813-14.rag

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                    OM protein - protein search, using sw model
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September 28, 2004, 08:51:21 ; Search time 52.525 Seconds
(without alignments)
118.345 Million cell updates/sec

US-10-084-813-14 118 1 APYNIVLLINTFQEFFGLNNCS score: Title: Perfect :

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext

1586107 Total number of hits satisfying chosen parameters:

1586107 segs, 282547505 residues

Searched:

length: 0 length: 2000000000 DB sed DB sed Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:\*
geneseqp1990s:\*
geneseqp2000s:\*
geneseqp2001s:\*
geneseqp2001s:\* geneseqp2003as:\*geneseqp2003bs:\*geneseqp2004s:\* 'A\_Geneseq\_29Jan04:\* 1: qeneseqp1980s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Aab88996 HIV gp120	Adc10142 Human NOV	Adc10144 Human NOV	Aaw26766 Human che	Aaw27407 Human CCR	Aaw27123 Human che	Aaw27125 Macaque c		Aaw23835 Human CC	HIV-1		Amino	Human	8 Human	Aag80111 Human CCR	Aae04321 Human che	Human	Aae07039 Human G-p	Aab46858 Human HDG	Non-en	Human	Aab82948 Human HIV	Aau97150 Human G-p	Aau97152 Human G-p	Aam52829 Human CCR
SUMMARIES		ΠD	AAB88996	ADC10142	ADC10144	AAW26766	AAW27407	AAW27123	AAW27125	AAW07602	AAW23835	AAW88232	AAY80128	AAG79089	AAE07046	AAE07048	AAG80111	AAE04321	AAE07037	AAE07039	AAB46858	ABB56342	AAB83354	AAB82948	AAU97150	AAU97152	AAM52829
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df	Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	1:00.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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Aam52828 Human CC Abg70597 Human G-P Abg92883 Human imm Abg92889 Human G-P Aae25808 Human G-P Aae25811 Human G-P Abb81054 G-protein Abb81054 Human Che Abg75540 Human Che Abg75540 Human Che Abg75540 Human Che Abg75540 Human CC Abus1331 Human CC Abus13331 Human CC Abw8193758 Amino aci Abg81333 Human CC Aaw23834 Human CC Aaw23834 Human CC Aaw23834 Human CC Aaw441280 Fusion pr Aaw441280 Fusion pr Ad444859 Rat Prote	
AAM52828 ABG92883 AAG92883 AAG22808 AAAE2808 AAAE2811 ABB81054 AAB81054 AAB75540 AAG75540 AAG75540 AAG75540 AAG75540 AAG75540 AAG75540 AAG75540 AAG75540 AAG75540 AAG75540 AAG75540 AAG75540 AAG75540 AAG75540 AAW5441280 AAW54037 AAD44859	
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## ALIGNMENTS

AAB88996 standard; peptide; 22 AA. (first entry) 23-MAY-2001 AAB88996; AAB8899 

HIV gp120 protein binding peptide #89

Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist; replication; CCR5; CXCR4; CTR133.

Homo sapiens.

WO200116182-A2.

08-MAR-2001.

25-AUG-2000; 2000WO-US023505

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

99US-0151270P

27-AUG-1999;

Saxinger C;

WPI; 2001-244398/25.

Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gpl20 under physiological conditions.

Claim 21; Page 38; 114pp; English.

The present invention describes a number of peptides which are able to bind to HIV glycoprotein 120 (gp120). These are similar to the human chemokine receptors CCRS, CXCR4 and STR13, as well as CD4. These are useful in the treatment of HIV, as they prevent replication of the virus. The present sequence is an example of a peptide of the invention

Sequence 22 AA;

ö Gaps ; Query Match 100.0%; Score 118; DB 4; Length 22; Best Local Similarity 100.0%; Pred. No. 1.1e-12; Matches 22; Conservative 0; Mismatches 0; Indels

1 APYNIVLLINTFQEFFGLNNCS 22

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1 APYNIVLLINTFQEFFGLNNCS 22

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cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective; antiinflammatory; gene therapy; antisense therapy; thyromimetic; NOVX; pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder; inflammatory disorder; chromosome mapping; tissue typing; predictive medicine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;
Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;
Gerlach VL, Gorman L, Guo X, Herrmann JL, Hjalt T, Ji W, Kekuda F
Khramtsov NV, Li L, Liu X, Malyankar JW, Miller CE, Millet I;
Ort T, Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK;
Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G, Spaderna SK;
                                                                                                                                                                                                                    Human NOVX polypeptide SEQ ID NO: 162.
                                                      ADC10142 standard; protein; 268 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001US-0295607P.
2001US-0295641P.
2001US-02964418P.
2001US-0296575P.
2001US-0296575P.
2001US-0296573P.
2001US-0296573P.
2001US-029630P.
2001US-0299230P.
2001US-0299230P.
2001US-0299230P.
2001US-0299133P.
2001US-0299133P.
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2001US-0301550P.
2001US-0302951P.
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2002US-0359121P.
2002US-0359964P.
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                                                                                                                                                                18-DEC-2003 (first entry)
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18-JUN-2001;
19-JUN-2001;
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22-JUN-2001;
26-JUN-2001;
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22-FEB-2002;
22-FEB-2002;
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12-JUN-2001;
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                                                                                                          ADC10142;
RESULT 2

AD C101422

ID C1014
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The invention relates to novel isolated polypeptides, mature form of the polypeptide, a sequence that is 95% identical to the polypeptide or the polypeptide comprising one or more conservative substitutions. The NOVX polypeptide is useful for treating or preventing a pathology associated with the polypeptide e.g. disorders associated with aberrant expression or activity of the polypeptide, such as cancer, diabetes, obesity, and endocrine, CNS and infilamatory disorders. They can also be used in various detection and screening assays, chromosome mapping, tissue typing and predictive medicine. This sequence corresponds to one of the polypeptides of the invention.
                                                                                          New isolated NOVX polypeptides and nucleic acid molecules useful for treating, preventing and diagnosing pathological conditions with NOVX-associated disorders, such as cancer, obesity, diabetes and inflammatory or CNS diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective; antidiamatory; gene therapy; antiseaspy; thycominetic; NOVX; pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder; inflammatory disorder; chromosome mapping; tissue typing;
 Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                          Claim 1; SEQ ID NO 162; 772pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human NOVX polypeptide SEQ ID NO: 164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 APYNIVLLLNIFQEFFGLNNCS 186
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2001US-0295661P.
2001US-0296404P.
2001US-0296418P.
2001US-0296575P.
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2001US-0295573P.
2001US-0297567P.
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21-JUN-2001; 2001US-0299949P.
22-JUN-2001; 2001US-0300177P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             22; Conservative
 Stone DJ, Lepley DM;
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                             WPI; 2003-210149/20.
N-PSDB; ADC10141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              predictive medicine.
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 268 AA;
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06-JUN-2001;
07-JUN-2001;
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12-JUN-2001;
12-JUN-2001;
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15-JUN-2001; 2
18-JUN-2001; 2
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Spytek KA,
Burgess CE,
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Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E, Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA; Gerdach VL, Gorman L, Guo X, Herrmann JL, Halt T, Ji W, Kekuda R; Khramtsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I; Ort T, Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK; Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP; Burgess CE,: Lepley DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated NOVX polypeptides and nucleic acid molecules useful for treating, preventing and diagnosing pathological conditions with NOVX-associated disorders, such as cancer, obesity, diabetes and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 164; 772pp; English.
26-JUN-2001, 2001US-0300883P.
28-JUN-2001; 2001US-0301530P.
28-JUN-2001; 2001US-0301550P.
03-JUL-2001; 2001US-030251P.
14-SEP-2001; 2001US-0302890P.
14-SEP-2001; 2001US-0322297P.
25-SEP-2001; 2001US-032459P.
14-DEC-2001; 2001US-0341652P.
14-DEC-2001; 2001US-0341652P.
14-DEC-2001; 2001US-0341652P.
12-FEB-2002; 2002US-0359034P.
22-FEB-2002; 2002US-0359034P.
22-FEB-2002; 2002US-0359034P.
22-FEB-2002; 2002US-0359034P.
22-FEB-2002; 2002US-0359034P.
27-FEB-2002; 2002US-0359034P.
27-FEB-2002; 2002US-0359034P.
27-FEB-2002; 2002US-0359034P.
12-MAR-2002; 2002US-0359130P.
12-MAR-2002; 2002US-0369444P.
10-ARY-2002; 2002US-0369444P.
                                                                                                                                                                                                                                                                                                                                         (CURA-) CURAGEN CORP
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N-PSDB; ADC10143.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 268 AA;
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The invention relates to novel isolated polypeptides, mature form of the polypeptide, a sequence that is 95% identical to the polypeptide or the polypeptide comprising one or more conservative substitutions. The NOVX polypeptide is useful for treating or preventing a pathology associated with the polypeptide e.g. disorders associated with aberrant expression or activity of the polypeptide, such as cancer, diabetes, obesity, and endocrine, CNS and inflammatory disorders. They can also be used in and predictive medicine. This sequence corresponds to one of the polypeptides of the invention.

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Gaps
                               .
0
     100.0%; Score 118; DB 7; Length 268; 100.0%; Pred. No. 2.1e-11;
                               Indels
                             0
                               Mismatches
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0
                               Conservative
Query Match
Best Local Similarity
Matches 22, Conserv
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AAW26766 standard; protein; 332 AA RESULT 4
AAW26766
ID AAW2
XX
AC AAW2
XX

(first entry) 21-MAY-1998

chemokine receptor MMLR-CCR. Human

Mammalian mixed lymphocyte receptor; chemokine receptor; MMLR-CCR; human; macrophage; chemotaxis; hematopolesis; infection; inflammation; proliferative disease; cardiovacular disease; tumour; rheumatod arthritis; alveolitis; atherosclerosis; tumour; cheumatod arthritis; alveolitis; atherosclerosis; diabetes; tumour; choring granulomatous disease; asthma; mysathenia gravis; diabetes; inflammatory bowel disease; toxic shock syndrome; septic shock; Chediak-Higashi syndrome; therapy; diagnosis.

Homo sapiens

107. .128 /note= "conserved peptide" Location/Qualifiers Peptide

/note= "a claimed polypeptide has isoleucine at residue  $121^\circ$ Misc-difference

06-NOV-1997.

97WO-US006993 25-APR-1997; 96US-00638081. 26-APR-1996;

(INCY-) INCYTE PHARM INC.

Wilde CG; Coleman R, Bandman O, Au-Young J,

WPI; 1997-549729/50. N-PSDB; AAT99542. Polynucleotide encoding MMLR-CCR or MPHG-CCR chemokine receptor - useful to study, diagnose and treat, e.g. infection, inflammation, solid tumour and proliferative and cardiovascular disease.

Claim 8; Page 37-38; 59pp; English.

This protein comprises human MMIR-CCR, a novel C-C chemokine receptor associated with monocyte/macrophage infiltration and chemotaxis and haematopoiesis. The amino acid sequence was deduced from a cDNA clone (see AAT99542) obtained from a cDNA library made from monouclear cells collected on day 2 of a mixed lymphocyte culture, i.e. cells associated with inflammation and immunomdulation. Another novel chemokine receptor, MPHG-CCR (see AAN36767), is also claimed. MMIR-CCR contains 7 transmembrane spanning segments connected by a serives of intracellular cand extracellular loops. MMIR-CCR and MPHG-CCR can be used to study, diagnose and treat disease states in which normal leukocyte function is perturbed by normal leukopoiesis or inappropriate activation via chemokine agoniers or antagoniers, such as infection, inflammation, proliferative disease, tumourigenesis, autoimmune disease, abnormal cell arthus, anysathenia gravis, diabetes, inflammatory bowel disease, toxic shock syndrome, septic shock and Chediak-Higashi syndrome

Sequence 332 AA;

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Gaps ö Length 332; Indels 100.0%; Score 118; DB 2; 100.0%; Pred. No. 2.7e-11; ive 0; Mismatches 0; Local Similarity 100. nes 22; Conservative Query Match Matches

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RESULT 5 AAW27407 ID AAW27407 standard; protein; 352 AA.

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AAW27407;

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This polypeptide sequence comprises novel human chemokine receptor 88C, a G protein coupled receptor that is involved in leukocyte trafficking. Its amino sequence was deduced from a CDNA clone (AATS161) isolated from a marcophage library. It shows 62% identity to CCCKR1. Chemokine receptor 88-28 (see AAW27124) has also been identified. 88C and 88-28 receptors and their polypeptide fragments can be produced in transformed host cells. The receptors, peptides comprising one or more of the extracellular or intracellular domains, and anti-receptor antibodies can be used to modulate receptor activities, particularly ligand and G brotein binding, and are potentially potentially useful in the treatment of atheroslerosis, rheumatoid arthritis, tumours, asthma, viral infection, AIDS, inflammatory conditions, pathological immune response, abnormal haematopoietic processes etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding chemokine receptors 88-2B and 88C - used modulate leukocyte trafficking, e.g. for treatment of inflammation, tumours, viral infections, auto-immune diseases, etc.
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100.0%; Pred. No. 2.9e-11;
iive 0; Mismatches 0;
                                                                             1. .32
/label= Extracellular_domain
56. .67 Intracellular_domain
89. .112
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/label= Extracellular_domain
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/label= Intracellular_domain
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                                                        Location/Qualifiers
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96US-00661393.
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/label= Ext
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Matches 22; Conservative
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                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is human CC (Cys-Cys) chemokine receptor 5 (CCR5), which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES chemokines, but not by monocyte chemoattractant protein 1 (WCP-1), MCP-2, MCP-3, interleukin-8 (IL-8) or growth related gene product alpha (GRO alpha) chemokines. Active CCR-5 is also a receptor of human immunodeficiency virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can used to diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid arthritis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriaais, viral infections, especially HIV-1 or HIV-2 infection, cancer, atherosclerosis and autoimmune disorders
                                                                                                                           Human Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention; inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma; idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer; atherosclerosis; autoimmune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Active and inactive forms of human CC chemokine receptor CCR-5 - useful to diagnose, prevent and/or treat inflammatory disorders, autoimmune disease and viral infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vassart G,
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                                                                                                                                                                                                                                                                                                                                                                              97WO-BE000023.
                                                                                                                                                                                                                                                                                                                                                                                                                    96EP-00870021.
96EP-00870102.
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N-PSDB; AAT90117.
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                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-1997;
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                                                            14-APR-1998
                                                                                                    Human CCR5
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Gaps

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AAW27123;

RESULT

ò 원 Length 352; Indels Homo sapiens.

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                                                                        Chemokine receptor 88C, atherosclerosis; rheumatoid arthritis; tumour; asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy; diagnosis; leukocyte trafficking; G protein coupled receptor; ligand; modulator; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This polypeptide sequence comprises macaque chemokine receptor 88C, a G protein coupled receptor that is involved in leukocyte trafficking. Its amino sequence was deduced from a 88C DMA (AARBSIGS) isolated by PCR amplification. It shows 97% identity to human 88C GAMW7123). 88C receptors and their polypeptide fragments can be produced in transformed host cells. The receptors, peptides comprising one or more of the extracellular or intracellular domains, and anti-receptor antibodies can be used to modulate receptor activities, particularly ligand and G protein binding, and are potentially potentially useful in the treatment of atheroslerosis, rheumatoid arthritis, tumours, asthma, viral infection, AIDS, inflammatory conditions, pathological immune response abnormal haematopoietic processes etc. A hybridoma that produces an antibody that specifically binds to macaque 88C is claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G-protein chemckine receptor; HDGNR10; signal transduction;
haematopoiesis; leukaemia; inflammation; rheumatoid arthritis; diagnosis;
therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding chemokine receptors 88-2B and 88C - used modulate leukocyte trafficking, e.g. for treatment of inflammation, tumours, viral infections, auto-immune diseases, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human G-protein chemokine receptor HDGNR10.
                                                                                                                                                                                                                                                                                                                                                                                       Raport CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 36; Page 57-58; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APYNIVLLINIFQEFFGLNNCS 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 APYNIVLLINTFQEFFGLNNCS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW07602 standard; protein; 352 AA.
                                                 Macaque chemokine receptor 88C.
                                                                                                                                                                                                                                                                    96WO-US020759.
                                                                                                                                                                                                                                                                                                    95US-00575967
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               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                     Gray PW, Schweickart VL,
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                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-341689/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT85163
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22;
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                                                                                                                                                                                                                                                                                                                     17-JUN-1996;
                 14-DEC-1997
                                                                                                                                                                                                                                  26-JUN-1997
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                                                                                                                                                                    Macaca sp.
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Matches
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ID AAW07602
IX XX AC AAW0
XX DDT 26-1
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XX G-P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC chemokine receptor 5; CCR5; G-protein coupled receptor; human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.
                                                                                                                                                                                                                      Human G-protein chemokine receptor, HDGNR10 - useful to identify (ant)agonists, for treatment of haematopoiesis, leukaemia, chronic and acute inflammation, rheumatoid arthritis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 352;
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// note= "extracellular loop-1 (Claim 19)"

7. 171

/label= IV
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.94. .219
                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 118; DB 2;
100.0%; Pred. No. 2.9e-11;
iive 0; Mismatches 0;
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/label= III
/note= "transmembrane domain"
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'note= "transmembrane domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human CC chemokine receptor 5 (CCR5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 APYNIVLLINTFQEFFGLINGS 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW23835 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                           Claim 1; Page 44-46; 61pp; English
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                                                                                                                                (HUMA-) HUMAN GENOME SCI INC.
                                                                            95WO-US007173
                                                                                                       95WO-US007173
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Best Local Similarity 100.
Matches 22; Conservative
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/label=
                                                                                                                                                                                 WPI; 1997-043072/04.
N-PSDB; AAT44042.
                                                                                                                                                        Li Y, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 352 AA;
                         WO9639437-A1
                                                                           06-JUN-1995;
                                                                                                    06-JUN-1995;
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                                                   12-DEC-1996.
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AAW23835
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ocation/Qualifiers

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chemokine receptor that has been designated CCRS. The sequence was deduced from an isolated CDNA clone (see AAT76920). An Ala127Leu variant (see W238340 of CCRS was also identified. The susceptibility of human macrophages to HIV infection depends on cell surface expression of CD4 and CCRS. CCRS is a member of the 7-transmembrane superfamily of G-protein coupled call surface molecules. It plays an essential role in the membrane fusion step of infection by some HIV isolates. The establishment of stable, non-human cell lines and transgenic mammals having cells that infection. Antibodies that bind to CCRS, CCRS variants, and CCRS-binding agents capable of blocking membrane fusion between HIV and target cells represent potential anti-HIV therapeutics for macrophage tropic strains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein sequence comprises of a novel human macrophage-selective CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion between HIV and a target cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 118; DB 2; Length 352;
Pred. No. 2.9e-11;
; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Berger EA, Alkhatib G, Murphy PM;
                                                                                                          261. .276
/note= "extracellular loop-3 (Claim 19)"
/label= VII
/note= "transmembrane domain"
                   /note= "transmembrane domain"
238. .258
/label= Wl
/note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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Local Similarity 100.0%;
les 22; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                    97WO-US009586.
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label= V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Combadiere C, Feng Y,
Broder CC, Kennedy PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-032650/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT76920.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 352 AA;
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                                                                                                                                                                                                                                                         W09745543-A2
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Best Local S
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                                              Domain
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AAM8823
XX AAW883
XX AC AAW883
XX XX BDT 15-MAL
XX BB HIV-1
XX HIV-1
XW Gene
XX CO HOMO OX
XX HOW GENE
XX CO HOMO OX
XX CO HOMO OX
XX CO HOMO OX
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Homo sapiens

Matches

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Answars of the infection by macrophage-tropic (W-tropic) strains of HIV-1. The invention relates to the identification of a CCRS variant (see Anwasz1), designated CCRSm303, comprising the first two transmembrane commans of wild-type CCRS, but lacking transmembrane domains 3-7. The presence of the CCRSm303 variant with the wild type CCRS allele shows a presence of the CCRSm303 variant with the wild type CCRS allele shows a craims, and may indicate slower progression of the disease. The detection of CCRS variants may be used to identify individuals at lower crise of intection who, if infected, may exhibit slower progression to AIDS. Probes and primers (see AAV84127-36) are provided for use in diagnostic methods for detecting the presence of such variants. A method is provided for inhibiting HIV-1 infection of a cell expressing the CCRS receptor. This involves introducing a nucleic acid encoding a CCRS variant into the cell, thereby reducing the number of functional CCRS molecules present on the cell surface
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is the amino acid sequence of wild-type human CCR5, which serves as
                                                                                      in wild-type CCR5, TGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Braun J;
                                                                               /note= "corresponds to TGT (Cys) (Stop) in CCr5m303"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 118; DB 2; Best Local Similarity 100.0%; Pred. No. 2.9e-11; Matches 22; Conservative 0; Mismatches 0;
                                                                                                                     103. .124
/note= "transmembrane domain 3"
                                                                                                                                                                                                              236. .260
/note= "transmembrane domain 6"
                                                                                                                                                                                                                                              275. .301
/note= "transmembrane domain 7"
                                                                                                                                                                "transmembrane domain 4"
                                                                                                                                                                                                "transmembrane domain 5"
                          "transmembrane domain 1"
                                                      'note= "transmembrane domain 2"
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                                                                                                                                                                                                                                                                                                                                                                                                                     (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 34-35; 55pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY80128 standard; protein; 352 AA.
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                                                                                                                                                                                                                                                                                                                                                        98WO-EP003437
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                                                                                                                                                142. .167
/note= "tr
200. .223
                                       .87
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                                                                                                                                                                                                   /note=
                            note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 352 AA;
                                                                        Misc-difference
                                                                                                                                                                                                                                                                                              WO9854317-A1
                                                                                                                                                                                                                                                                                                                                                           29-MAY-1998;
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 Key
Domain
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ID AAY8
XX
AC AAY8
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Human, receptor, DC-SIGN, dendritic cell, T lymphocyte, HIV, gpl20,
C-type lectin, ICAM3, HIV entry, T cell, macrophage, HIV infection, CCR5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 An antibody for the treatment or prevention of HIV-infection comprises gpl20 portion which binds to DC-SIGN or is exposed upon gpl20 binding o DC-SIGN due to concomitant conformational change.
Amino acid sequence of human CCR5 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 118-119; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        Van Kooyk Y,
                                                                                                                                                                                                                                                28-FEB-2001; 2001WO-US006322.
                                                                                                                                                                                                                                                                                           02-MAR-2000; 2000US-00517605.
                                                                                                                                                                                                                                                                                                                                    (UYNY ) UNIV NEW YORK STATE. (UYNI-) UNIV NIJMEGEN.
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                                                                                                                                                                                                                                                                                                                                                                                                          Kwon D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-602565/68.
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Best Local Similarity
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                                                                                                                                                       WO200164752-A2
                                                                                                                 Homo sapiens.
                                                                                                                                                                                                     07-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE07046;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a human G-protein chemokine receptor designated HDGNR10 polymucleotides are useful in methods of screening to compounds which bind to and either: (1) activate the HDGNR10 polypeptides causing stimulation of haematopolesis, wound healing, coagulation, and angiogenesis; treatment of solid tumours, chronic infections, leukaemia, T-cell mediated autoimmune diseases, parastic infections, psoriasis, and to stimulate growth factor activity; or (2) inhibit activation of the HDGNR10 polypeptides which is useful for preventing and/or treating allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation, histamine and immunoglobulin B-mediated allergic reactions, prostaglandin-independent fever, bone marrow failure, slicosis, sarcoidosis, theumatoid arthitis shock and hyper-eosinophilia syndrome. The polymucleotides are also useful for diagnostic assays for detecting diseases related to mutations in the nucleic acid sequences encoding the polympetides and for detecting an altered level of the soluble form of the receptor polypeptides. The polymucleotides are also useful for in vitro purposes related to altered level of the soluble form of the receptor polypeptides. The polymucleotides are also useful for in vitro purposes related to constitute of DNA vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                 Human, G-protein coupled receptor, G-protein chemokine receptor, HDGNR10, diagnosis; haematopoiesis; wound healing; coagulation; angiogenesis; nucur, infection; leukaemia; psoriasis; allergy; T-cell mediated autoimmune disease; atherogenesis; anaphylaxis; inflammation; allergic reaction; silicosis; sarcoidosis; theumatoid arthritis; hyper-eosinophilia syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acid encoding human G-protein chemokine receptor useful for diagnostic assays, scientific research and screening for compounds which bind to and activate or inhibit activation of the receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 118; DB 3; Length 352; 100.0%; Pred. No. 2.9e-11; tive 0; Mismatches 0; Indels
                                        Human G-protein chemokine receptor HDGNR10 SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 APYNIVLLINTFQEFFGLNNCS 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 1; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                    95US-00466343.
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(first entry)
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N-PSDB; AAZ91481.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li Y, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                  06-JUN-1995;
                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUN-1995;
19-MAY-2000
                                                                                                                                                                                                                                                                                         US6025154-A.
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ID AAG7
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AC AAG7
XX
DT 10-D
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Geijtenbeek T;

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The specification describes an antibody which is specific for an antigenic fragment of gpl20. This antigenic fragment binds to DC-SIGN or conformational change. Drinding of DC-SIGN due to concomitant conformational change. DC-SIGN is a receptor that is specifically expressed on dendritic cells and facilitates infection of T lymphocytes with HIV. DC-SIGN is identical to a HIV-1 gpl20-binding C-type lectin. DC-SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes) with high affinity. The antibody of the invention inhibits the trans enhancement of HIV entry into a T cell or macrophage facilitated by infection. The present sequence represents a human CCRS protein, which is a translocation promoting agent that interacts with CD4. This receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV; human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; cytostatic; immunosuppressive; nootropic; neuroprotective; gene therapy; neurodegenerative disorder; Kaposi's sarcona; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative collitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 118; DB 4; 100.0%; Pred. No. 2.9e-11; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 APYNIVLLINTFQEFFGLNNCS 270
                                                                                                                                                                                                                                                                                                                                                                     functions in HIV-1 entry into cells
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AAG79089 standard; protein; 352 AA

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(first entry)

10-DEC-2001

AAG79089;

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WO200158916-A2
Homo sapiens
                                                                           16-AUG-2001
   Key
Domain
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interaction. The disease or disorder may also be an infectious disease (e.g. a viral infection such as an early stage HIV infection, a cycomegalovirus infection, an autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The disease or disorder may be associated with aberrant CCR5 expression, lack CCCF ligand expression, or lack of CCR5 ligand expression, or lack of CCR5 ligand correase or decrease storage capabilities. CCR5 HGGMR10 protein is used as a food additive or preservative to increase or decrease storage capabilities. CCR5 HGGMR10 DNA, or correction, antibodies, agonists and antagonists are also useful in the protein, antibodies, agonists and antagonists are also useful in the diagnosis, treatment and prevention of cancer (breast, ovary, adrenal curogenital); immune disorders (Adabson's disease, allergies, autoimmune thyroiditis, diabetes mellitus, crohm's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular disorders (mycardial ischaemias) and wound healing. The present sequence is human CCR5 HDGNR10 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acid encoding a human G-protein chemokine receptor (CCRS) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, G-protein chemokine receptor, CCR5, HDGNR10, inflammation, HIV, human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; cytostatic; immunosuppressive, noctrobic, neuroprotective; gene therapy; reurodegenerative disorder; Kaposi's sarcoma; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestimal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 118; DB 4; Length 352; 100.0%; Pred. No. 2.9e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE07048 standard; protein; 352
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09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (first entry)
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N-PSDB; AAD13299.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 352 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to human G-protein chemokine receptor (CCR5) HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are useful for treating, preventing or ameliorating a disease or disorder associated with inflammation, defective or aberrant chemotaxis of immune cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen presenting cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid encoding a human G-protein chemokine receptor (CCRS) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
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|Jabel= Transmembrane_domain
|note= "Segment 7"
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/label= Intracellular_loop_1
68..88
                                                                                                                                                                                                                                                                         18. .88
| Jabel = Transmembrane_domain
| Jote = "Segment 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   25. .141
label= Intracellular loop 2
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|label= Transmembrane_domain
|note= "Segment 4"
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| Salabel = Extracellular_loop_3
                                                                                                        Extracellular domain
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|abel= Transmembrane_domain
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|label= Transmembrane_domain
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                                                             iocation/Qualifiers
                                                                                                                                                                                                            "Segment 1"
                                                                                                                                                                                                                                                                                                                                                                                                                            note= "Segment 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "Segment 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Segment 5"
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09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
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/label= Ex
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                                                                                      l. .36
/label= 1
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N-PSDB; AAD13282.
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Gaps

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Indels

Disclosure, Page 10; 26pp; German.

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The invention relates to human G-protein chemokine receptor (CCRS)

HDGNR10 polypeptides and polynucleotides. CCRS HDGNR10 antibodies are
useful for treating, preventing or ameliorating a disease or disorder
associated with inflammation, defective or aberrant chemotraxis of immune
cells, HTV infection (such as Pneumocystis carinii pneumonia or Kaposi's
sarcoma) or defective or aberrant T-cell antigen presenting cell
interaction. The disease or disorder may also be an infectious disease
control infection such as an early stage HTV infection, a
cytomegalovirus infection, or a poxvirus infection, a nautoimmune
control interaction arthritis) or a neurodegenerative disorder. The
disease or disorder may be associated with aberrant CCRS expression, lack
of cCRS function, aberrant CCRS ligand expression, or lack of CCRS ligand
function. CCRS HDGNR10 protein is used as a food additive or preservative
control increase or decrease storage capabilities. CCRS HDGNR10 DNA,
control of a disposite and antegonists are also useful in the
disposis, treatment and prevention of cancer (breast, ovary, adrenal
control, bone, bone marrow, gastrointestinal tract, liver, lung,
dispositial); immune disorders (Adabetes mellitus, Crohn's
curogenital); immune disorders (Adabetes mellitus, Crohn's
curogenital); immune disorders (Adabetes mellitus, Crohn's
curogenital); cardiovascular disorders (mycavalial ischaemias) and wound healing. The
control or present sequence is human CCRS HDGNR10 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection; inflammation; autoimmune disease; metastasis; bronchial asthma; lupus; chronic bowel inflammation; rheumatoid arthritis; cytostatic; antiinflammatory; attiasthmatic; immunosuppressive; dermatological; antirheumatic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 118; DB 4; Length 352; 100.0%; Pred. No. 2.9e-11; ive 0; Mismatches 0; Indels 0
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Example 40; Page 504-505; 518pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 APYNIVLLINTFQEFFGLNNCS 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 22, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-626256/72.
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This invention describes a novel diagnostic agent (A) comprising at least two different ligands (I) for receptors (II) that are implicated in disease. (A) are used for the diagnosis of tumors (especially colorectal or prostatio), organ rejection, inflammation and autoimmune diseases. Also inhibitors of (I) are used therapeutically against tumors (and their metastases), inflammation (particularly bronchial asthmat or chronic bowel inflammation), or autoimmune diseases (rheumatoid arthritis or lupus), where the (cardio) vaccular, lymphatic, respiratory, nervous, diseative, endocrine, motor or urogenital systems or skin are affected, and bone marrow diseases. The products of the invention are chemokine derivatives immunosuppressive, dermatological, antirheumatic, antiarthritic. Chemokines act on specific tumor and inflammatory cells through a constellation of chemokine cand inflammatory cells through a proliferation of these cells. Adagnots-AAG80128 represent human chemokine fragments used to illustrate the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; transformed mammalian cell; CD4; reporter gene; translocation; human immuno deficiancy virus; HIV; long terminal repeat; LTR; therapy; chemokine receptor; CKR; cellular dysfunction; HIV infection; cofactor; CC-CKR-5; envelope glycoprotein; anti-HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transformed mammalian cell (I) that contains a CD4 gene, reporter gene and HIV LTR for identification of drugs and antibodies for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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(UYNY ) UNIV NEW YORK STATE.
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96US-0020043P.
97US-00858660.
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Best Local Similarity 100.
Matches 22, Conservative
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contains a gene encoding CD4, a construct encoding a reporter gene under the regulation of an human immuno deficiency virus (HIV) long terminal repeat (LTR) and that has been transduced with a vector encoding a human chemokine receptor (CTR) where the CD4 and the CMR are present on the cell surface of transformed mammalian cell. The invention is useful for identifying drugs or antibodies that interfere with the translocation of HIV into transformed mammalian cell or for identifying a human chemokine receptor that facilitates the infection of a particular HIV strain into the transformed mammalian cell. Compounds identified can be used to treat sequence is a human chemokine receptor (CTR), CC-CTR-5 related protein. CC-CTR-5 is the principal coffector for entry mediated by the envelope glycoproteins of primary macrophage-tropic strains of HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV; human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; cytostetic; immunosuppressive; nocropic; neuroprotective; gene therapy; neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cardiovascular disorder; myocardial ischaemia.
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17. .58
1. Tabel= Transmembrane_domain
/note= "Segment 1"
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| label = Transmembrane_domain
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/label= Extracellular_loop_2
196. .223
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/label= Extracellular_domain
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label= Transmembrane_domain
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|abel= Intracellular_loop_1
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/label= Tr
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The present sequence is human G-protein chemokine receptor (CCR5) HDGDRIO protein. CCR5 HDGDRIO cDNA is included in ATCC Deposit No: 97183. CCR5 HDGNRIO antibodies are useful for treating, preventing or ameliorating a disease or disorder associated with inflammation, defective or aberrant chemotaxis of immune cells. HIV infection (such as Pneumocystis carini presenting cell interaction. HIV infection (such as Pneumocystis carini presenting cell interaction. A presenting cell interaction. The disease or disorder may also be an infection, a cytomegalovirus infection or a poxvirus infection, an infection, or a poxvirus infection, an infection, a cytomegalovirus infection, or a poxvirus infection, or a poxvirus infection, or a poxvirus or a neurodegenerative contoinmune disease (e.g. rheumatoid arthritis) or a neurodegenerative contoinmune disorder may be associated with aberrant CCR5 disorder. The disease or disorder may be associated with aberrant CCR5 captression, lack of CCR5 function. Aberrant CCR5 ligand expression, or a packed with aberrant CR5 contoin additive or preservative to increase or decrease storage capabilities. CCR5 HDGNRIO DNA are useful for chromosome identification and in gene conterned to overy adrenal gland, bone, bone marrow, gastrointestinal tract, care also useful in the disapnesis, treatment and prevention of cancer contemmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, colitis), cardiovascular disorders (myocardial ischaemias) and wound colitis), cardiovascular disorders (myocardial ischaemias) and wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated nucleic acid encoding a human G-protein chemokine receptor (CCRS) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
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                                                                                                                         7.05 1. .274
/label= Extracellular_loop_3
287. .305
/label= Transmembrane_domain
/note= "Segment 7"
306. .355
'label= Transmembrane_domain
                                                                   236. 260
/label= Transmembrane_domain
/note= "Segment 6"
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                                                   Intracellular_loop_3
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               /note= "Segment 5
224. .235
/label= Intracell
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09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
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                                                                                                                                                                                                                                                                                                                                                         09-FEB-2001; 2001WO-US004152
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N-PSDB; AAD13181.
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249 APYNIVLLINTFOEFFGLANCS 270

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The Sep 25 LD:49:5/ 2004

UB-TO-084-8T2-T4.F3d

Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation, HIV; human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; vyrostatic; immunosuppressive; noctropic; neuroprotective; gene therapy; neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative collitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia. Isolated nucleic acid encoding a human G-protein chemokine receptor (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders. Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2. Example 40; Page 486-487; 495pp; English. Li Y, Ruben SM; AAE07039 standard; protein; 352 AA 09-FEB-2000; 2000US-0181258P. 09-MAR-2000; 2000US-0187999P. 22-SEP-2000; 2000US-0234336P. 09-FEB-2001; 2001WO-US004152. (HUMA-) HUMAN GENOME SCI INC 16-OCT-2001 (first entry) Roschke V, WPI; 2001-488965/53. N-PSDB; AAD13198. WO200158915-A2. Homo sapiens. 16-AUG-2001. Rosen CA, AAE07039; RESULT 18
AABO7039
IXX
AABO7039
IXX
AABO7039
DT 16-OC
DX 16-OC
DX Human
XW Human
XW Human
XW Human
XW Gastr
XW Gastr
XW Gastr
XX Homo
CCC Gameli
CCC Gamel

The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10 protein. CCR5 HDGNR10 antibodies are useful for treating, preventing or ameliorating a disease or disorder associated with inflammation, ameliorating a disease or disorder associated with inflammation. CCC defective or aberrant chemotaxis of immune cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen presenting cell interaction. The disease or disorder may also be an infectious disease (e.g. a viral infection such as an early stage HIV infection, a cytomegalovirus infection, or a poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The disease or disorder may be associated with aberrant CCRS expression, lack of CCRS function, aberrant CCRS is an early of cression, and of CCRS ligand function. CCRS HDGNR10 protein is used as a food additive or preservative to increase or decrease storage capabilities. CCRS HDGNR10 DNA are useful for chromosome storage capabilities and antagonists are also useful in the diagnosis, treatment and prevention of cancer (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract, liver, lung, urogenital); immune disorders (Addison's disease, allergies, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple selerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular cultisorders (myocardial ischaemias) and wound healing

Sequence 352 AA;

Query Match

100.0%; Score 118; DB 4; Length 352;

Gaps ö Indels Pred. No. 2.9e-11; Mismatches 0; Local Similarity 100.0%; P. les 22; Conservative 0; Best Loc Matches

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AAB46858 standard; protein; 352

AAB46858;

16-AUG-2001 (revised) 02-AUG-2001 (revised) 04-MAY-2001 (first entry)

Human HDGNR10 protein.

HDGNR10; human; G-protein chemokine receptor; antiinflammatory; imticoagulant; antialregid; immunosuppressive; cytostatic; antiparasitic; antiparasitic; antiparasitic; antiparasitic; antiparasitic; antiparasitic; antiparatic; force theremay; infection; leukemia; growth factor activity; T-cell mediated autoimmune disease; pooriasis; allergy; atherogenesis; anaphylaxis; malignancy; inflammation, histamine; IgE; silicosis; shock; immunoglobulin E-mediated allergic reaction; rheumatoid arthitis; prostaglandin-independent fever; bone marrow failure; sarcoidosis; hyper-eosinophilic syndrome; vulnerary.

Homo sapiens.

US2001000241-A1.

12-APR-2001

29-NOV-2000; 2000US-00725285.

95US-00466343. 98US-00195662. 99US-00339912. 06-JUN-1995; 18-NOV-1998; 25-JUN-1999;

(LIYY/) LI Y. (RUBE/) RUBEN S M.

Li Y, Ruben SM;

WPI; 2001-226317/23. N-PSDB; AAF26390 New human G-protein chemokine receptor polypeptides and polynucleotides, useful for identifying (ant)agonists to the G-protein chemokine receptor

Claim la; Page 15; 22pp; English.

This invention describes a novel receptor polypeptide (I) selected from (I) a fully defined 329 amino acid sequence (II) fully disclosed in the specification; and (II) a polypeptide encoded by the cDNA contained in a plasmid, and fragments, analogs and derivatives of the polypeptide. The products of the invention have antiinflammatory, immunomodulatory, anticoagulant, antiallergic, immunosuppressive, vulnerary, cytostatic, antiparasitic, antiparatic, antianting cape therapy. The G-products of hemokine activate or inhibit activation of (I). The products of the invention can also be used for stimulating hematopoiesis, wound healing, coagulation, angiogenesis, treating solid tumours, chronic infections, psoriasis, and stimulating growth factor activity. HDGNRIO is useful for treating solute inflammation, histamine and immunoglobulin E (IgB) mediated allergic reactions, prostaglandin-independent fever, bone marrow failure,

Matches

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RESULT 20

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This sequence represents the human CCR5 protein sequence. The invention relates to a method for determining whether an agent is capable of modulating the interaction of chemotractic chemokine receptor 5 (CCR5) with gpl20, comprising incubating the agent with CCR5 and gpl20 and determining whether the agent modulates the interaction, where gpl20 is associated with CDR, and where the interaction is a low affilmity binding. The method is used to identify an agent capable of modulating the interaction of CCR5 with gpl20. An agent identified by the method is used to prepare a pharmaceutical composition for the treatment of a disease or condition associated with CCR5 and gpl20 interaction, to treat a subject with a disease or condition associated with CCR5 and gpl20 interaction, to treat a subject with a disease or condition associated with CCR5 and gpl20 interaction, and for preparing a pharmaceutical for treating human immunodeficiancy virus (HIV). It can also be treat anti-inflammatory diseases. The method is commercially useful, amenable to high throughput screening, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Determining if an agent can modulate CCRS-gp120 interaction, comprises incubating the agent with CCR5 and gp120 and determining if the agent
                                                                                                                                                        Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5; human immunodeficiency virus; anti-inflammatory disease; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 118; DB 4;
100.0%; Pred. No. 2.9e-11;
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standard; protein; 352 AA.
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12-JAN-2000; 2000GB-0000661.
12-JAN-2000; 2000GB-0000663.
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                                                                                                                      Human CCR5 protein sequence
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modulates the interaction.
                                                                               09-OCT-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dobbs S, Perros M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-477088/52.
N-PSDB; AAF87099.
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Matches 22; Conserv
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                                                                                                                                                                                                                                                                 EP1118858-A2
                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                        25-JUL-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying agonists of G protein-coupled receptors (GPCRs) for use in disease treatment, comprises contacting candidate compounds with versions of GPCRs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to G protein-coupled receptors (GPCRs) for which the endogenous ligand has been identified. Non-endogenous constitutively activated versions of known GPCRs are used in the invention for the direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists. Such agonists are useful as therapeutic agents for diseases or disorders associated with GPCRs. The present sequence is a non-endogenous version of a known human GPCR
                                                                                                                                                                 Gaps
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silicosis, sarcoidosis, rheumatoid arthritis, shock and hypereosinophilic syndrome. (N.B. This record was resubmitted to correct errors in the keyword formatting)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, G protein-coupled receptor; GPCR; non-endogenous; mutant; constitutively activated GPCR; agonist; disease.
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                                                                                                                      Length 352;
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                                                                                                                   y Match 100.0%; Score 118; DB 4; Local Similarity 100.0%; Pred. No. 2.9e-11; nes 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Non-endogenous human GPCR protein, SEQ ID NO: 477
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                                                                                                                                                                                                                             249 APYNIVLLINTFQEFFGLNNCS 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-648759/74.
N-PSDB; ABI97978.
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es 22; Conserv
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                                                                                                                          Query Match
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Gaps

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Human HIV-1 co-receptor CCR5

Best Loc Matches

RESULT 21 AAB83354

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Length 352; Indels

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THE DED TO TO: 43.07 7004
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us-10-084-813-14.rag

Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; fimmune cell chemotaxis; autoimmune disease; rheumatoid arthritis; neurodegemeration; viral infection; Kaposi sarcoma; cancer; hyperproliferative disease; neurological disease; receptor.

Homo sapiens

The present sequence is that of human HIV-1 co-receptor CCR5. Amino acids caste that determines the specificity of the interaction between CCR5 and HIV-1 gpl20. Post-translational sulfation of the tyrosine residues in the CCR5 N-terminus is required for gpl20 binding and may critically modulate the susceptibility of target cells to HIV-1 infection in vivo. The invention provides claimed sulfated peptides (see AAB82947) that are based on the CCR5 N-terminal region and which are effective for inhibiting HIV-1 binding to CCR5. These peptides are used in claimed methods of inhibiting HIV infection of CO4+ cells, of preventing CD4+ cells from becoming infected with HIV, of treating a subject whose CD4+ cells are infected with HIV, and of identifying an agent which inhibits binding of a CCR5 ispecially a human, infected (therapeutic method), not infected with HIV (prophylactic method), not in a subject who is not infected with, but has been exposed to, HIV CCR5; chemokine; co-receptor; human immunodeficiency virus type 1; HIV-1; infection; therapy; vaccine; anti-HIV-1. Novel compounds comprising specific amino acids within CCR5 (HIV 1 crreceptor) amino terminal domain including negatively charged and two sulfated tyrosine residues is useful for treating HIV infection in Gaps ö Length 352; Indels Human G-protein chemokine receptor (CCR5) HDGNR10 #1. Query Match
100.0%; Score 118; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 22; Conservative 0; Mismatches 0; Location/Qualifiers 2. .18 /note= "binds to HIV-1 gp120" (PROG-) PROGENICS PHARM INC. (AARO-) AARON DIAMOND AIDS RES CENT. 249 APYNIVLLINTFQEFFGLNNCS 270 Ş 1 APYNIVLLINIFQEFFGLNNCS 22 Claim 1; Page 30; 163pp; English. AAU97150 standard; protein; 352 29-FEB-2000; 2000US-0185667P. 19-MAY-2000; 2000US-0205839P. 07-FEB-2001; 2001US-0267231P. 28-FEB-2001; 2001WO-US006699. (first entry) Dragic T, Olson WC; WPI; 2001-611273/70. N-PSDB; AAH26903. Sequence 352 AA; WO200164710-A2 Key Binding-sitė Homo sapiens 13-AUG-2002 07-SEP-2001 AAU97150, humans. à g

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The present invention relates to the isolation of a novel human G-protein chemokine receptor (CCR5) designated HPGNR10, and polymucleotide sequences encoding it. The invention also describes antibodies that bind human G-protein chemokine receptor (CCR5) HPGNR10 and polymucleotide.

Chuman G-protein chemokine receptor (CCR5) HPGNR10 and polymucleotide.

Sequences encoding the antibodies. The antibodies are useful for treating or preventing inflammation, defective or aberrant chemotaxis of immune cells and T-cell/antigen-presenting cell interactions, infections and autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral infections (sepecially early stage human immune deficiency virus (HIV), cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions associated with aberrant or deficient expression of the CCR5 receptor or its ligands. The antibodies are also useful to determine CCR5 expression, e.g. for diagnosis, prognosis and monitoring of cancer and other hyperpoliferative diseases. The polymucleotide sequences encoding human combinant receptor, and in the treatment of a wide range of diseases such as infectious diseases (e.g. influenza), neurological diseases (e.g. HDGNR10 #H).

Parkinson's disease, and hyperproliferative disorders (e.g. cancer). The HDGNR10 #H]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding an antibody specific for the G-protein chemokine receptor CCRS, useful for treatment and diagnosis of e.g. inflammation.
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100.0%; Pred. No. 2.9e-11;
ive 0; Mismatches 0;
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09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
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Best Local Similarity 100.
Matches 22, Conservative
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(ROSC/) ROSCHKE V.
(LIYY/) LI Y.
(RUBE/) RUBEN S M.
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                                                                                                                                                 25-APR-2002.
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13-AUG-2002 (first entry)

/note= "Glu replaces wild-type Leu; encoded by

Location/Qualifiers 55

/note= "Encoded by AGC"

22-FEB-2002

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Human G-protein chemokine receptor (CCR5) HDGNR10 #2.
                                                                                                                                                                               Query Match
Best Local Similarity
      Human; G-protein
immune cell chemo
                                                                                                                                                                          Sequence 352 AA;
                           US2002048786-A1
                     Homo sapiens
                                 25-APR-2002
                                                                                                                                                                   HDGNR10 #2
                                                               (LIYY/)
(RUBE/)
                                                         ROSE/)
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human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome; drug screening; identification; variant.
                                                                                CC chemokine receptor 5; human; HIV infection;
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21-MAR-2000; 2000US-0190996P.
21-MAR-2000; 2000US-0191299P.
20-MAR-2001; 2001US-00813481.
20-MAR-2001; 2001US-00813651.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONS-) CONSENSUS PHARM INC.
                                         Human CCR5 Gln 55 variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nestor JJ, Wilson CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-010610/01.
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Misc-difference
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                                                                                                                                                                                                                                                                                                                                              WO200171346-A2
                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                     27-SEP-2001
The present invention relates to the isolation of a novel human G-protein chemokine receptor (CCR5) designated HDGNR10, and polymucleotide sequences encoding it. The invention also describes antibodies that bind human G-protein chemokine receptor (CCR5) HDGNR10 and polymucleotide sequences encoding the antibodies. The antibodies are useful for treating or preventing inflammation, defective or aberrant chemotaxis of immune cells and T-cell/antigen-presenting cell interactions, infections and autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral infections (especially early-stage human immune deficiency virus (HIV), cytomegalovius or pox virus infections, Kapoesi sarcoma, or conditions associated with aberrant or deficient expression of the CCR5 receptor or its ligands. The antibodies are also useful to determine CCR5 expression, e.g. for diagnosis, prognosis, and monitoring of cancer and other hyperproliferative diseases. The polymucleotide sequences encoding human d-protein chemokine receptor (CCR5) HDGNR10 can be used to produce the recombinant receptor, and in the treatment of a wide range of diseases councing a infectious diseases (e.g. influenza), neurological diseases (e.g. cancer). The present sequence represents human G-protein chemokine receptor (CCR5) protein chemokine receptor (CCR5) present sequence represents human G-protein chemokine receptor (CCR5) present sequence represents human G-protein chemokine receptor (CCR5) presents and pyperpocial diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding an antibody specific for the G-protein chemokine receptor CCR5, useful for treatment and diagnosis of e.g. inflammation.
                                                           immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;
neurodegeneration; viral infection; Kaposi sarcoma; cancer;
hyperproliferative disease; neurological disease; receptor.
                                           receptor; CCR5; HDGNR10; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 165-166; 180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruben SM;
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09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
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N-PSDB; ABK51870.
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Tan Hehir CA;

See RH,

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The invention relates to a method for identifying a binding compound for chemokine receptor 5 (CCR5). The method involves screening a library of test molecules (particularly peptides) with immobilised CCR5, and then dentifying those molecules which bind. The invention also relates to cdentifying chose molecules which bind. The invention also relates to crR5-binding molecules identified using the method of the invention, methods for identifying consensus motifs for CCR5-binding peptides, a cransfer vector encoding tagged CCR5, a computer-aided methods for determining the relative binding assay that utilises the three-dimensional computer aided drug screening assay that utilises the three-dimensional etricules of CCR5. Compounds identified using the methods of the invention are useful for treating or preventing HTW (human consense) in a patient. The methods of the invention may also be used to syndrome) in a patient. The methods of the invention may also be used to identify agonists or antagonists of the interaction of CCR5 with its natural ligand, and to determine a binding motif for CCR5. The present sequence represents a naturally occurring variant of human cCR5 in which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
Identifying CC chemokine receptor 5 binding compound for treating AIDS, comprises binding a molecule from library to a molecule having binding property corresponding to CCR5 and identifying bound molecule.
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                                                                                                                                                                               Example 3; Fig 4B; 50pp; English.
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Best Local Similarity 100.0
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Gaps

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100.0%; Score 118; DB 5; Length 352; 100.0%; Pred. No. 2.9e-11; ive 0; Mismatches 0; Indels (

APYNIVLLLNTFQEFFGLNNCS 270

249

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RESULT 25 AAM52829

1 APYNIVLLINTFOEFFGLNNCS 22

22; Conservative

Matches

AAM52829 standard; protein; 352 AA.

AAM52829;

RESULT 26 AAM52828

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us-10-084-813-14.rag
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Human; G-protein chemokine receptor; HDGNR10; CCRS receptor; hadman; G-protein chemokine receptor; HDGNR10; anglogenesis; solid tumour; chronic infection; leukaemia; T-cell mediated autoimmune disease; parasitic infection; psoriasis; growth factor activity; allergy; atherogenesis; anaphylaxis; mallignancy; inflammation; histamine; immunoglobulin B; IQB-mediated allergic reaction; sarcoidosis; prostaglandin-independent fever; bone marrow failure; shock; rheumatoid arthritis; hyper-eosinophilic syndrome; cytostatic; antiparasitic; antiparasitic; antiparasitic; antiparasitic; antiparasitic; antiparasitic; antiparatic; antiarthritic;

antipyretic; receptor

US2002099176-A1.

Homo sapiens.

Human G-protein chemokine receptor, HDGNR10.

(first entry)

03-DEC-2002

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The invention relates to a method for identifying a binding compound for CC chemokine receptor 5 (CCR5). The method involves screening a library of test molecules (particularly peptides) with immobilised CCR5, and then identifying those molecules which bind. The invention also relates to cCR5-binding molecules identified using the method of the invention, methods for identifying consensus motifs for CCR5-binding peptides, a transfer vector encoding tagged CCR5, a computer-aided methods for determining the relative binding assay that utilises the three-dimensional computer aided drug screening assay that utilises the three-dimensional computer aided drug screening assay that utilises the three-dimensional structure of CCR5. Compounds identified using the methods of the invention are useful for treating or preventing HIV (human immunodeficiency virus) infection or AIDS (acquired immunodeficiency syndrome) in a patient. The methods of the invention may also be used to identify agonists or antagonists of the interaction of CCR5. The present sequence represents human CCR5.
                                                                                                                                           CCR5; CC chemokine receptor 5; human; HIV infection; human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome; drug screening; identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying CC chemokine receptor 5 binding compound for treating AIDS, comprises binding a molecule from library to a molecule having binding property corresponding to CCR5 and identifying bound molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tan Hehir CA;
                                                                                                          Human CC chemokine receptor 5 (CCR5)
AAM52828 standard; protein; 352 AA.
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                                                                                                                                                                                                                                                                                                                                                                                      21 MAR-2000; 2000US-0190996F.
22-MAR-2000; 2000US-0191299P.
20-MAR-2001; 2001US-00813448.
20-MAR-2001; 2001US-00813651.
20-MAR-2001; 2001US-00813653.
                                                                                                                                                                                                                                                                                                                                  21-MAR-2001; 2001WO-US009155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CONS-) CONSENSUS PHARM INC.
                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nestor JJ, Wilson CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-010610/01.
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                                                                                                                                                                                                                          Homo sapiens
                                                                        22-FEB-2002
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Best Local S:
Matches 22
                                   AAM52828
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Novel human G-protein chemokine receptor polypeptide useful for identifying modulators for stimulating hematopoiesis, wound healing, leukemia, for treating allergy, rheumatoid arthritis, shock and as

WPI; 2002-690494/74. N-PSDB; ABS54272.

Novel

95US-00466343.

25-JUN-1999; 36-JUN-1995;

25-JUL-2002

(LIYY/) LI Y. (RUBE/) RUBEN S M.

Li Y, Ruben SM;

Claim 7; Fig 1; 22pp; English.

research agents.

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The present invention relates to the isolation of human G-protein chemokine receptor, HDGNR10 (CCR5 receptor), and the polymucleotide sequences are conding it. HDGNR10 polymeptide and polymucleotide sequences are or useful for diagnosing a disease or a susceptibility to a disease related to underexpression of HDGNR10. They are useful for identifying modulators for stimulating haematopoiesis, wound healing, coaquilation, angiogenesis, to treat solid tumours, chronic infections, psoriasis, or for stimulating growth factor activity. The sequences are also useful for preventing and/or treating allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation, histamine and immunoglobulin E (IgE)-mediated allergic reactions, prostaglandin-independent fever, bone marrow failure, sarcoidosis, rheumatoid arthitis, shock and hyperbone marrow failure, sarcoidosis, rheumatoid arthitis, shock and hypercessinophilic syndrome. Polymucleotide sequences encoding HDGNR10 can be used in gene therapy to treat conditions related to underexpression of HDGNR10. The present sequence represents human G-protein chemokine
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Best Local Similarity 100.0
Matches 22, Conservative
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Gaps

RESULT 28 ABG92883

249 APYNIVLLINTFQEFFGLNNCS 270

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ABG70597 standard; protein; 352 AA

RESULT 27
ABG70597
ID ABG70
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AC ABG70

ABG70597

1 APYNIVLLLNTFQEFFGLNNCS 22

Tue Sep 28 15:49:57 2004

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(HUMA-) HUMAN GENOME SCI INC.
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ABG92880;
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                                                                                                                                                                                                                                                             Human immunoglobulin variable heavy domain #1.
ABG92883 standard; protein; 352 AA
                                                                                                                                                                     (first entry)
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08-FEB-2002; 2002WO-US003634
                                                                                                            2001US-00779880
                           WO200264612-A2.
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Homo sapiens
                                                                                                             09-FEB-2001;
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                                                      22-AUG-2002
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; 2001WO-US004153. ; 2001US-0297257P. ; 2001US-0310458P. ; 2001US-0328447P. 2001US-0341725P 21-DEC-2001;

Ruben SM; Rosen CA, Roschke V,

WPI; 2002-643455/69. N-PSDB; ABS68606.

New human G-protein Chemokine Receptor gene (HDGNR10) useful for treating, preventing, ameliorating or monitoring diseases or disorders associated with aberrant expression of HDGNR10 e.g. cancer.

Example 55; Fig 4; 562pp; English

The invention describes an isolated polynucleotide encoding a first antibody at least 95-100% identical to a second antibody consisting of antibody at least 95-100% identical to a second antibody consisting of a variable heavy (VH) or variable light (VL) domain of the antibody consisting of a variable heavy (VH) or variable light (VL) domain of the antibody consisting of xF3.6A2, XF3.1089, XF22.3C9.6, XF22.9E6, XF27/28.18E5, XF27/28

Sequence 352 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d-protein chemokine receptor; CCR5, HDGNRI0; cancer; inflammation; d-protein chemokine receptor; CCR5, HDGNRI0; cancer; inflammation; immunologic deficiency syndrome; blood protein disorder; nephritis; nataxia telangiectasia; endotoxin lethality; inflammatory bowel disease; histiocytosis; chemotaxis; infectious disease; autoimmune disease; Addison's disease; dermatitis; rheumatoid arthritis; allergy; neurodegenerative disorder; viral infection; poxvirus infection; HIV; human immunodeficiency virus; cyromegalovirus; Kaposi's sarcoma; pneumocystis carnii infection; cardiovascular disorder; atherosclerosis;
                                                           Gaps
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                                                        0; Indels
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Score 118; DB 5;
Pred. No. 2.9e-11;
                                                           Mismatches
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   100.08;
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                                                           22; Conservative
                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunoglobulin;
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   Query Match
Best Local S
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2001WO-US004153. 2001US-0297257P. 2001US-0310458P. 08-FEB-2002; 2002WO-US003634 2001US-00779880 21-DEC-2001; 2001US-0341725P 2001US-0328447P 08-AUG-2001; 09-FEB-2001; 12-JUN-2001; 22-AUG-2002 

WO200264612-A2. Homo sapiens

(HUMA-) HUMAN GENOME SCI INC.

Ruben SM Rosen CA, Roschke V,

WPI; 2002-643455/69. N-PSDB; ABS68553.

New human G-protein Chemokine Receptor gene (HDGNR10) useful for treating, preventing, ameliorating or monitoring diseases or disorders associated with aberrant expression of HDGNR10 e.g. cancer.

Disclosure; Fig 1A-B; 562pp; English.

The invention describes an isolated polymucleotide encoding a first antibody at least 95-100% identical to a second antibody consisting of an antibody at least 95-100% identical to a second antibody consisting of an amino acid sequence comprising at least one, two or three CDR regions of a variable heavy (VH) or variable light (VL) domain of the antibody expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8, XF27/28.18B5, XF27/28.25G10, XF27/28.18B5, XF27/28.18

us-10-084-813-14.rag

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Gaps

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Indels

ch 100.0%; Score 118; DB 5; 1 Similarity 100.0%; Pred. No. 2.9e-11; 22; Conservative 0; Mismatches 0;

Local

249 APYNIVLLINTFQEFFGLNNCS 270

1 APYNIVLLINTFQEFFGLNNCS 22

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AAE25811 standard; protein; 352

DNA

chemokine receptor (CCR5), HDGNR10

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Sequence 352

Length 352;

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Best Loc
Matches
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dermatitis and rheumatoid arthritis, allergies, a neurodegenerative disorder, a viral infection e.g. HIV infection, cytomegalovins or poxvirus infection, a Pneumocystis carnii infection, Kaposi's sarcoma, cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a disease or disorder associated with aberrant expression of novel human Gprotein chemokine receptor (CCRS) HDGNR10. This is an amino acid sequence of Human G-protein chemokine receptor (CCRS) HDGNR10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding antibodies to the human CCRS receptor HDGNR10, useful for treatment, prevention and diagnosis of e.g. cancer, also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, G-protein chemokine receptor; CCRS; HDGNR10 protein; cancer; inflammation; viral infection; autoimmune disease; neurodegeneration; rheumatoid archirits; Pneumocystis carinii infection; Kaposi's sarcoma; hyperproliferative disease; receptor.
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                                                                                                                                                                             Length 352;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human G-protein chemokine receptor (CCR5), HDGNR10 #1
                                                                                                                                                                               100.0%; Score 118; DB 5; 100.0%; Pred. No. 2.9e-11;
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                                                                                                                                                                                                                                                                            APYNIVLLLNTFQEFFGLNNCS 270
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                                                                                                                                                                                                                                                                                                                                                                              AAE25808 standard; protein; 352 AA.
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09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
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                                                                                                                                                            Query Match
Best Local Similarity 100..

Servative 22; Conservative
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(ROSC/) ROSCHKE V.
(LIYY/) LI Y.
(RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-499674/53
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                                                                                                                                             Sequence 352 AA;
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The invention relates to human G-protein chemokine receptor (CCR5), antibodies are used for the treatment or prevention of inflammation, defective or aberrant chemotaxis of immune cells or T cell antigenpresenting cell interaction, viral infections (specifically human immune deficiency (including its early stages), cytomegalo or pox viruses), autoimmune deficiency Kaposi's sarcoma or any condition associated with aberrant expression of CCR5 or their ligands. They are also used for the detection, diagnosis, prognosis and monitoring of cancers or other hyperproliferative diseases. The present sequence is human G-protein chemokine receptor (CCR5), HDGNR10 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding antibodies to the human CCR5 receptor HDGNR10, useful for treatment, prevention and diagnosis of e.g. cancer, also related antibodies.
                                                                                                                                                Human, G-protein chemokine receptor; CCR5, HDGNR10 protein; cancer;
inflammation; viral infection; autoimmune disease; neurodegeneration;
rheumatoid arbhritis; Pneumocystis carinii infection; Kaposi's sarcoma;
hyperproliferative disease; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 118; DB 5; Length 352;
Pred. No. 2.9e-11;
                                                                                                                      Human G-protein chemokine receptor (CCR5), HDGNR10 #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 170; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
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09-MAR-2000; 2000US-0167999P.
22-SEP-2000; 2000US-0234336P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Li Y,
                                                                                                                                                                                                                                                                                                                       09-FEB-2001; 2001US-00779880.
                                                                                         (first entry)
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N-PSDB; AAD42426.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                         24-FEB-2003
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                                                           AAE25811;
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Matches

8

RESULT 32

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The present sequence is that of a polypeptide encoded by the human chemokine (C-C motif) receptor 5 (CCR5) gene of the invention (See ABA97319). The specification describes haplotyping the CCR5 gene of an individual by determining if the individual has one of the CCR5 specification also describes an isolated polymothetoride comprising a nucleotide sequence which is a polymorphic variant of the reference CCR5 gene sequence which is a nisogene defined by a haplotype described nucleotide sequence and comprises an isogene defined by a haplotype described in the specification and its encoded polypeptide. The methods of the invention are useful to diagnose and develop treatment for diseases a ssociated with abnormal expression or function of the gene. The CCR5 isogenes and the screened compounds are useful for treating human communodeficiency virus (HIV)-1 infection and the progression to acquired immunodeficiency virus (HIV)-1 infection and the progression to acquired immunodeficiency syndrome (AIDS). The invention has antiviral complications are specification describes genotyping the CCR5 gene of an individual; predicting a haplotype pair for the CCR5 gene of an individual; predicting a passociation between a trait and a haplotype or haplotype pair for the CCR5 gene. The specification describes a composition comprising a genotyping oligonucleotide for detecting a CCR5 polymorphism; a recombinant non-human organism transformed with CCR5 polymorphism; a recombinant non-human organism transformed with expressing an isolated antibody specific for the CCR5 polypeptide and a method for screening drugs targeting the CCR5 polypeptide.
                                                                                                  Human chemokine C-C motif receptor 5; CCR5; haplotype pair; isogene; single nucleotide polymorphism; SNP; human immunodeficiency virus 1; HIV-1 infection; acquired immunodeficiency syndrome; AIDS; antiviral; genotype; polymorphic variant; transgenic; drug screening; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New haplotypes of the human chemokine (C-C motif) receptor 5 gene, to diagnose and treat diseases associated with its abnormal express function, including human immunodeficiency virus-1 infection.
                                                              Human chemokine (C-C motif) receptor 5 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 118; DB 5;
100.0%; Pred. No. 2.9e-11;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                             Location/Qualifiers
55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 29; Fig 3; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENA-) GENAISSANCE PHARM INC.
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Conservative C
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N-PSDB; ABA97318, ABA97319.
                     18-JUN-2002 (first entry)
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Best Local Similarity
Matches 22; Conserv
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                                                                                                                                                                                                                                                                                                                 Misc-difference
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                                                                                                                                                                                                     chromosome 3p21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              which has been identified as a G-protein chemokine receptor. The GPCR HDGNR10 polypeptide can be expressed by standard recombinant methodology. Compounds that activate or inhibit the receptor polypeptide, optionally expressed from DNA in gene therapy vectors; are used to treat diseases that require: (a) activation of the receptor (e.g. stimulation of haematopoiesis, treatment of solid tumours, T-cell mediated autoimmune diseases, parasitic infections, psoriasis etc.); or (b) inhibition of the receptor (e.g. allergy, inflammation, rheumatoid arthritis, silicosis etc.). The present sequence represents the human HDGNR10 receptor
                                                                                                                                                                                                                                                                                                                                                                                  7-transmembrane receptor; G-protein coupled receptor; GPCR; HDGNR10; G-protein chemokine receptor; haemacopoleric; immunosuppressant; antiparasitic; antiparasitic; antiparasitic; antiballergic; antiballergic; antiballergic; antiballergic; antiballergic; antiballergic; antiballergic; antiballergic; antiballergic; antiparthritic; gene therapy; human; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polynucleotide encoding a human G protein chemokine receptor HDGNR10,
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Gaps
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100.0%; Pred. No. 2.9e-11;
tive 0; Mismatches 0;
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Mismatches
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                                             1 APYNIVLLINTFOEFFGLNNCS
                                                                        249 APYNIVLLINTFQEFFGLNNCS
                                                                                                                                                                                                       ABB81054 standard; protein; 352
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                                                                                                                                                                                                                                                                                             05-NOV-2002 (first entry)
Conservative
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N-PSDB; ABN86542.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LIYY/) LI Y. (RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ruben SM;
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Local Sim
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Best Local &
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New

ABB1054
ABB1054
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AAC ABB8
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ABB105-1XXX
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ABB105-1XXX
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Gaps

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Length 352; Indels

Matches

RESULT 33

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ABB08343

Gaps

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Indels

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Pred. No. 2.9e-11;

100.0%; Prea. ...

22; Conservative

Matches

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Best Local Similarity

22

1 APYNIVLLINIFOEFFGLNNCS

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The invention discloses a G-protein chemokine receptor (sometimes creferred to as a 7-transmembrane receptor) polypeptide, HDGNR10, and the polymucleotide encoding it. G-protein chemokine receptors are involved in a gignal transduction pathways. The polymucleotide and polypeptide can be used to identify compounds which activate or inhibit activation of the used to identify compounds are useful for treating a patient having need to activate or inhibit a G-protein chemokine receptor. The compound is administered by providing to the patient DNA encoding the agonist. Or antagonist and expressing them in vivo (gene therapy). The polymucleotides and polypeptide are also useful for for diagnosing a disease or susceptibility to a disease related to an under-expression of the protein. For chromosome identification or as immunogens for producing antibodies. Agonists are useful in strimulating haematopoiesis, whond healing, coaqulation, angiogenesis, to treat solid tumours, chronic infections, portains and to stimulate growth factor activity.

Antagonists are useful in the prevention and treatment of allergy, attentogenesis, anaphylaxis, malignancy, chronic and acute inflammation, histermine and igE-mediated allergic reactions, prosteals and to stimulate growth factor activity.

Antagonists are useful in the prevention and reatment of allergy, attentogenesis, anaphylaxis, malignancy, chronic and acute inflammation, shock and hyper-eosinophilic syndrome. The sequence presented is the thurn HDGNR10 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human G-protein chemokine receptor polypeptide useful for diagnostic purposes and for identifying modulators of the polypeptide useful for treating leukemia, autoimmune diseases, psoriasis and allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; receptor; G-protein chemokine receptor; 7-transmembrane receptor; HDGMR10; signal transduction; gene therapy; haematopoiesis; wound healing; coagulation; angiogenesis; tumour; chronic infection; leukaemia; T-cell mediated auto-immune disease; parasitic infection; psoriasis; growth factor; allergy; atherogenesis; anaphylaxis; prostay; inflammation; histamine; Igg-mediated; prostaglandin-independent fever; bone marrow failure; silicosis; paracoidosis; rheumatoid arthritis; shock; hyper-eosinophilic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human G-protein chemokine receptor, HDGNR10, protein.
APYNIVLLINTFQEFFGLNNCS 270
                                                                                                                                                                                                                                           ABG75540 standard; protein; 352 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-208944/20.
N-PSDB; ABX10635.
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                                                                                                                                                                                                                                                                                                                     ABG75540;
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                                                                                                                                                                 RESULT 34
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ABG75540

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ABG75540

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ABG75540

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ABG75540

ABG7540

ABG75540

ABG7554
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Sequence 352 AA;
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6; Length 352;

DB

100.0%; Score 118;

Query Match

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The present invention describes an isolated nucleic acid molecule, which comprises the sequence of any of the genes that are up-regulated or down-cegulated in specific cancers (e.g. about 1031 genes up-regulated in acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer related gene nucleotide sequences which encode the proteins given in ABR585121 to ABR58709. Also described: (1) determining the presence or absence of a pathological cell in a patient; (2) an expression vector comprising a nucleic acid molecule described above; (3) a host cell comprising the vector; (4) an isolated polypeptide, which is encoded by the nucleic acid; (5) an antibody that specifically binds the polypeptide of (4); (6) specifically targeting a compound to a pathological cell in a patient by administering to the patient the antibody above; and (7) a cut greening assay. The nucleic acid is useful for therapeutic targete. In particular, the nucleic acid is useful for diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow, colladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary, abhances, prostate, skin and uterus), wounds, ischemia, heart diseases, ather seconds and endometriosis. The nucleic acid is also useful in a control of any seconds and endometriosis. The nucleic acid is also useful in a control of any seconds and endometriosis. The nucleic acid is also useful in a control of any seconds and endometriosis. The nucleic acid is also useful in a control of any seconds and endometriosis. The nucleic acid is also useful in the control of the patient by administry for identifying agents for treating these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New genes that are up-regulated or down-regulated in cancers, useful a markers for diagnosing e.g. cancer, ischemia or heart diseases, or as therapeutic targets for screening drugs for treating these diseases.
                                                                                                                                                                                                                                                                                            Human, cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
heart disease; atherosclerosis; endometriosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
                                                                                                                                                                                                                                                     Human cancer related protein SEQ ID NO:259.
249 APYNIVLLLNTFQEFFGLNNCS 270
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                                                                                                                        ABR58602 standard; protein; 352 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-NOV-2001; 2001US-035066FP.
08-FEB-2002; 2002US-0355145P.
08-FEB-2002; 2002US-0355257P.
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                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                    ABR58602;
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                                                                                RESULT 35
ABR58602
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us-10-084-813-14.rag

ABU61654 standard; protein; 352 AA.

Human G-protein chemokine receptor (HDGNR10) polypeptide. Human; G-protein chemokine receptor; receptor; HDGNR10; 7-transmembrane receptor.

(first entry)

08-AUG-2003

95US-00466343. 98US-00195662. 99US-00339912.

06-JUN-1995; 18-NOV-1998;

25-JUN-1999;

(HUMA-) HUMAN GENOME SCI INC

WPI; 2003-456307/43. Li Y, Ruben SM;

03-SEP-2002; 2002US-00232686.

US2003023044-A1.

30-JAN-2003

Homo sapiens

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                                                                                                                                                                                                                                                                                                                                              Human; urological disorder; stress urinary incontinence; prostate cancer; beign prostatic hyperplasia; overactive bladder; oversensitive bladder; oversensitive bladder; overselve urinary incontinence; gene therapy; nephrotropic; prostatitis; kidney disorder; C-C chemokine receptor type 5; CCR5; receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying a compound, capable of treating urological disorder e.g., benign prostatic hyperplasia, by assaying the ability of the compound modulate 313, 333, 5464, 188717 or 33524 nucleic acid expression or polypeptide activity.
                                      Gaps
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Length 352;
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                                      0; Indels
                                                                                                                                                                                                                                                                                                             Human C-C chemokine receptor type 5 (333) protein.
100.0%; Score 118; DB 6; ilarity 100.0%; Pred. No. 2.9e-11; Conservative 0; Mismatches 0;
                                                                                            249 APYNIVLLINTFQEFFGLNNCS 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 81; 87pp; English.
                                                                       1 APYNIVLLINTFORFFGLNNCS 22
                                                                                                                                                                                                 AAO29514 standard; protein; 352
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                                                                                                                                                                                                                                                                          (first entry)
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N-PSDB; AAL59912.
                 Best Local Similarity
Matches 22; Conser
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les 22; Conserv
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                                                                                                                                                                                                                                      AA029514;
   Query Match
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Matches
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The invention relates to a method of producing an antibody, involving immunising an animal with a human G-protein chemokine receptor (HDGNR10) polypeptide (also referred to as a human 7-transmembrane receptor) and recovering an antibody which binds the polypeptide. The method is useful for producing an antibody which binds specifically to the human G-protein chemokine receptor polypeptide. This sequence represents the HDGNR10 polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                         Producing an antibody, involves immunizing an animal with a polypeptide or with a polypeptide encoded by the human G-protein chemokine receptor clone in ATCC 97183, and recovering the antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, chemokine receptor, CCR5, viral infection, surface protein, respiratory virus infection, respiratory syncytial virus infection, RSV infection, bronchiolitis, bronchitis, pneumonia, asthma.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 118; DB 6; Length 352; 100.0%; Pred. No. 2.9e-11; cive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of human chemokine receptor CCR5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 APYNIVLLINTFQEFFGLNNCS 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP97728 standard; protein; 352
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 1; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-MAY-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
1es 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ACA61721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003014153-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP97728;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 38
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Gaps

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249 APYNIVLLLNTFQEFFGLNNCS 270

RESULT 37 ABU61654

1 APYNIVLLINTFOEFFGLINGS 22

Conservative

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                                                                                                                                                                                                                                                                                                                                         The present sequence represents human chemokine receptor CCR5. The specification describes a method for modulating viral infection of a cell. the method comprises modulating a binding interaction between a cell chemokine-receptor and a surface protein of the virus. The proviso is that the cell chemokine-receptor is not CX3CR1 and that the proviso is that the method is useful for treating or preventing respiratory virus infection in vertebrates, more particularly respiratory syncytial virus infections, and related diseases, e.g. bronchiolitis, bronchitis, pneumonia or asthma
                                                                                                                                                                                                                      Modulating viral infection of a cell, for treating or preventing respiratory virus infections, bronchitis, pneumonia or asthma, by modulating a binding interaction between a cell chemokine-receptor and surface protein of the virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 118; DB 6; Length 352; 100.0%; Pred. No. 2.9e-11; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human C-C chemokine receptor 5 protein SEQ ID NO:352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                Disclosure; Page 96-98; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 APYNIVLLINTFQEFFGLNNCS 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP81933 standard; protein; 352 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-DEC-2000; 2000US-0257144P.
                                 12-AUG-2002; 2002WO-CA001248
                                                                   10-AUG-2001; 2001US-0311088P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry
                                                                                                   TOPIGEN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22; Conservative
                                                                                                                                       Renzi P, Zemzoumi K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                           WPI; 2003-256541/25.
                                                                                                                                                                                             N-PSDB; ABZ68881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 352 AA;
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                                                                                                     (TOPI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 39
ABP81933
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The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (I) an assay for the detection of a particular Grand to an isolated antibody having high specificity and high affinity or and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for corresponding GPCRs. The antigenic peptides for treating immune-related disease, immunological-related diseases, collicated diseases, immunological-related diseases, collicated diseases, immunological-related cell proliferative diseases or autoimmune diseases, eg. ALDS, Alzheimer's disease, contential, fungal, protozoan or viral infections, altergies, osteoprossis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohm's disease, pain, psoriasis, concer, cardiomyopathy, chronic and acute inflammation, allergies, multiple sclerosis, pain, psoriasis, concer, espilepsy, asthma, tuberroulosis, obesity, nausea, hyperension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABB22523 to ABB42869 encode GPCR proteins given in ABP81675 to ABB42252 to ABB42869 encode cemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor; human; anti-HIV; virucide; HIV; SIV; 88-C; 88-2B; chemokine receptor; envelope protein; atherosclerosis; rheumatoid arthritis; tumour growth suppression; asthma; viral infection; AIDS; inflammatory condition.
                                                                                                                                      " isolated antigenic peptides e.g., for G protein-coupled receptors PCR), useful for diagnosing and designing drugs for treating conditions which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                    Disclosure; Fig 1; 523pp; English
(LIFE-) LIFESPAN BIOSCIENCES INC
                                        Brown JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human chemokine receptor 88-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-2002; 2002US-00106623.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
                                        Burmer GC, Roush CL,
                                                                                                                                                                                                              autoimmune diseases.
                                                                                  2003-046718/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2002150888-A1.
                                                                                  WPI; 2003-046718
N-PSDB; ABZ42781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 352 AA;
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                                                                                                                                               New isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-DEC-2003
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The invention relates to screening for a modulator of human immunodeficiency virus (HIV) or simian immunodeficiency virus (SIV)
infection, comprising contacting a first composition having an human (ADC03341) or macaque (ADC03359) 88C chemokine receptor polypeptide with a second composition having an HIV or SIV envelope protein in the presence or absence or acompound. Also included are screening for a modulator of HIV infection, detecting HIV infection of colls (comprising contacting a cell that has been recombinantly modified to express at least one of human chemokine receptors 88C and 88-28 with HIV, and detecting HIV infection of cells (comprising contacting cells with an antibody to at least one of human chemokine receptors 88C and 88-28 with HIV, and detecting HIV infection of cells (comprising contacting cells with an antibody to at least one of human chemokine receptors 88C and 88-28 with HIV, and detecting HIV infection of the cell after the contacting step). The methods and compositions of the present invention are useful for the diagnosis and crivity of 88C or 88-28 bith HIV, and detecting HIV infection of activity of 88C or 88-28 chemokine receptors, such as atherosolerosis, rheumatoid arthritis, tumour growth suppression, asthma, viral infection, AIDS and other inflammatory conditions. The genes for human 88-C and 88-28 are located on chromosome 3921. The present sequence represents human chemokine receptor 88-C.
                                                                                                                                                                                                                                                                                                                                Screening for a modulator of HIV and SIV infection utilizing polymucleotides that encode the 88C or 88-2B chemokine receptors, useful for diagnosing and treating disorders such as atherosclerosis, arthritis, AIDS and asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 17-18; 29pp; English.
                    95US-00575967.
96US-00661393.
96US-00771276.
                                                                                                                                                                                                                 Gray PW, Schweickart VL,
                                                                                                            (GRAY) GRAY P W.
(SCHW/) SCHWEICKART V L.
(RAPO/) RAPORT C J.
                                                                                                                                                                                                                                                            WPI; 2003-182491/18.
N-PSDB; ADC03340.
                    20-DEC-1995;
07-JUN-1996;
20-DEC-1996;
```

Raport CJ;

0; Gaps Query Match 100.0%; Score 118; DB 7; Length 352; Best Local Similarity 100.0%; Pred. No. 2.9e-11; Matches 22; Conservative 0; Mismatches 0; Indels 0 Sequence 352 AA; ò

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Search completed: September 28, 2004, 09:03:38
Job time : 52.525 secs

Appli

Sequence 2 Sequence 5 Sequence 5 Sequence 5 Sequence 5 Sequence 6 Sequence 7 Sequence 6 Sequence 6 Sequence 7 Sequence 6 Sequence 6

US-08-681-192-2 US-09-087-232A-22 US-08-012-988A-2 US-08-450-393A-5 US-08-446-669-5 US-09-286-3194-14 US-09-866-319A-14 PCT-US95-00476-5 US-08-833-752-9 US-08-833-752-9 US-08-833-752-9 US-08-875-573-6 US-09-232-878-2 US-09-232-878-2 US-09-232-878-2 US-09-534-185-55 US-09-534-185-55 US-09-534-185-55 US-09-534-185-55 US-09-534-185-55 US-09-103-107-12

Sequence

ALIGNMENTS

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Sequence 13, Appl
Sequence 2, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 4, Appl
Sequence 6, Appl
Sequence 51, Appl
Sequence 20, Appl
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                    September 28, 2004, 09:00:23; Search time 19:8 Seconds (without alignments) 57.362 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                           Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-466-343D-2
US-09-087-232A-13
US-08-681-105-114
US-08-675-967A-2
US-09-045-583-52
US-09-514-165-52
US-09-514-165-52
US-09-514-165-52
US-09-514-165-52
US-09-514-165-52
US-09-514-185-52
US-08-724-984A-2
US-08-724-984A-3
US-08-724-984A-3
US-08-724-984A-3
US-08-724-984A-3
US-08-724-33A-4
US-08-456-583-50
US-09-045-583-51
US-09-045-583-51
US-09-045-583-51
US-09-131-827A-2
US-09-131-827A-2
US-09-131-827A-2
US-08-446-669-2
US-08-446-669-2
US-08-446-669-2
                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                         389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                      US-10-084-813-14
118
1 APYNIVLLINTFQEFFGLNNCS 22
                                              - protein search, using sw model
                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
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                                                                                                                                                                      Scoring table:
                                                  OM protein
                                                                                                                                                                                                                                                                                                                                               Database :
                                                                                                                                                 Sequence:
                                                                                                                                                                                                            Searched:
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No.
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SESULT 1

US-06-466-343D-2

Sequence 2, Application US/08466343D

Sequence 2, Application US/08466343D

Sequence 2, Application US/08466343D

Partent No. 6025154

SEQUENCES 111, X1

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN C-PROTEIN

TITLE OF INVENTION: CHEMOKINE RECEPTOR HIGGRID (AS AMENDED)

NUMBER OF SEQUENCES:
APDRESSES:
APDRESSES:
ACREA SEQUENCES:
APDRESSES:
ACREA SEQUENCES:
APPLICATION WASHINGTON

STATE: 1100 NWW YORK AVE., NW, SUITE 600

CONTREY: USA

ZIP: 20005

CORPITATE IN PC COMPATIBLE
CONTREST: Defect In Release #1.0, Version #1.30

CORPITATION SYSTEM: US/08/466,343D

FILING DATE: Patent In Release #1.0, Version #1.30

CORPUTATION NUMBER: US/08/466,343D

FILING DATE: OF COMPATION:
APPLICATION NUMBER: US/08/466,343D

ATTCAREVAGE (ACREA)

ATTCAREVAGE (ACREA)

FILING DATE: OF COMPATION:
APPLICATION NUMBER: 148.1150000/EKS/KIM

FELENOWHOUT ON NORMATION:
TELEBONG: (202) 371-2540

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 Amino acid

TOPOLOGY: linear

TOPOLOGY: linear
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RESULT

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ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6265184and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32918
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-861-105-14
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US-08-575-967A-2
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US-08-861-105-14

// Sequence 14, Application US/08861105
// Sequence 14, Application US/08861105
// DELECT INFORMATION:
// APPLICANT: LITTMAN, DAN R.
// APPLICANT: ELIMBIER, WILPRIED
// APPLICANT: LANDAW, NATHANIEL R.
// APPLICANT: LANDAW, NATHANIEL R.
// APPLICANT: LIU RONG
// TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
// TITLE OF INVENTION: MACROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
// TITLE OF INVENTION: USS THERES:
// OWNERS POWDENCES: 14
// CORRESPONDES: 14
// C
                       Sequence 13, Application US/09087232A

Batent No. 6153431
GENERAL INFORMATION:
APPLICANT: QUILLEN et al.
TITLE OF INVENTION: HUAN INFUNDEFICIENCY VIRUS CO-RECEPTOR
TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
NUMBER OF SEQUENCES:
ADDRESSEB: Baker & Botts, L.L.P. attn. Lisa Kole
STREET: 30 Rockefeller Plaza
CITER: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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100.0%; Score 118; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.1e-12;
Matches 22; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/087,232A
FILING DATE: 28 MAY 1998
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/048,057
APPLICATION NUMBER: 60/048,057
ATTORNEY/AGENT INFORMATION:
NAME: KOJE, LISA B.
FRIGHT NUMBER: 3225
FRIGHT NUMBER: APPLICATION NUMBER: 3225
FRIGHT NUMBER: APPLICATION NUMBE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: (212) 765-2519
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein US-09-087-232A-13
US-09-087-232A-13
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Gaps
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Patent No. 6265184

GENERAL INFORMATION:

APPLICANT: Gray et al.

TITLE OF INVENTION: Chemokine Receptor Materials and Methods

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 S. Wacker Drive

COUNTRY: USA

COUNTRY: USA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,105
FILING DATE:
CLASSIPICATION: 436
PRIOR APPLICATION: 436
PRIOR APPLICATION: 436
FILING DATE: 19-JUN-1996
CLASSIPICATION DATA:
APPLICATION NUMBER: US 08/66,020
FILING DATE: 19-JUN-1996
CLASSIPICATION DATA:
APPLICATION NUMBER: US 08/227,319
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: JGCKSON ENG. DAVIG
REFERENCE/DOCKET NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-004 NI
TELEPRAX: 201-447-5800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TENGTH: 352 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: proposes: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: HOMO Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 22; Conservative
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Query Match
Best Local Similarity 100.v
                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-517-605-5
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US-09-534-185-52
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US-09-045-583-52
Sequence 52, Application US/09045583
Sequence 52, Application US/09045583
Fatent No. 62878105
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
APPLICANT: Graham, Gerard J. et al.
APPLICANT: Graham, Gerard J. et al.
AUMERAL INVENTION: No. 6287805e1 Molecules of the G Protein-Coupled
NUMBER OF INVENTION: No. 6287805e1 Molecules of the G Protein-Coupled
CORRESPONDENCE ADDRESS: 56
CORRESPONDENCE ADDRESS: 1
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 48 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER RELABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ELS Floppy disk
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: CO-MAR-98
CLASSIFICATION DATA:
APPLICATION NUMBER: WS.99
FILING DATE:
APPLICATION NUMBER: ANY E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MI-044
TELEPHONE: (617)227-1400
                                                                                                                                                        ; NAME_KEY: misc_feature
; OTHER INFORMATION: /= "88C amino acid sequence"
US-08-575-967A-2
                                                                                                                                                                                                                                                              100.0%; Score 118; DB 3; 100.0%; Pred. No. 4.1e-12;
                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                 1 APYNIVLLLNTFQEFFGLNNCS 22
  LENGTH: 200-485-1900
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TYPE: Amino acid
TYPE: Alinear
MOLECULE TYPE: protein
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDART: 25 COURTY: Boston
STATE: Massachusetts
COUNTRY: USA
TP: 02109
                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / MOLECULE TYPE: peptide
// FRAGMENT TYPE: internal
US-09-045-583-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 22; Conserve
TELEPHONE:
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Gaps

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US-VB-VA-P344A-S.

US-VB-VA-P34A-S.

Sequence 2, Application US/08724984A

Patent No. 6388055

GENERAL INFORMATION:

TITLE OF INVENTION: No. 6388055e1 Mouse Genomic Clone of the CC-TITLE OF INVENTION: CRRS Receptor

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road, P.O. Box 1539

CITY: King of Prussia

STATE: PA

COUNTRY: USA

COUNTRY: USA

INCOMPTER: IBM 48

COMPUTER: IBM 486

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-796-202-1

Sequence 1, Application US/09796202

Sequence 1, Application US/09796202

Sequence 1, Application US/09796202

GENERAL INFORMATION:

APPLICANT: Dragic, Tatjana

APPLICANT: Dragic, Tatjana

TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION

FILE REFERENCE: 2048/61010/JPW/SHS

CURRENT APPLICATION NUMBER: US/09/796,202

CURRENT APPLICATION NUMBER: US/09/796,202

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                           Length 352;
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       CURRENT APPLICATION NUMBER: US/09/502,783A
CURRENT FILING DATE: 200.1-08-23
PRIOR APPLICATION NUMBER: 08/466,343
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249 APYNIVILLINIFQEFFGLINGS 270
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                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-502-783A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 1
LENGTH: 352
TYPE: PRT
ORGANISM: human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-08-724-984A-2
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Patent No. 6511826
GENERAL INFORMATION:
APPLICANT: Li, Yi
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: POlymorleotides Encoding Human G-Protein Chemokine Receptor (CCRS TITLE OF INVENTION: HDGNR10
FILE REFERENCE: 1488.1150006
                                                                                                                                                                                                                                                  ö
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Belent No. 64487375

GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: PARAENTHER, MARC
APPLICANT: VASSART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOXINES RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                          100.0%; Score 118; DB 4; Length 352; 100.0%; Pred. No. 4.1e-12; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,752
FILING DATE: 9-APR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Attention NUMBER: 34,115
REFISENCE/DOCKET NUMBER:
INFORMATION NO SEG ID NO: 5:
SEQUENCE CHARACTERISTICS:
249 APYNIVLLINTFOEFFGLNNCS 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 APYNIVLLINTFQEFFGLNNCS 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
                                                                                                                                                                                                                                                                                                                  1 APYNIVLLLNTFQEFFGLNNCS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 APYNIVLLINTFOEFFGLNNCS 22
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nino acid
                                                                                                                                                                              Query Match
Best Local Similarity 100.(
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / TOPOLOGY: linear
// MOLECULE TYPE: protein
US-08-833-752-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino
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US-09-502-783A-2
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US-08-833-752-5
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Gaps

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US-08461-244-3
US-08461-244-3
Sequence 3, Application US/08461244
Sequence 3, Application US/08461244
Sequence 3, Application
Sequence 3, Application
Sequence 3, Application
Sequence 3, Application
APPLICANT: Soppet, Daniel R.
APPLICANT: Wi, Li
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBER32
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STREET: 6 Becker Farm Road
CITY: Roseland
STREET: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match

Best Local Similarity 90.0%; Pred. No. 1.4e-09;
Matches 18; Conservative 2; Mismatches 0; Indels
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MEDIUM TYPE: Flopy disk
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,244
FILING DATE: O5-JUN 1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: FFETENCY, GREGOTY D.
REGISTRATION NUMBER: 35,134
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: 325800-445
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION 1707
TELECHMUNICATION 1707
TELECHMUNICATION: 201-994-1700
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,343D
FILING DATE: 06-JUN 1995
CLASSIFICATION: 435
ATTONENTY/AGENT INPORMATION:
NAME: STEPFE, ERIC K.
REGISTRATION NUMBER: 1488.1150000/EKS/KLM
TELECOMMULCATION INFORMATION:
TELEFACOM (202) 371-2500
TELEFACOM CORET NUMBER: 1280
TELEFACOM CORET NUMBER: 1280
TELEFACOM (202) 371-2500
TELEFACOM CORET NUMBER: 1280
TELEFACOM CORET NUMBER: 1280
TELEFACOM (202) 371-2540
TELEFACOM CORET NUMBER: 1280
TELEFACOM CORET NUMBER: 1280
TELEFACOM (202) 371-2540
TELEFACOM CORET NUMBER: 1280
TELEFACOM CORET NUMBER: 1280
TELEFACOM (202) 371-2540
TYPE: AMINO CORET NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 344 AMINO COID
STRANDENDESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 PYNIVLLINTFOEFFGLNNC 21
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SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-466-343D-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/09502783A
Sequence 9, Application US/09502783A
Patent No. 6511826
GENERAL INFORMATION:
APPLICANT: Li. Yi
APPLICANT: NUMBER: 1488.1150006
GURRENT APPLICATION NUMBER: 08/466,343
PRIOR APPLICATION NUMBER: 08/466,343
PRIOR APPLICANT: 2001-08-23
PRIOR APPLICANT: 2001-08-23
PRIOR APPLICANT: PATE: PATE: 2001-08-23
PRIOR APPLICANT: PATE: 2001-08-23
PRIOR PATE: PATE: 2001-08-23
PRIOR APPLICANT: PATE: 2001-08-23
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PRIOR APPLICANT: PATE: 2001-08-23
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PRIOR PATE: PATE: 2001-08-23
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PRIOR PATE: 2001-08-23
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Fatent No. 6025154

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 9

NORMESPONDENCE ADDRESS:

ADDRESSERE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVE., NW, SUITE 600

CITY: WASHINGTON

STRATE: DC

COUNTRY: USA
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Best Local Similarity 90.0%; Pred. No. 1.4e-09;
Matches 18; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 91.5%; Score 108; DB 4; Length 354; Best Local Similarity 95.2%; Pred. No. 2.1e-10; Matches 20; Conservative 0; Mismatches 1; Indels
                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: William T. Han
REGISTATION NUMBER: 34,344
REFERENCE DOCKET NUMBER: 4156023
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270 5024
TELEPAK: 610 270 5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252 PYNIVLLITTFOEFFGLNNCS 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 PYNIVILINTFQEFFGLSNC 245
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                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: Amino Acid
TOPOLOGY: Linear
US-08-724-984A-2
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LENGTH: 329
TYPE: PRT
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US-08-466-343D-9
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US-09-502-783A-9
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MAMMALIAN MONOCYTE CHEMOATTRACTANT PROTEIN RECEPTORS
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; MOLECULE TYPE: protein
US-08-446-669-4
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US-09-045-583-50
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| Sequence 4, Application US/08450393A
| Sequence 4, Application US/08450393A
| Patent No. 57070815
| Patent No. 57070815
| APPLICANT: Charo, Israel
| APPLICANT: Coughlin, Shaun
| TITLE OF INVENTION: MANMALIAN MONOCYTE CHEMOATTRACTANT
| TITLE OF INVENTION: PROTEIN RECEPTORS
| NUMBER OF SEQUENCES: 14
| CORRESPONDENCE ADDRESS: 15
| CORRESPONDENCE ADDRESS: 16
| CORRESPONDENCE ADDRESS: 17
| CORRESPONDENCE ADDRESS: 18
| CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 PYNIVLLLNTFQEFFGLNNC 21
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LENGTH: 360 amino acids
TYPE: amino acid
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-461-244-3
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MOLECULE TYPE: protein
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Sequence 50, Application US/09045583

Sequence 50, Application US/09045583

Patent No. 6287805

GENERAL INFORMATION:
TITLE OF INVENTION: No. 628780561 Molecules of the G Protein-Coupled NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESSES: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTAN
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto
CITY: Palo Alto
STATE: California
COUNTRY: USA
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STATE: Massachusetts
COUTRY: USA
ZIP: USA
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US-09-045-583-51
Sequence 12. Application US/09045583
Sequence 13. Application US/09045583
GENERAL INFORMATION:
APPLICANT: GENERAL
TITLE OF INVENTION: No. 628780551 Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCES: 56
CORRESPONDENCES DAHLVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                             0
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CITY: Boston
STATE: Massachusetts
CONTRY: USA
ZIP: 02109
ZIP: SPEADBLE FORM:
MEDIUM TYPE: FLODPY disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFICATION NUMBER: 30-307
REPERICATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELEPHONE: (617) 742-4214
INPORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: Innear
REGISTRATION NUMBER: 36,207
REPERRINCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHX: (617)227-4214
INFORMATION FOR SEQ ID NO: 50: SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
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                                                                                                                                                                                                                             ) MOLECTLE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-045-583-50
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FRAGMENT TYPE: internal
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Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels
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| Sequence 20, Application US/09131827A
| GENERAL INFORMATION:
| APPLICANT: O'STICH: Stephen J.
| APPLICANT: Carrington, Mary
| APPLICANT: Carrington, Mary
| TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
| TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
| TITLE OF INVENTION: DIALYED PROGRESSION TO AIDS BY A
| TITLE OF INVENTION: DIALYED PROGRESSION TO AIDS BY A
| TITLE OF INVENTION: DIALYED PROGRESSION TO AIDS BY A
| TITLE OF INVENTION: DIALYED PROGRESSION TO AIDS BY A
| TITLE OF INVENTION: DIALYED PROGRESSION TO AIDS BY A
| TITLE OF INVENTION UNMERR: US/09/131,827A
| CURRENT APPLICATION NUMBER: US/09/131,827A
| PRIOR FILLING DATE: 1997-08-14
| WUMBER OF SEQ ID NOS: 20
| SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Dean, Michael
APPLICANT: O'Brien, Stephen J.
APPLICANT: O'Brien, Stephen J.
APPLICANT: O'Brien, Stephen J.
APPLICANT: Carrington, Mary
ITILE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
ITILE OF INVENTION: DELAYED ALLELE OF THE CCR2 GENE
ITILE REFERENCE: 14014.0333
CURRENT FAPLICATION NUMBER: US/09/131,827A
CURRENT FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/055,659
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-131-827A-2
; Sequence 2, Application US/09131827A
; Patent No. 6600030
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MOLECULE TYPE: No. 6448375e
US-08-833-752-7
           LENGTH: 360 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-09-131-827A-2
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; ORGANISM: HOMO
US-09-131-827A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 2
LENGTH: 360
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LENGTH: 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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| Sequence 10. 6448355
| Patent No. 6448355
| GENERAL INFORMATION:
| APPLICANT: SAMSON, MICHEL
| APPLICANT: PARKENTIER, MARC
| APPLICANT: LIBERT, FREDERICK
| APPLICANT: LIBERT, FREDERICK
| TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEWOKINES RECEPTOR
| TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
| VMMBER OF SEQUENCES: 17
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Knobbe, Martens, Olson & Bear
| STREET: 620 Newport Center Drive 16th Floor
| CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PRACADIN Release #1.0, Version #1.25
CURRANT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,185
FILING DATE: 24-Mar-2000
CLASSIFICATION: UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/045,583
FILING DATE: AUKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: MANIES MANIES: NAMY E.
RECIT MANIES (617) 722-740

TELEPRACISE (617) 742-4214

INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTK::

ZIP: 92660
COMPUTER: READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,752
TITING DATE: 9-ARR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 87.3%; Score 103; DB 4; Length 360; Best Local Similarity 90.0%; Pred. No. 1.5e-09; Matches 18; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECTLE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 PYNIVILLNTFQEFFGLSNC 277
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CLASSIFICATION: 536
ATTORNEY/ACENT INFORMATION:
NAME: Altman, Daniel
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 PYNIVLLINTFORFFGLNNC 21
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US-08-833-752-7
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87.3%; Score 103; DB 1; Length 374; 90.0%; Pred. No. 1.6e-09; live 2; Mismatches 0; Indels
                 COMPARTS READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPOTHER: IBM FC compatible
COMPOTHER: IBM FC compatible
COMPOTHER: IBM FC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/450,393A
FILING DATE: May 25, 1995
CLASSITCATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CSETY, LUBBER: 31,822
REFERENCE/DOCKET NUMBER: 31,822
REFERENCE/DOCKET NUMBER: 31,822
RELECOMMUNICATION INFORMATION:
TELEPOMMUNICATION INFORMATION:
TELEPOMMUNICATION INFORMATION:
TELEPOMMUNICATION INFORMATION:
TELEPOMMUNICATION INFORMATION:
TELEPOMMUNICATION: A15-843-5165
TELEPAK: 415-843-5163
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TELBEAK: 415-805,
TELBEK: 380816COOleyPA
INFORMATION FOR SEQ ID NO: 2;
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 90.03
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
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US-08-446-669-2
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Query Match

87.3%; Score 103; DB 4; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                 RESULT 24

PCT-US95-00476-4

| Sequence 4, Application PC/TUS9500476
| GENERAL INFORMATION:
| APPLICANT: The Regents of the University of California TITLE OF INVENTION: MAWALLAN MONOCYTE CHEMOATTRACTANT TITLE OF INVENTION: MAWALLAN MONOCYTE CHEMOATTRACTANT TITLE OF INVENTION: MAWALLAN MONOCYTE CHEMOATTRACTANT TITLE OF INVENTION: PROTEIN RECEPTORS
| NUMBER OF SEQUENCES: 14 CARFESPORS ADDRESSEE: California STREET: 201 N. Figueroa Street, 5th Floor STREET: California COUNTRY: USA ZIP: 90012-2628
| STREET: California COUNTRY: USA ZIP: 90012-2628
| COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC compatible OPERATING SYSTEM: PC COLOS/MS: CARSINT APPLICATION NUMBER: PCT/US95/00476
| FLLING DATE: CLASSIFICATION NUMBER: 20,121 REFERENCE/DOCKET NUMBER: 5555-291 TELECOMMULICATION INFORMATION: TELECOMMULICATION: TELECOMMULICATION: TELECOMMULICATION INFORMATION: TELECOMMULICATION INFORMATION: TELECOMMULICATION INFORMATION: TELECOMMULICATION INFORMATION: TELECOMMULICATION INFORMATION:
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| Sequence 2, Application US/08450393A
| Patent No. 5707815
| GENERAL INFORMATION |
| APPLICANT: Cauchlin, Shaun |
| TITLE OF INVENTION: PROTEIN RECEPTORS |
| TITLE OF INVENTION: PROTEIN RECEPTORS |
| NUMBER OF SEQUENCES: 14 |
| CORRESPONDENCE ADDRESS: Cooley Godward Castro Huddleson & Tatum |
| STREET: 5 Palo Alto Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 PYNIVILLNTFQEFFGLSNC 277
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                                                                                                           2 PYNIVLLINIFQEFFGLNNC 21
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SEQUENCE CHARACTERISTICS:

ILENGTH: 360 amino acids

TYPE: amino acid

TYPE: amino acid

MOLECULE TYPE: protein

PCT-US95-00476-4
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TELEFAX: 310-977-1003
TELEX:
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US-08-450-393A-2
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JUSTON-4945-669-2, Application US/08446669

Patent No. 6132987

GENERAL INPORMATION:

APPLICANT: Coughlin, Shaun

TITLE OF INVENTION: PROTEIN RECEPTORS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

STREET: 5 Palo Alto

GENERAL OF INVENTION: PROTEIN RECEPTORS

NUMBER OF SEQUENCES: 14

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COMPUTER: Falo Alto

STATE: Palo Alto

STATE: ABADBLE FORM:

MEDIN TYPE: Floppy disk

COMPUTER: IBM PC compatible

OMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OMPUTER: IBM PC compatible

OMPUTER: IBM PC compatible

OMPUTER: MAY 25, 1995

CURRENT APPLICATION DATA:

HAPLICATION: 435

ATTONEY AGENT INFORMATION:

NAME: Neeley, Richard

REGISTRATION NUMBER: 30,092

REFERENCE/DOCKET NUMBER: 30,092

REFERENCE/DOCKET NUMBER: 30,092

REFERENCE/DOCKET NUMBER: 30,092

RELECHONE: 415-847-0663

FELLECHONE: 415-847-0663

FELLECHONE: 415-847-0663 TELERAX: 415-857-0663
TELEX: 380816CooleyPA
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids

Palo Alto California

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RESULT 29
US-09-087-232A-22
Sequence 22, Application US/09087232A
; Sequence 22, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
    APPLICANT: QUillent et al.
    TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
    TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
    STREET: 30 Rockefeller Plaza
; STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 344;
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APPLICATION NUMBER: US/09/087 277
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59.3%; Score 70; DB 3; I

Best Local Similarity 57.1%; Pred. No. 0.00063;

Matches 12; Conservative 4; Mismatches 5;
       NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Schreck, Particia A.
REGISTRATION NUMBER: 33,777
REFERENCE/DOCKET NUMBER: 33,777
TELECHONE: 610-270-5031
TELEFAX: 610-270-5031
                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SUCHWARE: FASKERG Version 1.5
SUGRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/681,192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acida
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: N-terminal ORIGINAL SOURCE: US-08-681-192-2
                                                                                                                                                                  ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
STATE: New York
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                                                                                                                           Length 374;
                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application PC/TUS9500476
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California APPLICANT: The Regents of the University of California TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson STREET: 201 N. Figueroa Street, 5th Floor CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     % Sequence 2, Application US/08681192

Sequence 2, Application US/08681192

Patent No. 6287801

Patent No. 6287801

APPLICANT: BERGSMA, DERK

APPLICANT: BLSHOURBAGY, NABIL

APPLICANT: SARAY, HENRY

APPLICANT: GREAU HENRY

APPLICANT: GREAU HENRY

TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR HNFDS78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00476
FILING DATE:
                                                                                                                           Query Match 87.3%; Score 103; DB 3; Best Local Similarity 90.0%; Pred. No. 1.6e-09; Matches 18; Conservative 2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: Beliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555-291
TELECHONIS: 310-977-1001
TELEFAX: 310-977-1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 90012-2628
CCMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Comparible
OPERATING SYSTEM: PC-DOS/NE-DOS
SOFTWARE: Patentin Palescon.
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                                                                                                                                                                                                                     2 PYNIVLLINIFOEFFGLNNC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 PYNIVLLLNTFOEFFGLNNC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 374 amino acids TYPE: amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 87.3
Best Local Similarity 90.0
Matches 18; Conservative
, TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-669-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
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Sequence 2, Application US/08012988A
Petent No. 5652133

GENERAL INFORMATION:

TITLE OF INVENTION: Cloning and Expression of Human
TITLE OF INVENTION: Abrilip M.

TITLE OF INVENTION: Abrain / Rancophage Inflammatory Protein-1 alpha (MIP-1
TITLE OF INVENTION: Abrain / Rancophage Inflammatory Protein-1 alpha (MIP-1
TITLE OF INVENTION: Abrain / Rancophage Inflammatory Protein-1 alpha (MIP-1
TITLE OF INVENTION: Abrain / Rancophage Inflammatory Protein-1 alpha (MIP-1
TITLE OF INVENTION: Abrain / Rancophage Inflammatory Protein-1 alpha (MIP-1
TITLE OF INVENTION: Abrain / Rancophage Inflammatory Protein-1 alpha (MIP-1
TITLE OF INVENTION: USA
COMPTRE: California
COMPTRE: California
COMPTRE: California
COMPTRE: Laboration of SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATH:
APPLICATION NUMBER: US/08/012,988A
FILLING DATE: 19930128
FILLING DATE: 19930128
TELEPONMUNICATION NUMBER: 15280-118
TELECOMMUNICATION NUMBER: 15280-118
TELEPONMUNICATION NUMBER: 15280-118
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47.5%; Score 56; DB 1; Length 355;
Best Local Similarity 40.0%; Pred. No. 0.16;
Matches 8; Conservative 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.7%; Score 61; DB 3; Length 25; 100.0%; Pred. No. 0.00092; tive 0; Mismatches 0; Indels
                     CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 30 MAY 1997
ATTORNEY/AGENT INFORMATION:
NAME: KOLE. LISA B.
REGISTRATION NUMBER: 35,225
REGISTRATION NUMBER: AP 31115
TELEPHONE: (212) 408-2628
TELEPHONE: (212) 765-2519
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-087-232A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 MAY 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 APYNIVLLLNTF 25
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   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-012-988A-2
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Gaps
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Patent No. 612287;
GENERAL INFORMATION:
APPLICANT: Chazo, Israel
APPLICANT: Chazo, Israel
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT;
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 40.0%; Pred. No. 0.16;
Matches 8; Conservative 6; Mismatches 6; Indels
                                                                      GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
                                                                                                                                                                                                                                                                                                                                                                   CCUNTRY: USA

ZIP: 9430-2155

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: MAY 25, 1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Cserr: Luann
NAME: Cserr: Luann
REGISTRATION NUMBER: 31,822
REFERENCE/POCKET NUMBER: 31,822
RELEFAX: 415-883-5165
FELEFAX: 415-885-0663
FELEFAX: 415-885-0663
FELEFAX: 388016CooleyPA
INPORMATION POR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
FENGTH: 355 amino acids
US-08-450-393A-5; Sequence 5, Application US/08450393A; Patent No. 5707815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 PYNLTILISVFQDFLFTHEC 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 355 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                              CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-450-393A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 32
US-08-446-669-5
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254 PYNLTILISVFQDFLFTHEC 273

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2 PYNIVLLINTFOEFFGLNNC 21

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Tue Sep 28 15:49:57 2004

Gaps 0; Score 56; DB 3; Length 355; Pred. No. 0.16; 6; Mismatches 6; Indels Query Match
Best Local Similarity 40.0%;
Matches 8; Conservative 6

US-08-446-669-5

g

RESULT 33 US-09-239-938-1

; Sequence 1, Application US/09239938 ; Patent No. 6329510

GENERAL INFORMATION:

APPLICANT: Qin, Shixin

APPLICANT: Qin, Shixin

APPLICANT: Newman, Walter

APPLICANT: Newman, Masim

APPLICANT: Leukosite, Inc.

TITLE OF INVENTION: ANTI-CCR1 ANTIBODIES AND METHODS OF USE

TITLE OF INVENTION: THEREFOR

TITLE OF INVENTION: THEREFOR

TITLE OF INVENTION: THEREFOR

TITLE OF INVENTOR OF 13

CURRENT FILICATION NUMBER: US/09/239,938

CURRENT FILICATION NUMBER: 1999-01-29

NUMBER OF SEQ ID NOS: 1

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 1

LENGTH: 355

, ORGANISM: Homo sapien US-09-239-938-1

Query Match 47.5%; Score 56; DB 4; Length 355; Best Local Similarity 40.0%; Pred. No. 0.16; Matches 8; Conservative 6; Mismatches 6; Indels |||::||::| 254 PYNLTILISVFQDFLFTHEC 273 2 PYNIVLLINTFQEFFGLNNC 21

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RESULT 34 US-09-886-319A-14 ; Sequence 14, Application US/09886319A

APPLICANT: Regenbogen, Johannes
APPLICANT: Regenbogen, Johannes
APPLICANT: Goppelt, Andreas
TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound
TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
TITLE OF INVENTION: Active Substances
FILE REPERENCE: 50125/014002
CURRENT APPLICATION NUMBER: US/09/886,319A
CURRENT FILING DATE: 2000-06-10
FRIOR APPLICATION NUMBER: US 60/222,081
FRIOR FILING DATE: 2000-06-10
FRIOR PELICATION NUMBER: DE 10030149.5
FRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0 Werner, Sabine Halle, Jorn-Peter

SEQ ID NO 14 LENGTH: 355 TYPE: PRT

ORGANISM: Homo sapiens US-09-886-319A-14

ö Length 355; Query Match
47.5%; Score 56; DB 4;
Best Local Similarity 40.0%; Pred. No. 0.16;
Matches 8; Conservative 6; Mismatches

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Gaps

254 PYNLTILISVFODFLFTHEC 273 2 PYNIVLLINTFQEFFGLNNC 21 ò g

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PCT-US95-00476-5 RESULT 35

Sequence 5, Application PC/TUS9500476
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: Robbins, Berliner & Carson STREET: 201 N. Figueroa Street, 5th Floor

STREET: 201 N. Fign CITY: Los Angeles STATE: California COUNTRY: USA

ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00476

FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Berliner, Robert
REGIESTRATION UNUBER: 20, 121
REFERENCE/DOCKET UNMER: 5555
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-977-1001
TELEPHONE: 310-977-1003

5555-291

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SEQUENCE CHARACTERISTICS: LENGTH: 355 amino acids TYPE: amino acid INFORMATION FOR SEQ ID NO:

TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein

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INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR? SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 PYNLTIIISVEQDFLFTHEC 273
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; MOLECULE TYPE: No. 6448375e
US-08-833-752-9
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UG-08-833-752-8

Sequence 8, Application US/08833752

Sequence 8, Application US/08833752

Sequence 8, Application US/08833752

Sequence 8, Application US/08833752

GREATAL INFORMATION:
APPLICANT: WASSART GLLBERT
APPLICANT: WASSART GLLBERT
APPLICANT: WASSART GLLBERT
APPLICANT: WASSART; FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: ACTIVE AND INACTIVE 16th Floor
CORRESSEE: Knobbe, Martens, Olson & Bear
STRIET CA.
COMPUTER: Bach Compactible
COMPUTER: BADBLE FORM:
MEDIUM TYPE: IBM PC compactible
COMPUTER: BADBLE FORM:
MEDIUM TYPE: BADBLE FORM:
COMPUTER: BADBLE FORM:
MEDIUM TYPE: BADBLE FORM:
MEDIUM TYPE: BADBLE FORM:
MANE: PALENAL FORMING STRIEN:
MANE: APPLICATION NUMBER: 34,115
RECISTANTION NUMBER: 34,115
RECISTANTION FOR SEQ ID NO: 8:
INFORMATION PARCHASISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-08-033-752-9
| Sequence 9, Application US/08033752
| Patent No. 6440375
| Patent No. 6440375
| GENERAL INFORMATION:
| APPLICANT: PARWENTIER, MARC
| APPLICANT: VASSART, GILBERT,
| APPLICANT: LIBERT, FREDERICK:
| APPLICANT: APPLIC
                                                                                                                                                                                                                                                                                                                                          ö
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47.5%; Score 56; DB 5; Length 355;
Best Local Similarity 40.0%; Pred. No. 0.16;
Matches 8; Conservative 6; Mismatches 6; Indels
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TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: alinear
MOLECULE TYPE: No. 6448375e
                                                                               ANTI-SENSE: NO PCT-US95-00476-5
                               HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-833-752-8
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Gaps US-08-875-573-6

1 Sequence 6, Application US/08875573

1 Sequence 6, Application US/08875573

2 Sequence 6, Application US/08875573

2 GENERAL INFORMATION:

APPLICANT: Wells, Timothy N.C.

APPLICANT: Power, Christine A.

TITLE OF INVENTION: A CHEWOKINE RECEPTOR ABLE TO BIND TO

TITLE OF INVENTION: MCP-1, MIP-1 ALPHA AND/OR RANTES. ITS USES

NUMBER OF SEQUENCES: 20

CORRESPONDENCES: 20

CORRESPONDENCES: 100 No. 6150132th Glebe Rd. 8th floor

CITY: Arlington

STATE: WA

COUNTRY: USA

COUNTRY: USA

COUNTRY: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

OFFRATION NUMBER: PC-DOS/MS-DOS

SOFFWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: PCT/GB96/00143

FILING DATE: 24-JAN-1995

PRILING DATE: 24-JAN-1995

ATTORNEY/AGENT INFORMATION:

FILING DATE: 27-JAN-1995

ATTORNEY/AGENT INFORMATION: .. TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SA CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

ADDRESSE:
CORRESCE:
CITY: Remobe, Martens, Olson & Bear STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach STATE: CA COUNTRY: U.S.A.

ZIP: 92660
COMPUTER REMOBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER REMOBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING DATE: 9268 #33.752
FILING DATE: 9-APR-1997
CLASSIFICATION NUMBER: US/08/833,752
FILING DATE: 9-APR-1997
CLASSIFICATION NUMBER: 34,115
REFERENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acide
TYPE: amino acide
TYPE: amino acide
TYPE: amino acide
TYPE: amino acide Query Match
Best Local Similarity 35.0%; Pred. No. 0.35;
Matches 7; Conservative 7; Mismatches 6; Indels

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SEQ ID NO 2
LENGTH: 360
                                                                                                                                                                                                                                               RESULT 40
US-09-232-878-2
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Sequence 20, Application US/08875573
Patent No. 6150132
GENERAL INFORMATION:
APPLICANT: Wells, Timothy N.C.
APPLICANT: Power, Christine A.
TITLE OF INVENTION: MCP-1, MIP-1 ALPHA AND/OR RANTES. ITS USES NUMBER OF SUGURNICES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: AIINO No. 6150132th Glebe Rd. 8th floor
CITY: AIINGTON
STATES VANDER OF SUMPLY OF STATES.
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0
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44.9%; Score 53; DB 3; Length 170;
Best Local Similarity 52.4%; Pred. No. 0.22;
Matches 11; Conservative 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
44.9%; Score 53; DB 3; Length 360;
Best Local Similarity 52.4%; Pred. No. 0.53;
Matches 11; Conservative 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: VA

ZIP: 22201-4741

COMPUTER READABLE FORM:

MEDIUM TYPE: Floepy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/875,573

FILING DATE: 31-OCT-1997

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: QCT/GB96/00143

FILING DATE: 24-CAN-1996

PRIOR APPLICATION NUMBER: GB 9501683.8

FILING DATE: 27-CAN-1995

ATPLICATION NUMBER: ADATA:

APPLICATION NUMBER: ADATA:

ADATA: ADATA:

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NAME: Wilson, Mary J.
REGISTRATION NUMBER: 32,955
REPERENCE/DOCKET NUMBER: 146
TELECOMMUNICATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                        TELEFAX: 703-845-4100
| INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 170 amino acids TYPE: amino acid TYPE: amino acid HOSECULE TYPE: protein US-08-875-573-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Wilson, Mary J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 147
TELECOMMUNICATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
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Db 257 PYNIVILIATEOFFEGIANUS 22

NESULT 40

US-09-228-878-2

Sequence 2, Application US/09232878

Sequence 2, Application US/09232878

Sequence 2, Application US/09232878

Sequence 3, Application US/09232878

Septiment No. Gat5332

GENERAL INFORMATION:

APPLICANT: Campbell, James

APPLICANT: Rottman, James

NUMBER OF EEQ ID NOS: 6

NUMBER OF EEQ ID NOS: 6

SEQ ID NO 2

TYPE: PRT

APPLICANT: Rottman

SEQ ID NO 2

TYPE: PRT

APPLICANT: Rottman

APPLICANT: Rot
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September 28, 2004, 09:06:23; Search time 72.875 Seconds (without alignments) 97.074 Million cell updates/sec
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18: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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118
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Describeron:	Sequence 14, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Seguence 2, Appli	Sequence 22, Appl	Sequence 2, Appli	Sequence 22, Appl	Seguence 15, Appl	Sequence 17, Appl	Sequence 1, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 5, Appli	Sequence 5, Appli
t.	- 1	US-10-084-813-14	US-10-095-876A-2	US-09-725-285-2	US-09-759-841-2	US-09-779-879A-2	US-09-779-879A-22	US-09-779-880A-2	US-09-779-880A-22	US-09-813-653-15	US-09-813-653-17	US-09-796-202-1	US-09-195-662A-2	US-09-339-912A-2	US-09-938-719-5	US-09-939-226-5
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APYNIVLLINTFQEFFGLNNCS 22

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RESULT 2 US-10-055-876A-2 Sequence 2, Application US/10095876A ; Publication No. US20030148294A1

Sequence 5, Appli Sequence 14, Appli Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli	equence 9, equence 9, equence 9,
	95-662A 39-912A 02-783A
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11 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	4 4 4 6 4 7

## ALIGNMENTS

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NESOLI 14

Sequence 14, Application US/10084813

PUBLICATION 0. USZO030068615A1

GENERAL INFORMATION:

APPLICANT: SAXINGER, CARL

TITLE OF INVENTION:

APPLICANT: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE

TILE REFERENCE: 215875

TILE REPERENCE: 2000-08-25

PRIOR APPLICATION NUMBER: US/10/084,813

CURRENT APPLICATION NUMBER: US/000/23505

PRIOR APPLICATION NUMBER: US 60/151,270

PRIOR FILING DATE: 1999-08-27

NUMBER OF SEQ ID NOS: 1242

SEQ ID NO 14

LENGTH: 2

PRIOR ARTICLE

PREATURE:

ORGANISM: Artificial Sequence

FRATURE:

ORGANISM: Artificial Sequence

FRATURE:

OTHER INFORMATION: Description of Artificial Sequence: binding peptide

US-10-084-813-14

QUETY MATCH

QUETY MATCH

QUETY MATCH

QUETY MATCH

QUETY MATCH

PREATURE:

OTHER INFORMATION: 00.0%; Pred. No. 1e-11;

MATCHES 22; CONSERVATIVE 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPLICATION WEREAUTHER 0; MISMATCHES 0; Indels 0; Gaps 0;
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US-US-1/3-6/94-2

Sequence 2. Application US/09779879A

Fatent No. US2002048786A1

GENERAL INFORMATION:

APPLICANT: Roschke, Viktor

APPLICANT: Roschke, Viktor

APPLICANT: Li, Yi

APPLICANT: Li, Yi

APPLICANT: Li, Yi

APPLICANT: Nuben, Steven, M.

TITLE REFERENCE: 1488.115000A

CURRENT FILING DATE: 2001-02-09

FRICA PILING DATE: 2000-02-09

FRICA PILING DATE: 2000-02-09

FRICA FILING DATE: 2000-02-09

FRICA FILING DATE: 2000-03-09

FRICA FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 58

SOFTWARE: PatentIN version 3.0

SEQ ID NO 2

LENGTH: 352
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100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels C
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Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels
           TITLE OF INVENTION: Assay Method
FILE REFERENCE: PC10348APME
CURRENT APPLICATION NUMBER: US/09/759,841
CURRENT TILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: GB 0000661.9
PRIOR APPLICATION NUMBER: GB 0000663.5
PRIOR PLING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: GB 0000663.5
PRIOR PILING DATE: 2000-01-12
PRIOR PRICH DATE: 2000-01-12
PRIOR FILING DATE: 2000-01-12
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Patent No. US20020048786A1
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Roschke, Viktor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 APYNIVLLINTFOEFFGLNNCS 22
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Perros, Manoussos
                                                                                                                                                                                                                                                                                                                                                          ; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; CRGANISM: Homo sapiens
US-09-759-841-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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US-09-779-879A-22
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APPLICANT: Li, Yi
APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10
TITLE OF INVENTION: (CCR5 Receptor)
FILE REFERENCE: 1488.1150003
CURRENT APPLICATION NUMBER: US/09/725,285
CURRENT FILING DATE: 2000-11-29
PRIOR PILING DATE: 09/339,912
PRIOR PAPLICATION NUMBER: 09/339,912
PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 08/466,343
PRIOR PILING DATE: 1998-11-18
PRIOR FILING DATE: 1998-06-06
NUMBER: 08 SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 352
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                 APPLICANT: Au-Young, Janice; Bandman, Olga
APPLICANT: Au-Young, Janice; Bandman, Olga
APPLICANT: Coleman, Roger; Wilde, Craig G.
TITLE OF INVENTION: DNA ENCODING NOVEL CHEMOKINE RECEPTORS
FILE REFERENCE: PF-0060-1 CON
CURRENT APPLICATION NUMBER: US/10/095,876A
CURRENT APPLICATION NUMBER: US 08/638,081
PRIOR PILING DATE: 1996-04-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PERL PROGram
SOFTWARE: PERL PROGram
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:

"NAME/KEY: misc_feature

"OTHER KINY: nisc_feature

"OTHER MATION: Incyte ID No. US20030148294A1 478861
US-10-095-876A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 118; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.9e-10;
Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: Deduced Amino Acid Sequence US-09-725-285-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence: Genomic
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Patent No. US20010000241A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                   LENGTH: 332
TYPE: PRT
ORGANISM: Homo sapiens
  GENERAL INFORMATION:
```

Gaps

APPLICANT: Li, Yi
APPLICANT: Ruben, Steven, M.

US-09-759-841-2 ) Sequence 2, Application US/09759841 Patent No. US20010039026A1 ; GENERAL INPORMATION:

APPLICANT: Rickett, Graham A APPLICANT: Dobbs, Susan

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Gaps

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WESOUR 3. 653-15

Sequence 15, Application US/09813653

Sequence 15, Application US/09813653

Sequence 15, Application US/09813653

Sequence 15, Application US/00064770A1

SERENT No. US20020064770A1

APPLICANT: Nestor, John

APPLICANT: Wilson, Christina

APPLICANT: Tan Hehir, Christina

FILE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds

FILE REPERENCE: CNO-03-20

PRICR APPLICATION NUMBER: US 60/190,996

PRICR APPLICATION NUMBER: US 60/190,996

PRICR APPLICANTION NUMBER: US 60/191,299

PRICR FILING DATE: 2000-03-21

NUMBER OF SEQ ID NOS: 44

SEQ ID NO 15

LENGTH: 352
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100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels
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Local Similarity 100.0%; Pred. No. 2e-10;
nes 22; Conservative 0; Mismatches (
    PILE REFERENCE: 1488.115000C
CURRENT APPLICATION WUMBER: US/09/779,880A
PRIOR APPLICATION NUMBER: US 60/181,258
PRIOR FLING DATE: 2000-02-09
PRIOR FLING DATE: 2000-02-09
PRIOR FLING DATE: 2000-03-09
PRIOR FLING DATE: 2000-03-09
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 2000-03-05
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin version 3.0
SERVARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
US-09-779-880A-22
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US-09-813-653-17
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GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GAPPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
CURRENT APPLICANT:
GENERAL APPLICATION NUMBER:
GURRENT APPLICATION NUMBER:
GURRENT APPLICATION NUMBER:
GURRENT APPLICATION NUMBER:
GON-02-09
FRIOR APPLICATION NUMBER:
FRIOR SEPLING DATE:
FRIOR FILING DATE:
FR
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TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNRIO FILE REPERENCE: 1488-115000A
CURRENT APPLICATION NUMBER: US/09/779,879A
CURRENT FILING DATE: 2001-02-09
PRIOR PILING DATE: 2000-02-09
PRIOR FILING DATE: 2000-02-09
PRIOR FILING DATE: 2000-02-09
PRIOR FILING DATE: 2000-02-09
PRIOR FILING DATE: 2000-02-09
PRIOR PILING DATE: 2000-03-09
PRIOR PILING DATE: 2000-03-09
PRIOR PILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PETENTI Version 3.0
SEQ ID NO 2.2
LENGTH: 352
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APPLICANT: Roschke, Viktor
APPLICANT: Li, Zi, Zieven, M.
APPLICANT: Ruben, Steven, M.
IIILE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNRIO
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100.0%; Score 118; DB 9; Length 352;

Best Local Similarity 100.0%; Pred. No. 2e-10;

Matches 22; Conservative 0; Mismatches 0; Indels (
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100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels
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Sequence 22, Application US/09779880A

Patent No. US20020061834A1

GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
US-09-779-879A-22
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
US-09-779-880A-2
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Sequence 17, Application US/09813653
Patent No. US2002064770A1
GENERAL INFORMATION:
APPLICANT: Welsor, John
APPLICANT: See, Raymond
APPLICANT: Tan Hehlr, Christina
APPLICANT: Tan Hehlr, Christina
APPLICANT: Be INVENTION: Binding Compounds
FILE REFERENCE: CNS-005 ö

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APPLICANT: Li, Yi
APPLICANT: Ruben, Steven, M.
APPLICANT: Ruben, Steven, M.
APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10
TITLE OF INVENTION: (CCR5 Receptor)
FILE REFERENCE: 1488.1150003
FILE REFERENCE: 1488.1150003
CURRENT PAPLICATION NUMBER: 0.80/95/339, 912A
CURRENT FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 09/195,662
PRIOR APPLICATION NUMBER: 09/195,662
PRIOR PILING DATE: 1998-11-18
PRIOR PILING DATE: 1998-06-06
SOFTWARE: PALENTING DATE: 1998-06-06
SOFTWARE: PALENTING NOWNER: PALENTING DATE: 1995-06-06
LENGTHARE: PALENTING DATE: 1998-11-18
RIGHT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSARY, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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ZIP: 9260
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                           Query Match 100.0%; Score 110; DB 9; Length 352; Best Local Similarity 100.0%; Pred. No. 2e-10; Matches 22; Conservative 0; Mismatches 0; Indels
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100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels
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ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
... OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-319-912A-2
; OTHER INFORMATION: Deduced Amino Acid Sequence US-09-195-662A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence: Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 APYNIVLLINTFOEFFGLINICS 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-339-912A-2
, Sequence 2, Application US/09339912A
; Patent No. US20020099176A1
; GENERAL INFORMATION:
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Patent No. US20020106742A1
GENERAL INFORMATION:
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APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Ruben, Beeven, M.

TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGNR10 (CCR5 Receptor)
TITLE OF INVENTION: 1488.11500.2

CURRENT FILING DATE: 1998.11-18
CURRENT FILING DATE: 1998.11-18
PRICA APPLICATION NUMBER: 08/466,343
PRICA FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
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Patent No. US20020068813A1

Patent No. US20020068813A1

Patent No. US20020068813A1

APPLICANT: Dragic, Tatjana

TITLE OF INVENTION: SULFATED CCRS PEPTIDES FOR HIV-1 INFECTION

TITLE REFERENCE: 2048/610/JPW/SHS

CURRENT FILING DATE: 2001-02-28

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin version 3.0

SEQ ID NO 1.
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100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels
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Pred. No. 2e-10;
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       PRIOR APPLICATION NUMBER: US/09/813,653
PRIOR APPLICATION NUMBER: US 60/190,946
PRIOR FILING DATE: 2000-03-21
PRIOR PLING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/190,996
PRIOR PLING DATE: 2000-03-21
PRIOR PLING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin version 3.0
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ORGANISM: Artificial Sequence: Genomic
PEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%;
Matches 22; Conservative 0;
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US-09-813-653-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CRGANISM: human
US-09-796-202-1
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SEQ ID NO 2
LENGTH: 352
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US-09-195-662A-2
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US-09-796-202-1
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Gaps

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WE-09-502-783A-2

Sequence 2, Application US/09502783A

TILLE OF INVENTION: Polymucleotides Encoding Human G-Protein Chemokine Receptor (CCR5)

TILLE OF INVENTION: HDGNRIO

FILE REFERENCE: 1488.1150006

CURRENT APPLICATION NUMBER: US/09/502,783A

CURRENT PILING DATE: 2001-08-23

PRIOR APPLICATION NUMBER: 08/466,343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SANSON, MICHEL
PARMENTIER, MARC
VASSARY, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: CA
COUNTRY: U.S.A.

ZIP: 95660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatibl
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             Indels
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ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
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100.0%; Score 118; DB 9;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0;
             Mismatches
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               249 APYNIVLLINTFQEFFGLNNCS 270
                                                                                                                                              249 APYNIVLLINTFQEFFGLINICS 270
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Patent No. US20020110870A1
GENERAL INFORMATION:
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STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
             22; Conservative
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             Matches
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Sequence 5, Application US/09939226
Sequence 5, Application US/09939226
Sequence 5. Application US/09939226
Sequence 5. Application US/0805A1
GENERAL INFORMATION, MICHEL
PARMENTIER, MARC
VASSARY, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Newboll
STATE: CA
COUNTR: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/339,226
FILING DATE: 24-Aug-2001
CLASSIFICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Danial B
REGISTRATION NUMBER: 34,115
FREDISTRATION NUMBER: 34,115
STERENCE/DOCKET NUMBER: <Unknown>
STERENCE/DOCKET NUMBER: <UNKNOWN
STERENCE/DOCKET NUMBER: <U
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CORRESPONDENCE ADDRESS:
ADDRESSE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
FILING DATE: 24-Aug-2001
CLASSIPEICATION CURKNOWN>
PRIOR APPLICATION NUMBER: 09/626,939
FILING DATE: 27-ULLY-2000
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: cunknown>
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: milio acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 TOPOLOGY: Ilhear 7 TOPOLOGY: Ilhear 7 SEQUENCE DESCRIPTION: SEQ ID NO: 5: US-09-938-719-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein SEQ ID NO: 5: US-09-939-226-5
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Best Local Similarity
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US-09-939-226-5
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Sequence 477. Application US/09826509;
Sequence 477. Application US/09826509;
Publication No. US20030204073A1
| GENERAL INFORMATION:
APPLICANT: Lehmann-Bruinsma, Karin
| APPLICANT: Lehmann-Bruinsma, Karin
| APPLICANT: Liaw, Chen W. |
| TITLE OF INVENTION: Protein-Coupled Receptors |
| TITLE OF INVENTION: Protein-Coupled Receptors |
| FILE REFERENCE: AREN-207 |
| CURRENT FILING DATE: 2001-04-05 |
| PRIOR APPLICATION NUMBER: 09/170,496 |
| PRIOR FILING DATE: 1998-10-13 |
| NUMBER OF SEQ ID NOS: 589 |
| SEQ ID NO 477 |
| LENGTH: 352 |
| LENGTH: 352 |
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Publication No. US20030064071A1

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: Litteman, Dan R.

APPLICANT: Van Koopk, Yvette

APPLICANT: Van Koopk, Yvette

APPLICANT: Van Koopk, Yvette

APPLICANT: Geijtenbeck, Tneo

TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY

TITLE OF INVENTION: (CELLS)

TITLE OF INVENTION: (CELLS)

FILE REPRENCE: 1049-1-017

CURRENT APPLICATION NUMBER: US/10/151,274

CURRENT FILING DATE: 2000-05-20

PRIOR FILING DATE: 2000-03-02

NUMBER OF SEQ ID NOS: 17

SOOTWARE: PATENTIN VET. 2.0

SEQ ID NOS: 17

SEQ ID NOS: 17
                                                                     Gaps
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                       Length 352;
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                  Query Match 100.0%; Score 118; DB 10; Best Local Similarity 100.0%; Pred. No. 2e-10; Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 118; DB 11; Best Local Similarity 100.0%; Pred. No. 2e-10; Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                249 APYNIVLLINTFQEFFGLNNCS 270
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                           RESULT 19
US-09-826-509-477
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Publication No. US20030096221A1
GENERAL INFORMATION:
DENG, HONGKUI
ELLMEIER, WILFRIED
LANDAU, NATHANIEL R.
LIU, RONG
TITLE OF INVENTION: G-COULLED RECEPTORS ASSOCIATED WITH
MACKOPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
USES THEREOF
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100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels
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ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTWARE: Patentln Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/734,221A

RIING DATE: 11-Dec-2000

PRIOR APPLICATION NUMBER: US 08/66,020

FILING DATE: 19-D-UN-1996

APPLICATION NUMBER: US 08/27,319

FILING DATE: 13-ARR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1049-1-004 NZ

TELEMPHONE: 201-487-5800
                                                                                                                                                                                                                                2e-10;
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SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                   1 APYNIVLLLNTFQEFFGLNNCS 22
                       NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 352
PRIOR FILING DATE: 1995-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                    TYPE: PRT CORGANISM: Homo sapiens US-09-502-783A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-734-221A-14
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-106-623-20
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SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino scids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
CORGANISM: Homo sapiens
US-10-232-686-2
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Sequence 20, Application US/2088A1
GENERAL INFORMATION:
APPLICANT: Gray, Patrick W.
Raport, Carol J.
TITLE OF INVENTION: Chemokine Receptor Materials and Methods
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                      Query Match
100.0%; Score 118; DB 13; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                      CONTEXT USA

CONTEXT USA

ZIF: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATION SYSTEM: PC-DOS/NN-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/106,623

FILING DATE: 26-Mar-2002

CLASSIFICATION: UNKNOWN-

PRIOR APPLICATION NUMBER: 08/771,276

FILING DATE: CUNKNOWN-

APPLICATION NUMBER: 08/771,276

FILING DATE: CUNKNOWN-

NAME: NO. US20020150888Aland, Greta E.

REFERRATION NUMBER: 35,302

REFERRATION NUMBER: 31,302

REFERRATION FOR SEQ 1D NO: 2:

CONTINUE OF SEQ 1D NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: misc feature
; OTHER INFORMATION: /= "88C amino acid sequence"
;
US-10-106-623-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249 APYNIVLLINTFQEFFGINNCS 270
                                   249 APYNIVLLINTFQEFFGLNNCS 270
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               1 APYNIVLLLNTFOEFFGLNNCS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 352 antino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 22
US-10-106-623-20
                                                                                                                     RESULT 21
US-10-106-623-2
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ö ö RESULT 23
US-10-232-686-2
; Sequence 2, Application US/10232686
; Publication No. US20030023044A1
; GENERAL INFORMATION:
; APPLICANT: Li, YI
; APPLICANT: Li, YI
; TILE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.115000N
; FILE REFERENCE: 1488.115000N
; CURRENT APPLICATION NUMBER: US/10/232,686
; CURRENT FILING DATE: 2002-09-03
; PRIOR FILING DATE: 1999-06-25
; PRIOR FILING DATE: 1999-06-25
; PRIOR FILING DATE: 1999-06-25
; PRIOR FILING DATE: 1998-11-18
; PRIOR FILING DATE: 1998-11-18
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352 Gaps Gaps ; 0 ö Query Match
100.0%; Score 118; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Query Match 100.0%; Score 118; DB 13; Length 352; Best Local Similarity 100.0%; Pred. No. 2e-10; Matches 22; Conservative 0; Mismatches 0; Indels 0 STATE: 1111015
COUNTY: USA
ZIP: 6066
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/106,623
FILING DATE: 26-Mar-2002
FILING DATE: 4UNKNOWN>
PRIOR APPLICATION NUMBER: 08/771,276
FILING DATE: 4UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: NO. US20020150888Aland, Greta E.
REFERENCE/DOCKET NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 37,303
TELEPHONE: 312-44-6300
TELEPHONE: 312-44-6300

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Tue Sep 28 15:49:58 2004

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RESULT 27
US-10-290-058A-6
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Fublication No. US20330100058A1
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
FILE REPERENCE: 1488.115001
CURRENT APPLICATION NUMBER: US/10/067,800
CURRENT APPLICATION NUMBER: PCT/US01/04153
FRICR FILING DATE: 2001-02-09
FRICR FILING DATE: 2001-02-09
FRICR FILING DATE: 2001-02-09
FRICR FILING DATE: 2001-06-12
FRICR FILING DATE: 2001-06-12
FRICR FILING DATE: 2001-06-12
FRICR FILING DATE: 2001-10-12
FRICR FILING DATE: 2001-10-13
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Sequence 1, Application US/10086814

Publication No. US20030092632A1

Publication No. US20030092632A1

APPLICANT: Dragic, Tatjana

APPLICANT: Olson, Wiliam C.

TITLE OF INVENTION: SULFATED CCRS PEPTIDES FOR HIV-1 INFECTION

TITLE OF INVENTION NUMBER: US/10/086,814

CURRENT FILING DATE: 2002-02-28

NUMBER OF SEQ ID NOS: 38

SOFTWARE: Patentin version 3.1

LENGTH: 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 14; Length 352;
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249 APYNIVLLINIFQEFFGLNNCS 270
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ORGANISM: Homo sapiens
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US-10-067-800-2
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US-10-067-800-2
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TYPE: PRT
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Squence 6, Application US/10290058A

Squence 6, Application US/10290058A

Squence 6, Application Wo. US20030104455A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Wethods and Compositions for Treating
TITLE OF INVENTION: UFOLOGICAL Disorders Using 313, 333, 5464, 18817 or 33524

FILE REPERENCE: MPIO1-289PIRM
CURRENT APPLICATION NUMBER: US/10/290,058A

CURRENT FILING DATE: 2002-11-07

PRIOR APPLICATION NUMBER: 60/344,552

PRIOR APPLICATION NUMBER: 60/344,552

PRIOR APPLICATION OF STORMARY STORMARY
FILING DATE: 2001-11-07

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6

LENGTH: 352
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JOURNAL OF SEQUENCE 22, Application US/10067800

Sequence 22, Application US/10067800

Publication No. US20030100058A1

JERREAL INFORMATION:

APPLICANT: Rosen, Craig A.

APPLICANT: Rosen, Craig A.

APPLICANT: Ruben, Steven, M.

TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGNRIO

CURRENT APPLICATION NUMBER: US/10/067,800

CURRENT APPLICATION NUMBER: US/10/067,800

CURRENT APPLICATION NUMBER: PC/10/061/0615

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-06-12

PRIOR PLING DATE: 2001-06-12

PRIOR FILING DATE: 2001-06-12

PRIOR FILING DATE: 2001-10-10-12

PRIOR FILING DATE: 2001-10-12

PRIOR PLING DATE: 2001-10-12

PRIOR PLING DATE: 2001-10-12

PRIOR PLING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: 60/341,725

PRIOR PLING DATE: 2001-12-21

PRIOR PLING DATE: 2001-12-21

PRIOR PLING DATE: 2001-13-11

PRIOR PLING DATE: 2001-13-11

PRIOR PLING DATE: 2001-13-11

PRIOR APPLICATION NUMBER: 60/341,725

PRIOR PLING DATE: 2001-13-11

PRIOR APPLICATION NUMBER: 60/341,725

PRIOR PLING DATE: 2001-13-11

PRIOR APPLICATION NUMBER: 60/341,725

PRIOR APPLICATION NUMBER: 60/341,725
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Best Local Similarity 100.0
Matches 22; Conservative
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; ORGANISM: Homo sapiens
US-10-067-800-22
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US-10-290-058A-6
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RESULT 28 US-10-225-567A-352

249 APYNIVLLLNTFQEFFGLNNCS 270

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WESULO.

19.10-164-69-52

19.5equence 52, Application US/10164649

19.10-164-610-104

19.5equence 52, Application US/10164649

19.5equence 52, Application No. US2001062943Alel

19.5equence 52, Application No. US2001062943Alel

19.5equence 52, Application No. US20030162943Alel

19.5equence 52, Application No. US20045, 583

19.5equence 52, Application No. US20045, 583

19.5equence 52, Application No. US20045, 583

19.5equence 52, Application No. USAN. 1998

19.5equence 52, Application No. USAN. 198

19.5equence 52, Application No. USAN. 198

10.5equence 52, Application No. Solution No. Solu
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100.0%; Score 118; DB 14;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0;
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100.0%; Score 118; DB 14
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches C
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MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-10-164-649-52
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; Publication No. US20030165988A1
; GENERAL INFORMATION:
                    ; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-301-1
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RESULT 30

US-10-072-301-1

Sequence 1, Application US/10072301

Publication No. US20030152913A1

GENERAL INFORMATION:

APPLICANT: Hua, Shao-bing

APPLICANT: Pauling, Michelle H.

APPLICANT: Pauling, Michelle H.

APPLICANT: Pauling, Michelle H.

APPLICANT: Pauling, WIRNION: VIRUS

TITLE OF INVENTION: VIRUS

FILE REFERENCE: 25636-718

CURRENT FILING DATE: 2002-02-08

NUMBER OF SEQ ID NOS: 54

SOFTWARE: Patentin version 3.1
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US-10-323-314-1
VS-10-323-314-1
Sequence 1, Application US/10323314
Publication No. US20030139571A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Olson, William
TITLE OF INVENTION: SULFATED CCRS PEPTIDES FOR HIV-1 INFECTION
FILE REPERENCE: 2048/GIOLO-1/JFW/MAF/DJK
CURRENT APPLICATION NUMBER: US/10/323,314
CURRENT APPLICATION NOWHER: 202-12-19
NUMBER OF SEO ID NOS: 17
SOFTWARE: Patentin version 3.0
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Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0;
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US-10-225-567A-352
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ORGANISM: human
US-10-323-314-1
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LENGTH: 352
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Length 352;

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Query Match 100.0%; Score 118; DB 14; Best Local Similarity 100.0%; Pred. No. 2e-10; Matches 22; Conservative 0; Mismatches 0;
                                            PRIOR APPLICATION NUMBER: US/09/779,879A
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/187,999
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 2000-03-09
PRIOR PILING DATE: 2000-09-22
NUMBER OF SEC ID NOS: 58
SOFTWARE: Patentin version 3.0
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Publication No. US20030186889A1
                                 2002-05-01
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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APPLICANT: Hua, Shao-bing
APPLICANT: Pauling, Michelle H.
APPLICANT: Dauling, Michelle H.
APPLICANT: Stu, in
TITLE OF INVENTION: HIGH THROUGHDUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST ITILE OF INVENTION: FRAGMENTS DERIVED FROM MEMBRANE PROTEINS
FILE REPERBENCE: 25636-717
CURRENT APPLICATION NUMBER: US/10/071,866
CURRENT FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
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APPLICANT: Rosen, Craig A.
APPLICANT: Rosenke, Viktor
APPLICANT: Lid. St.
APPLICANT: Lid. St.
APPLICANT: Lid. Steven, M.
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
FILE REFERENCE: 1488.11500A
CURRENT FILING DATE: 2002-05-01
PRIOR PRIOR APPLICATION NUMBER: US/09/779,879A
PRIOR FILING DATE: 2001-02-09
PRIOR PRLING DATE: 2000-03-09
PRIOR PLING DATE: 2000-03-09
PRIOR PRIOR PLING DATE: 2000-03-09
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Publication No. US20030166024A1
GENERAL INFORMATION:
APPLICANT: Roschke, Viktor
APPLICANT: Li, Yi
APPLICANT: Li, Xi
CURRENT APPLICATION NUMBER: US/10/135,839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 2, Application US/10135839; Publication No. US20030166024A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-071-866-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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Best Local Similarity
Matches 22; Conserv
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PAPELICANT: PORSSMANN, Wolf-Georg; FORSSMANN, Ulf; ADERWANN, Knut;
APPLICANT: PORSSMANN, Wolf-Georg; FORSSMANN, Ulf; ADERWANN, Knut;
APPLICANT: HEITLAND, Alekandra; SPODSBERG, Nikola;
APPLICANT: HEITLAND, Alekandra; SPODSBERG, Nikola;
TITLE OF INVENTION: Diagnostic Agent and Medicanent for Examining the
TITLE OF INVENTION: Deferably with the Aid of Specific Chemokine
TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction
FILE REFERENCE: 022217us
FILE REFERENCE: 2002-09-23
RIOR PAPLICATION NUMBER: US/10/239,423
CURREAT FILING DATE: 2002-09-23
RIOR APPLICATION NUMBER: DE10016013.1
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PatentIN Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Sequence 2. Application US/10439845
Publication No. US20030195348A1
GENERAL INFORMATION:
APPLICANT: COMMADIATION: CC CHEMOKINE RECEPTOR 5 DNA, NEW ANIMAL MODELS
TITLE OF INVENTION: AND THERAPEUTIC AGENTS FOR HIV INFECTION
NUMBER OF SEQUENCES:
OCRRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0883G
TELECOMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEPHONE: 619/678-5099
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 anino acids
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Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT; ORGANISM: Homo sapiens
US-10-360-828-1
CLASSIFICATION:
                                                                                                                                                                                                                                                                   US-10-439-845-4
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                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/439,845
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/864,458
FILING DATE: May 28, 1997
APPLICATION NUMBER: Provisional 60/018,508
FILING DATE: May 28, 1996
CLASSIFICATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMENT Release #1.0, Version #1.30
CURRATI APPLICATION DATA:
APPLICATION NUMBER: US/10/439,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/864,458
FILING DATE: MAY 28, 1997
APPLICATION NUMBER: Provisional 60/018,508
FILING DATE: MAY 28, 1996
                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 08830/030001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 APYNIVLLINIFQEFFGLNNCS 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
IENGTH: 352 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: peptide US-10-439-845-2
                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
La Jolla
                                  COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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Sequence 5, Application US/10661798
; Sequence 5, Application US/10661798
; Publication No. US20040110127A1
; GENERAL INFORMATION:
; APPLICANT: Parmentier, Marc
; APPLICANT: Variant, Libert
; APPLICANT: Variant, Libert
; TITLE OF INVENTION: Screening Methods for Identifying Compounds which Decrease HIV Ent; FILE REFERENCE: 9409/2023F
; FILE REFERENCE: 9409/2023F
; CURRENT APPLICATION NUMBER: US/10/661,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/10360828

Sequence 1, Application US/10360828

Publication No. US20030206909A1

SENERAL INPORMATION:
APPLICANT: Hau, Shaobing
APPLICANT: Tauluing, Michelle H.
APPLICANT: Thu, Lii
TILES OF INVERTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
FILE REFERENCE: 25636-727

CURRENT FILING DATE: 2003-02-07

PRIOR APPLICATION NUMBER: US 10/071,866

PRIOR PELING DATE: 2002-02-07

PRIOR FILING DATE: 2002-02-08

PRIOR FILING DATE: 2002-02-08

PRIOR FILING DATE: 2002-02-08

PRIOR FILING DATE: 2002-02-08

PRIOR FILING DATE: 2002-04-08

NUMBER OF SEQ ID NOS: 64

SOFTWARE: Patentin Version 3.1

SEQ ID NO 1
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100.0%; Pred. No. 2e-10;
tive 0; Mismatches 0;
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08830/030001
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2003-09-12

CURRENT FILING DATE:

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| US-10791-901-905|
| Publication No. US20040151719A1
| GENERAL INCRRAMITION:
| APPLICANT: Li, Yi
| APPLICANT: Ruben, Steven, M. |
| TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGNR10
| TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGNR10
| TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGNR10
| TITLE OF ILLNG DATE: 2004-03-04
| CURRENT APPLICATION NUMBER: 09/127,764
| RICR FILING DATE: 2006-02-11
| PRIOR FILING DATE: 1999-06-25
| PRIOR FILING DATE: 1999-06-25
| PRIOR PILING DATE: 1999-06-25
| PRIOR FILING DATE: 1999-11-18
| PRIOR FILING DATE: 1999-06-25
| PRIOR FILING DATE: 1995-06-06
| NUMBER OF SEQ ID NOS: 9
| SEQ ID NO 2 |
| LENGTH: 352 |
| TYPE: PRI |
| TYPE: PRI |
| TYPE: PRI |
| ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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100.0%; Score 118; DB 16; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0
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PRIOR PLILING DATE: 2002-09-12
PRIOR FILING DATE: 2001-09-24
PRIOR FILING DATE: 2001-08-24
PRIOR PLING DATE: 2001-08-24
PRIOR PLING DATE: 2000-07-27
PRIOR PLING DATE: 2000-07-27
PRIOR FILING DATE: 1997-04-09
PRIOR PILING DATE: 1997-03-03
PRIOR PLING DATE: 1997-03-03
PRIOR PLING DATE: 1997-03-03
PRIOR FILING DATE: 1996-08-06
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 5
LENGTH: 352
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Best Local Similarity 100.1
Matches 22, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CRGANISM: Homo sapiens
US-10-661-798-5
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US-10-791-905-2
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September 28, 2004, 08:57:36; Search time 11.825 Seconds (without alignments) 178.961 Million cell updates/sec Run on:

Title: US-10-084-813-14
Perfect score: 118
Sequence: 1 APYNIVLLINTFQEFFGLNNCS 22

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:\*
i: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	chemokine (C-C) re	chemokine (C-C) re	(c-c)		0-0 0-0	probable DNA-direc	e (C-C) r	(C-C)	chemokine (C-C) re	Y		muscarinic acetylc			muscarinic acetylc	muscarinic acetylc	hypothetical prote	hypothetical prote	histidinol-phospha	MIP-1 alpha recept	muscarinic acetylc	muscarinic acetylc	muscarinic acetylc	O	muscarinic acetylc	υ	d de	υ	muscarinic acetylc
SUMMARIES	ID	A43113	JC2443	45	JC5942	17	_	10	~	$\sim$	•	•	$\sim$	S10856	m	$\sim$	A35546	m	34	20	m	S48657	B29514	-	-	IO.	0	9	10	12
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	Length	352	360	374	344	355	1075	360	355	360	383	466	466	466	466	589	490	294	300	342	359	484	589	590	590	590	639	352	478	479
do	Query		7.	•	ę.	47.5	•	44.9		•	44.1		44.1	44.1	•	43.2	42.4	•	40.7	ö	•	ö	•	•						6
	Score	1	103	0	70		54.5	53	52	52	52	52	52	52	52	51	20	48	4,8	48	4.8	48	48	48	48	48	48	47	47	47
	Result No.	1	7	m	4	ហ	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	50

muscarinic acetylc probable sugar tra	hypothetical prote	glutamine ABC tran	macrophage inflamm	G protein-coupled	G protein-coupled	hypothetical prote	DNA-directed RNA p	hypothetical prote	probable G protein	G protein-coupled	pentamidine resist	guanylate cyclase-	guanylate cyclase	guanylate cyclase-
S33776 T01844	T31013	E69633	I49339	S42628	S32785	T28952	C29959	T25510	I58186	JC5067	867163	568838	C55331	B55331
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479 507	87	216	355	374	374	613	1070	312	354	355	423	199	201	202
39.8	39.4	39.0	39.0	39.0	39.0	39.0	38.6	38.1	38.1	38.1	37.7	37.3	37.3	37.3
47	46.5	46	46	46	46	46	45.5	45	45	45	44.5	44	44	44
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## ALIGNMENTS

RESULT 1	
A43113 Chanchae (C-C) receptor 5 - human NyAnchrate names: C-C CKR-5; CCR5	
C;Specites: Homo sapiens (man) C;Date: 12-Uul-1996 #sequence revision 12-Jul-1996 #text_change 20-Jun-2000 C;Accession: A43113; S71808; Ā58834; A58832; G02653; A58 <u>8</u> 33	
R;Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M. Biochemistry 35, 3362-3367, 1396 abiochemistry S. Mitter Mollemistry S. Mitter Mollemi	300
43113; MUID:96241590; PMID:8639485	receptor
A;Molecule type: mRNA A;Residues: 1-352 <sam1></sam1>	
A;Cross-references: GB:X91492; NID:91262810; PIDN:CAA62796.1; PID:91262811 R;Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragostj	Saradosti
M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Pai Nature 382, 722-725, 1996	, G.; Paı
A,Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant allele A:Reference number: S11808: MITD-96345670: PMTD:8751444	alleles of
A;Accession: S71808	
Apparent increase actu bequence not shown; not compared with conceptual translation A; Molecule type: DNA	107
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A;Status: nucleic acid sequence not shown; not compared with conceptual translation	ion
A;MOLECULE TYPE: DNA A;Residues: 1-184,'IKDSHLGAGPAAACHGHLLLGNPKNSASVSK' <sam3></sam3>	
.1; PID:g1524063 al receptor but confers	s a degre
nd may have had a selective advantage by conferring resistance to Yersinia plague inf R:Combadiere, C.; Ahuia, S.K.; Tiffanv, H.L.; Murohy, P.M.	e infecti
J. Leukoc. Biol. 60, 147-152, 1996	
A;Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine rece A;Reference number: A58832; WUID:96295970; PMID:8699119	kine rece
A;Accession: A58832	
A;Molecule type: mkna A;Residues: 1-352 <com1></com1>	
A;Cross-references: GB:US7840; NID:g1502408; PIDN:AAB17071.1; PID:g1502409  3.Experimental equate: Glone 8 endopoxin etimulated northberal blood monocytes	
R. Combadiere, C.	
Submitted to the EMBL Data Library, May 1996	
A; Accession: G02653	
A;Status: translated from GB/EMBL/DDBJ A:Molecule type: mRNA	
A; Residues: 1-69, 11, 91-352 < COM2>	
Rikaport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.	
u. blol. Chem. 2/1/ 1/101-1/105/ A;Title: Molecular cloning and functional characterization of a novel human CC chemokine A;Reference number: A58833; MUID:9621862; PMID:8663314	nemokine

.; 0

Gaps

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chemokine (C-C) receptor 2, splice form A - human
NyAlternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemo C; Species: Homo Sapiens (man)
C; Species: Homo Sapiens (man)
C; Species: Homo Sapiens (man)
C; Accession: 138450
R; Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A; Title: Molecular cloning and functional expression of two monocyte chemoattractant prot A; Reference number: A53477; MUID:94195821; PMID:8146186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Map position: 3921-3921
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate resolutions of superior coupled receptor; glycoprotein; transmembrane #status predicted <TM1>
F; 79-99/Domain: transmembrane #status predicted <TM2>
F; 115-136/Domain: transmembrane #status predicted <TM3>
F; 208-226/Domain: transmembrane #status predicted <TM5>
F; 208-226/Domain: transmembrane #status predicted <TM6>
F; 208-208/Domain: transmembrane #status predicted <TM6>
F; 208-208/Domain: cransmembrane #status predicted <TM6>
F; 208-208/Domain: cransmembrane #status predicted <TM6>
F; 208-208/Domain: veransmembrane #status predicted <TM7>
F; 208-208/Domain: veransmembrane #status predicted <TM8-208/Domain: v
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C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Molecule type: DNA
A,Residues: 1-344 FRAN-
A,Cross-references: GB:U97123; NID:g2897070; PIDN:AAC39595.1; PID:g2897071
C,Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R.Fan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y. Biochem. Biophys. Res. Commun. 243, 264-268, 1998
A.Title: Cloning and characterization of a novel human chemokine receptor. A;Reference number: JC5942; MUID:98139902; PMID:9473515
A;Accession: JC5942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: EMBL:U03882; NID:g472555; PIDN:AAA19119.1; PID:g472556
F_114/Binding site: carbohydrate (Asn) (covalent) #status predicted F_1113-190/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 374;
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59.3%; Score 70; DB 2; Length 344
Best Local Similarity 57.1%; Pred. No. 0.0018;
Matches 12; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Pred. No. 9.6e-09;
2; Mismatches 0;
                                                                                                                                                       Score 103; DB 2;
Pred. No. 9.3e-09;
2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDB:337364; OMIM:601267
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                                                                                                                                                                                                                                                                                                                                                                                                                                         258 PYNIVILLNTFQEFFGLSNC 277
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                                                                                                                                                                                                                                                                                                                                                                                 2 PYNIVLLLNTFQEFFGLNNC 21
                                                                                                                                                                  87.3%;
90.0%;
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90.0%;
                                                                                                                                                            Query Match
Best Local Similarity 90.0°
Matches 18; Conservative
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Best Local Similarity 90.0
Matches 18; Conservative
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A;Molecule type: mRNA
A;Residues: 1-374 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene: GDB:CMKBR2
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C, Superfamily: vertebrate rhodopsin.
C, Superfamily: vertebrate rhodopsin.
C, Superfamily: vertebrate rhodopsin.
C, Reywords: AIDS, G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane #status predicted <TM1>
F, 57-87 Domain: transmembrane #status predicted <TM2>
F, 5103-124 / Domain: transmembrane #status predicted <TM4>
F, 193-216 / Domain: transmembrane #status predicted <TM4>
F, 193-218 / Domain: transmembrane #status predicted <TM6>
F, 2526-257 / Domain: transmembrane #status predicted <TM7>
F, 2526-257 / Domain: transmembrane #status predicted <TM6>
F, 2526-257 / Domain: transmembrane #status predicted <TM7>
F, 2526-257 / Domain: transmembrane #status predicted <TM7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chemokine (G-C) receptor 2, splice form B - human
NyAlternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chem
C;Species: Homo sapiens (man)
C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
C;Accession: JC2443, 138463
R;Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
A;Title: CDNA cloning and functional expression of a human monocyte chemoattractant prot
A;Reference number: JC2443; MUID:94324942; PMID:8048929
                                                                                                                           A;Residues: 1-352 <RAP>
A;Cross-references: GB:U54994; NID:g1457945; PIDN:AAC50598.1; PID:g1457946
A;Cross-references: GB:U54994; NID:g1457945; PIDN:AAC50598.1; PID:g1457946
C;Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see C;Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Cross-references: DDBJ:D29984; NID:g531246; PIDN:BAA06253.1; PID:g531247
R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A.Title: Molecular cloning and functional expression of two monocyte chemoattractant propagate researce number: A53477; MUID:94195821; PMID:8146186
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C,Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate splicing; G protein-coupled receptor; glycoprotein; transmembrane #status predicted <TM1>
F;43-70/Domain: transmembrane #status predicted <TM2>
F;11-10/Domain: transmembrane #status predicted <TM3>
F;115-136/Domain: transmembrane #status predicted <TM3>
F;115-136/Domain: transmembrane #status predicted <TM3>
F;154-178/Domain: transmembrane #status predicted <TM4>
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A;Cross-references: EMBL:U03905; NID:g472557; PIDN:AAA19120.1; PID:g472558
C;Genetics:
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F;268/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;356,337,342/Binding site: phosphate (Ser) (covalent) #status predicted
F;340,343/Binding site: phosphate (Thr) (covalent) #status predicted
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Pred. No. 3.5e-11;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                      AjGane: GDB:CMKBR5; CCR5; CKR-5; CC-CKR-5; CKR5; ChemR13
A;Cross-references: GDB:1230510; OMIM:601373
A;Map position: 3p21-3p21
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A;Cross-references: GDB:337364; OMIM:601267
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Conservative 0
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Best Local Similarity
Matches 22; Conserv
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Status: preliminary
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AjGane: CDB: CMKBR4
AjGane: CDB: CMCBL4
AjGane: CDB: CMCB-1921
AjMap position: 3921-3921
Cj. Superfamily: vertebrate rhodopsin
Cj. Superfamily: vertebrate fractus predicted <TML>
Fj. CD-70/Domain: transmembrane flatatus predicted <TMS>
Fj. CD-70/Domain: transmembrane flatatus predicted <TMS>
Fj. CD-20/Domain: transmembrane flatatus predicted <TMS>
Fj. CD-20/Dinding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted Fj. Sj. Sj. Mbinding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted Fj. Sj. Mbinding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted Fj. Sj. Mbinding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted Fj. Sj. Mbinding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted Fj. Sj. Mbinding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted Fj. Sj. Mbinding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted Fj. Sj. Mbinding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted Fj. Sj. Mbinding site: phosphate (Thr) (covalent) (covale
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A; Biol. Chem. 270, 19495-19500, 1995
A; Title: Molecular cloning and functional expression of a novel CC chemokine receptor CD? A; Reference number: A57160; MUID:95370289; PMID:7642634
A; Accession: A57160
A; Status: preliminary; not compared with conceptual translation
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 04-Mar-2000
C;Accession: G02436; A57237
R;Ponath, P.D.
submitted to the EMBL Data Library, February 1996
A;Reference number: H0127
A;Accession: G02436
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alternate names: C-C CKR-4
Species: Homo sapiens (man)
Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
Cross-references: EMBL:D17510; NID:9529643; PIDN:BAA04326.1; PID:91262609; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Molecule type: mRNA
;Residues: 1-360 <POW>
;Cross-references: GB:X85740; NID:g1370103; PIDN:CAA59743.1; PID:g971452
;Note: source clone KS-5
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                                                                                                                                                                                                                                                                                                                                               Score 54.5; DB 2; Length 1075;
Pred. No. 1.8;
2; Mismatches 2; Indels 3;
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Best Local Similarity 52.4%; Pred. No. 1;
Matches 11; Conservative 2; Mismatches 8; Indels
                                                                                                            A;Gene: rpoB
A;Genome: chloroplast
C;Superfamily: DNA-directed RNA polymerase beta chain
C;Keywords: chloroplast; nucleotidyltransferase; transcription
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     355 PONLVISTLIKNIPODFFG 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chemokine (C-C) receptor 3 - human N.Alternate names: C-C CXR-3
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 63.2%;
Matches 12; Conservative
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Chemokine (C-C) receptor 1 - human

NiAlternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor

Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens

R;Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.

A;Reference number: A45177; MUID:93161416; PMID:7679328

A;Reference number: A45177

A;Status: Homo sapiens

A;Molecule type: MRNA

A;Molecul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . Exp. Med. 177, 1421-1427, 1993
Title: Structure and functional expression of the human macrophage inflammatory 1 alph
Reference number: I55671; MUID:93240122; PMID:7683036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - Japanese black pine chlor C; Species: chloroplast Pinus thunbergiana (Japanese black pine)
C; Species: chloroplast Pinus thunbergiana (Japanese black pine)
C; Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 18-Aug-2000
C; Date: 170748
R; Wakasugi, T.; Tsudzuki, J.; Ito, S.; Nakashima, K.; Tsudzuki, T.; Sugiura, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 9794-9798, 1994
A; Title: Loss of all nch genes as determined by sequencing the entire chloroplast genome A; Reference number: 216030; MUID:95024047; PMID:7937893
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-1075 < WAK>
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A;Molecule type: mRWA
A;Molecule type: mRWA
A;Residues: 1-355 <RES-
A;Cross-references: GB:L10918; NID:g292416; PIDN:AAAA36543.1; PID:g292417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Experimental source: HL60 cells
A;Note: sequence extracted from NCBI backbone (NCBIP:124876)
R;Gao, J.
                                                                                                                           252 APYNIAFFLSTFKEHFSLSDC 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 PYNLTILISVFQDFLFTHEC 273
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A;Status: preliminary
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transment
F;23-48,Domain: transmembrane #status predicted <TM1>
F;61-85/Domain: transmembrane #status predicted <TM3>
F;98-119/Domain: transmembrane #status predicted <TM4>
F;139-162/Domain: transmembrane #status predicted <TM5>
F;88-207/Domain: transmembrane #status predicted <TM6>
F;89-409/Domain: transmembrane #status predicted <TM6>
F;389-409/Domain: transmembrane #status predicted <TM6>
F;421-442/Domain: transmembrane #status predicted <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               muscarinic acetylcholine receptor M2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 24-Nov-1999
C;Accession: JH0197, D37121
R;Lai, J; Bloom, J;W; Yamamura, H;I; Roeske, W.R.
Life Sci. 47, 1001-1013, 1990
A;Title: Applification of the rat m2 muscarinic receptor gene by the polymerase chain res
A;Reference number: JH0197; MUID:91041524; PMID:2172674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Molecule type: DNA
A,Residues: 1-466 <LAI>
A,Residues: 1-466 <LAI>
B,K.sintenban, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.
B; Biol. Chem. 265, 13702-13708, 1990
A,Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues involaterence number: A37121; MUID:90337982; PMID:2380182
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R;Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.
EMBO J. 6, 3923-3929, 1987
G protein-coupled receptor El - equine herpesvirus 2
C.Species: equine herpesvirus 2
C.Species: equine herpesvirus 2
C.Species: equine herpesvirus 2
C.Accession: S55594
B.Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249; 520-528, 1995
A.Pitle: The DNA sequence of equine herpesvirus 2.
A.Fitle: The DNA sequence of equine herpesvirus 2.
A.Fitle: S55594; MUID:95302501; PMID:7783207
A.Stetus: preliminary; nucleic acid sequence not shown
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C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 24-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-383 <TEL>
A;Ressidues: 1-383 <TEL>
A;Cross-references: GB-1120824; NID:g695172; PIDN:AAC13788.1; PID:g695173
A;Cross-references: GB-1120824; NID:g695172; PIDN:AAC13788.1; PID:g695173
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 52; DB 2; Length 466;
Pred. No. 1.9;
4; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.1%; Score 52; DB 390.9%; Pred. No. 1.6; tive 1; Mismatches
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401 APYNVMVLINTF 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 90.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 PYNIVLLISTF 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 APYNIVLLLNTF 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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C;Species: Mus musculus (house mouse)
C;Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C;Accession: JG4587, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996
A;Titles Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to
A;Reference number: JG4587; MUID:96136324; PMID:8573157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Map position: 3921-3921
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane #status predicted <TM1>
F; 36-60/Domain: transmembrane #status predicted <TM2>
F; 71-91/Domain: transmembrane #status predicted <TM3>
F; 108-129/Domain: transmembrane #status predicted <TM3>
F; 108-129/Domain: transmembrane #status predicted <TM4>
F; 108-233/Domain: transmembrane #status predicted <TM5>
F; 205-223/Domain: transmembrane #status predicted <TM5>
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C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Keywords: glycoprotebin; phosphoprotebin; receptor; thymus
F;2,193,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
                                                       A;Cross-references: EMBL:U49727; NID:g1477560; PIDN:AAB09726.1; PID:g1477561
R;Combadiere, C.; Ahuja, S.K.; Murphy, P.M.
J. Biol. Chem. 270, 16491-16494, 1995
A;Title: Cloning and functional expression of a human eosinophil CC chemokine receptor. A;Reference number: A57237; MUID:95348056; PMID:7622448
                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-106,'N',108-275,'S',277-280,'R',282-355 <COM>
A;Cross-references: GB:U28694; NID:g1199579; PIDN:AAC50469.1; PID:g1199580
A;Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC50469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F)240-261/Domain: transmembrane #status predicted <TM6>
F)288-205/Domain: transmembrane #status predicted <TM7>
F)284-273,106-183/Disulfide bonds: #status predicted
F)345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
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A;Residues: 1-360 <HOO>
A;Cross-references: EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g1167852
A;Experimental source: thymus
C;Genetics:
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44.1%; Score 52; DB 2; Length 360;
Best Local Similarity 47.6%; Pred. No. 1.5;
Matches 10; Conservative 3; Mismatches 8; Indels
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Pred. No. 1.4;
6; Mismatches
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                                                                                                                                                                                                                                                                                                          Status: nucleic acid sequence not shown Molecule type: mRNA
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PYNVAILLSSYQSILFGNDC 273
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Best Local Similarity 40.0%;
Matches 8; Conservative (
               A; Molecule type: DNA
A; Residues: 1-355 < PON>
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A Experimental source atrial miscle
A, Note: the protein sequence derived from the mRNA clones differs from that of the genomi
R; Castro., J.
FEBS Lett. 209, 367-372, 1986
A; Title: Primary structure of porcine cardiac muscarinic acetylcholine receptor deduced for A; Title: Primary structure of porcine cardiac muscarinic acetylcholine receptor deduced for A; Accession: A25656, MUID: 87080790; PMID: 3792556
A; Accession: A25656
A; Accession: A25666
A; Accession: A2566
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Feb-2000
C;Accession: A29476
R;Braun, T.; Schofield, P.R.; Shivers, B.D.; Pritchett, D.B.; Seeburg, P.H.
B;Ochem Biophys. Res. Commun. 149, 125-132, 1987
A;Title: A novel subtype of muscarinic receptor identified by homology screening.
A;Reference number: A29476; MuID:88077068; PMID:3120722
A;Reference number: A29476
A;Molecule type: mRNA
A;Residues: 1-589 <-BRA
A;Cross-references: GB:M18088; NID:g202657; PIDN:AA40659.1; PID:g202658
A;Residues: 1-589 <-BRA
A;Residues: 1-589 <-BRA
A;Residues: 1-589 <-BRA
A;Residues: 1-580 <-BRA
A;Re
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C;Species: Gallus gallus (chicken)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 21-Jul-2000
Cross-references: GB:M16331; NID:g164311; PIDN:AAA30986.1; PID:g164313
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Pred. No. 3.5;
5; Mismatches 0; Indels
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R;Tietje, K.M.; Goldman, P.S.; Nathanson, N.M.
J. Biol. Chem. 265, 2828-2834, 1990
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Best Local Similarity 61.5%;
Matches 8; Conservative
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505 PYNIMVLVNTFRD 517
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401 APYNVMVLINTF 412
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Matches 8; Conservative
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A35546
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A;Title: Distinct primary structures, ligand-binding properties and tissue-specific exprayreference number: $04326; MUD:88166632; PMID:3443095
A;Accession: $10126
A;Accession: $10126
A;Accession: SI0126
A;Accession: SI0126
A;Accession: SI0126
A;Coss-references: EMBL:X15264; NID:g32319; PIDN:CAA33335.1; PID:g32320
B;Coss-references: EMBL:X15264; NID:g32319; PIDN:CAA33335.1; PID:g32320
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphory: $750-89;Domain: transmembrane #status predicted <TM1>
F;00-89;Domain: transmembrane #status predicted <TM3>
F;189-162;Domain: transmembrane #status predicted <TM4>
F;189-162;Domain: transmembrane #status predicted <TM4>
F;189-409;Domain: transmembrane #status predicted <TM5>
F;189-409;Domain: transmembrane #status predicted <TM6>
F;2007;Domain: transmembrane #status predicted <TM6>
F;2007;Domain: transmembrane #status predicted <TM7>
F;2007;Domain: transmembrane #sta
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A; Residues: 1-466 <GOC>
A; Residues: 1-466 <GOC>
A; Cross-references: EMBL:03025; NID:g203461; PIDN:AAA40926.1; PID:g203462
A; Cross-references: EMBL:03025; NID:g203461; PIDN:AAA40926.1; PID:g203462
C; Superfamily: Vertebrate rhodopsin
C; Reywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphot
C; Reywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphot
C; Reywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphot
C; Reywords: G protein-coupled receptor; glycoprotein; neuronsmembrane #status predicted <TM3>
F; 193-420 Domain: transmembrane #status predicted <TM4>
F; 184-207/Domain: transmembrane #status predicted <TM6>
F; 185-207/Domain: transmembrane #status predicted
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Manuscarinic acetylcholine receptor, cardiac - pig

Miscarinic acetylcholine receptor, cardiac - pig

MyAlternate names: muscarinic acetylcholine receptor M2

C;Species: Sus scrofa domestica (domestic pig)

C;Species: L5-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 31-Dec-2000

C;Accession: A27386; A25656

R;Peralta, E.G.; Winslow, J.W.; Peterson, G.L.; Smith, D.H.; Ashkenazi, A.; Ramachandran Soience 236, 600-605, 1987

A;Title: Primary structure and biochemical properties of an M-2 muscarinic receptor.

A;Reference number: A27386; MUD:87206169; PMID:3107123

A;Accession: A27386

A;Accession: A27386

A;Residues: 1-466 <PER>
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Wiscarinic acetylcholine receptor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 24-Nov-1999

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 24-Nov-1999

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 24-Nov-1999

R;Gocayne, 0.7 Robinson, D.A.; FitzGerald, M.G.; Chung, F.Z.; Kerlavage, A.R.; Lentes, R

Proc. Natl. Acad. Sci. U.S.A. 84, 8295-8300, 1987

Proc. Natl. Acad. Sci. U.S.A. 84, 8295-8300, 1987

A;Title: Primary structure of rat cardiac beta-adrenergic and muscarinic cholinergic rec

A;Reference number: S10855; MUID:88068581; PMID:2825184
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Pred. No. 1.9;
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401 APYNVMVLINTF 412
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nes 8; Conservative
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C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
C;Accession: 669502
C;Accession: 669502
B;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.
Smith, H.O.; Woese, C.R.; Venter, J.C.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Reference number: A69250; MUID:98049343; PMID:9389475
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A;Molecule type: DNA
A;Residues: 1-342 < KLES.
A;Cross-references: GB:AE000963; GB:AE000782; NID:g2689286; PIDN:AAB89229.1; PID:g264851(C;Superfamily: probable histidinol-phosphate transaminase
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Kgao, J. L.; Murphy, P.M.

J. Biol. Chem. 270, 17494-17501, 1995

A,Title: Cloning and differential tissue-specific expression of three mouse beta chemokir

A,Reference number: 149339; MUID:95340546; PMID:7542241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 histidinol-phosphate aminotransferase (hisC-2) homolog - Archaeoglobus fulgidus
                          A;Cross-references: GB:AE007870; PIDN:AAK90282.1; PID:915160307; GSPDB:GN00170 C;Genetics:
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C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1998
                                                                                                                                                                                                                                                                                               Length 300;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: I49341
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-359 A:RES
A;Cross-references: EMBL:U28406; NID:g881551; PID:g881552
C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 40.7%; Score 48; DB 2;
Best Local Similarity 45.0%; Pred. No. 6.4;
Matches 9; Conservative 3; Mismatches 8
                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.7%; Score 48; DB 2
50.0%; Pred. No. 6.1;
ative 5; Mismatches
                                                                                                                                                                                                                                                                                      Query Match
40.7%; Score 48; DB 3
Best Local Similarity 52.4%; Pred. No. 5.4;
Matches 11; Conservative 3; Mismatches
                                                                                                                A;Gene: AGR L 3415
A;Map position: linear chromosome
C;Superfamily: inner membrane protein ugpA
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248 PFNSSFVLLLKVYREAFQLNN 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 PYN -- IVLLINTFQEFFGLNN 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 YNIVLLINTFOEFFGL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 50.00,
100 8; Conservative
A;Residues: 1-300 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 20
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                                                                                                           A/ROCIOLIE 1779: DNA
A/Residues: 1-490 <TIE>
A/Residues: 1-490 <TIE>
A/Residues: 1-490 <TIE>
A/Residues: 1-490 <TIE>
C/Superfamily: vertebrate rhodopsin
C/Superfamily: vertebrate rhodopsin
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; glycoprotein, neurotransmitter receptor; transmembrane fatetus predicted <TML>
F/2-67/Domain: transmembrane fatetus predicted <TML>
F/30-104/Domain: transmembrane fatetus predicted <TML>
F/117-138/Domain: transmembrane fatetus predicted <TML>
F/18-191/Domain: transmembrane fatetus predicted <TML>
F/203-226/Domain: transmembrane fatetus predicted <TML>
F/413-433/Domain: transmembrane fatetus predicted <TML>
F/413-445/Domain: transmembrane fatetus predicted <TML>
F/445-466/Domain: transmemb
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Hy98144
hy98144
hy98145
hypothetical protein AGR_L_3415 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C;Accession: H98344
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Title: Cloning and functional analysis of a gene encoding a novel muscarinic acetylchd
A;Reference number: A35546; MUID:90153912; PMID:2154460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Species: Agrobacterium tumefaciens
C; Date: 11.-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C; Accession. AG293.
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell & Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dupont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein Atu3101 [imported] - Agrobacterium tumefaciens (strain C58,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Molecule type: DNA
Residues: 1294 «KUR»
(Eross-references: GB:AE008689; PIDN:AAL43917.1; PID:g17741468; GSPDB:GN00187;
Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 4.2;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 294;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Map position: linear chromosome
C; Superfamily: inner membrane protein ugpA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 PFNSSFVLLLKVYREAFQLNN 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 PYN--IVLLINTFQEFFGLNN 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42.4%;
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Best Local Similarity 52.4%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||:::|:||| | 426 PYNVMVLINTFCE 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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RESULT 21

A,Accession: H98344 A,Status: preliminary A,Molecule type: DNA

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3; Mismatches
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Best Local Similarity
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A;Accession: B94293
A;Molecule type: mRNA
A;Residues: 1-269;463-589 cB02>
A;Experimental source: cerebral cortex
A;Experimental source: cerebral cortex
A;Experimental source: cerebral cortex
B;Experimental source: cerebral cortex
B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C)Suberfamily: vertebrate thodopsin

C)Suberfamily: vertebrate thodopsin

C)Seywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme

F)33-289 Domain: transmembrane #status predicted <TM1>

F)1-95/Domain: transmembrane #status predicted <TM3>

F)108-129/Domain: transmembrane #status predicted <TM4>

F)19-17/Domain: transmembrane #status predicted <TM5>

F)19-17/Domain: transmembrane #status predicted <TM5>

F)407-427/Domain: transmembrane #status predicted <TM5>

F)407-427/Domain: transmembrane #status predicted <TM5>
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C, Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme
E;67-90, Domain: transmembrane #status predicted <TML>
F;104-124/Domain: transmembrane #status predicted <TML>
F;104-124/Domain: transmembrane #status predicted <TML>
muscarinic acetylcholine receptor MR - African clawed frog
C;Species: Kenopus laevis (African clawed frog)
C;Species: Ls-dul-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C;Accession: 846657; 824948
R;Herrera, L.; Carvallo, P.; Antonelli, M.; Olate, J.
R;Herrera, L.; Carvallo, P.; Antonelli, M.; Olate, J.
A;Title: Cloning of a Xenopus laevis muscarinic receptor encoded by an intronless gene.
A;Reference number: $48657; MUID:95010703; PMID:7925970
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A,Residues: 1-589 <BO1>
R:Bonner, T.1: Buckley, N.J.; Young, A.C.; Brann, M.R.
Science 237, 527-532, 1987
A;Title: Identification of a family of muscarinic acetylcholine receptor genes.
A;Reference number: A94293; MUID:87263421; PMID:3037705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muscarinic acetylcholine receptor M3 - rat
Cispecies: Rattus norvegicus (Norway rat)
Cibate: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 18-Feb-2000
CiAccession: B94518; B9423; B37121; B29514
R.Bonner, T.I.
A.Feerence number: A94518
A.Feerence number: A94518
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A;Residues: 1-484 <HER>
A;Cross-references: GB:X65865; NID:g64900; PIDN:CAA46694.1; PID:g64901
R;Olate, J.
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Pred. No. 8.7;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: S24948
A;Molecule type: mRNA
A;Residues: 1-131,'X',133-484 <OLA>
A;Cross-references: EMBL:X65865; NID:g64900; PID:g64901
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; nef;33-58/Domain: transmembrane #status predicted <TMI>F;71-95/Domain: transmembrane #status predicted <TMI>F;71-95/Domain: transmembrane #status predicted <TMI>F;71-95/Domain: transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, April 1992
A;Reference number: S24948
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Best Local Similarity 63.57
Tr Conservative
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                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: S48657
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Cispecies: Homo sapiens (man)
Cispecies: J1-be-1990 #sequence_revision 31-be-1990 #text_change 18-Feb-2000
Riberalta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J
Riberalta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J
A/Tile: Distrinct primary structures, ligand-binding properties and tissue-specific expre
A/Reference number: S04326; MUD:88166632; PMID:3443095
A/Accession: S10128
A/Accession: S1028
A/Accession: S10128
A/Accession: S10128
A/Accession: S04326; MUD:932323; PIDN:CAA33337.1; PID:q32324
Cisperfamily: vertebrate rhodopsin
Cisperfamily: vertebrate rhodopsin
Cisperfamily: vertebrate rhodopsin
Cisperfamily: vertebrate specificed <TM1>
Fig. 131.100main: transmembrane #status predicted <TM2>
Fig. 131.1252/Domain: transmembrane #status predicted <TM5>
Fig. 131.252/Domain: transmembrane #status predicted <TM5>
Fig. 131.252/Domain: transmembrane #status predicted <TM6>
Fig. 131.252/Domain: transmembrane #status predicted <TM6>
Fig. 131.252/Domain: transmembrane #status predicted <TM6>
Fig. 141/Binding site: carbohydrate (Asn) (covalent) #status predicted
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M.Alternate names: muscarinic acetylcholine receptor III
C.Species: Sus exrofa domestic pig)
C.Species: Sus exrofa domestic pig)
C.Species: Sus exrofa domestic pig)
C.Species: Sus exrofa domestic of domestic pig)
R.Accession: SO114
R.Akiba, I.; Kubo, T.; Maeda, A.; Bujo, H.; Nakai, J.; Mishina, M.; Numa, S.
F.BBS Lett. 235, 257-261, 1988
A.Filtle: Primary structure of porcine muscarinic acetylcholine receptor III and antagonis A.Reference number: SO1114; MUD: 88296835; PMID: 3402600
A.Reference number: SO1114; MUD: 88296835; PMID: 3402600
A.Residues: 1-590 - AKI.
A.Residues: 1-590 - AKI.
A.Residues: 1-590 - AKI.
A.Residues: 1-500 - AKI.
A.Coss-references: EMBL: X12712; NID: gl861; PIDN: CAA31215.1; PID: gl862
C.Superfamily: Vartebrate rehodopsin
C.Superfamily: Vartebrate rehodopsin
C.Superfamily: Vartebrate rehodopsin
C.Superfamily: Vartebrate rehodopsin
F;68-91/Domain: transmembrane #status predicted <TM3>
F;143-164/Domain: transmembrane #status predicted <TM3>
F;131-252/Domain: transmembrane #status predicted <TM4>
F;528-546/Domain: transmembrane #status predicted <TM5>
F;528-54/Domain: transmembrane #status predicted <TM6>
F;528-54/Domain: transmembrane #status predicted <TM6}
F;528-54/Fyreane **
F;528-54/Fyreane **
F;52
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F;184-206/Domain: transmembrane #status predicted <TM4>
F;20-251/Domain: transmembrane #status predicted <TM5>
F;492-512/Domain: transmembrane #status predicted <TM6>
F;527-545/Domain: transmembrane #status predicted <TM7>
F;527-545/Domain: transmembrane #status predicted <TM7>
F;6,15,41,48,52/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                               40.7%; Score 48; DB 2; Length 589; 72.7%; Pred. No. 11;
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Nature 390, 249-256, 1997

Ajuthors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallert icch, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucel, Y.; M.; Ogawara, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Pottetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, akeuchi, M.; Tamakoshi, A.; Tanakoshi, T.; Yasumoto, K.; Yasumoto, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Tanaka, T.; Yoshikawa, H.; Danchin, A.
A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Accession: B6990; MUID:98044033; PMID:934377

A; Residues: 1-352 «KUN»

A; Residues: 1-352 «KUN»

A; Residues: 1-352 «KUN»

A; Residues: Gersalia source: strain 168

C; Genetics:
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A; Residues: 1-233;373-478 <BO2>
A; Residues: 1-233;573-478 <BO2>
A; Residues: 1-233;573-478 <BO2>
A; Residues: 1-233;573-478 <BO2>
A; Residues: 1-25, 13702-13708, 1990
A; Biol. Chem. 255, 13702-13708, 1990
A; Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues invol
A; Reference number: A37121, MUID:90337982; PMID:2380182
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;Reywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphor;31-56/Domain: transmembrane #status predicted <TML>
;69-93/Domain: transmembrane #status predicted <TML>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Riboner, T.I.

submitted to GenBank, July 1987

A;Reference number: A94518

A;Accession: C94518

A;Molecule type: mRNA

A;Residues: 1-478 < BO)

Science 237, 527-522, 1987

A;Title: Identification of a family of muscarinic acetylcholine receptor genes.

A;Reference number: A94293; MUID:87263421; PMID:3037705

A;Accession: C94293.
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C;Species: Rattus norvegiuus (Norway rat)
C;Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text_change 24-Nov-1999
C;Accession: C94518; C94293; \( \overline{\ov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 47; DB 2;
Pred. No. 9.1;
3; Mismatches
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C,Superfamily: omega-3 fatty acid desaturase
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Molecule type: protein
Residues: 68-130 <KUR>
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Matches 9; Conserv
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muscarinic acetylcholine receptor, M3 isoform - chicken
muscarinic acetylcholine receptor, M3 isoform - chicken
c;becises acalus gallus (chicken)
c;becisesion: A55019
R;Gadbut, A.P.; Galper, J.B.
G;biol. Chem. 269, 25823-25829, 1994
A;Title: A novel M-3 muscarinic acetylcholine receptor is expressed in chick atrium and A;Reference number: A55019; MUID:95014393; PMID:7929287
A;Status: preliminary
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C;Species: Bacillus subtilis
C;Species: Dacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Accession: B69901
B;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               muscarinic acetylcholine receptor m3 - bovine

C/Species: Bos primigenius taurus (cattle)

C/Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 18-Feb-2000

C/Accession: 847572

Files. P.H.K.; Hodges, P.K.; Glickman, F.; Chang, K.J.

Biochim. Biophys. Acta 1223; IS1-154, 1994

A/Fitle: Cloning and expression of a cDNA encoding bovine muscarinic acetylcholine m3 x

A/Secence number: 847572; MUID:94339178; PMID:8061048

A/Scatus: preliminary
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Molecule type: mRNA
Residues: 1-590 <LEE>
Cross-references: EMBL:U08286; NID:9520465; PIDN:AAA51866.1; PID:9520466
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A;Residues: 1-639 <GAD>
A;Cross-references: GB:L10617; NID:g530097; PIDN:AAA65961.1; PID:g530098
C;Superfamily: vertebrate rhodopsin
C;Keywords: neurotransmitter receptor
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                                            Score 48, DB 2; Length 590;
Pred. No. 11;
3; Mismatches 0; Indels
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llarity 72.7%; Pred. No. 11;
Conservative 3; Mismatches
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A;Residues: 1-590 <LEE>
A;Cross-references: BMBL:U08286; NID:9
C;Superfamily: vertebrate rhodopsin
C;Keywords: neurotransmitter receptor
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                          Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                          506 PYNIMVLVNTF 516
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PYNIMVLVNTF
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Best Local Similarity
Thes 8, Conserve
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Matches 8; Conserv
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Query Match

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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Date: 05-Dec-1997 #text_change 20-Jun-2000
C;Date: 05-Dec-1997 #text_change 20-Jun-2000
C;Date: 05-Jun-2000
C;D
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Cipate: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
Cipate: 02-Sep-2000 #sequence_revision 02-Sep-2000
Extremophiles 2, 417-425, 1998
Extremophiles 2, 417-425, 1998
Ayititle: Ganetic profile of pNOB8 from Sulfolobus: the first conjugative plasmid from an Ayititle: Ganetic profile of pNOB8 from Sulfolobus: the first conjugative plasmid from an Ayicession: T31013
Ayititle: September: 220959; MUID:99044580; PMID:9827331
Ayititle: September: Septemb
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                                                                                                                                                                                                                                                                                                           probable sugar transport protein F9D12.9 - Arabidopsis thaliana
C;Species: Arabidopais thaliana (mouse-ear cress)
C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
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39.4%; Score 46.5; DB 2;
Best Local Similarity 47.4%; Pred. No. 2.6;
Matches 9; Conservative 5; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 47; DB 2;
Pred. No. 13;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Interons: 44/1; 150/3; 359/3
A;Note: F9D12.9
C;Superfamily: glucose transport protein
C;Keyworfas: sugar transport; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 YNIVLL-LNTFOEFFGLNN 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Map position: 4
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$3376
muscarinic acetylcholine receptor m4 - mouse

C;Species: Mus musculus (house mouse)
C;Date: 08-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 24-Nov-1999
C;Accession: 33776; 33135
R;van Koppen, C.J.; Lenz, W.; Nathanson, N.M.
Biochim. Biophys. Acta 1173; 342-344, 1993
A;Title: Isolation, sequence and functional expression of the mouse m4 muscarinic acetyl
A;Reference number: S33776; MUID:93305731; PMID:7916637
A;Accession: S33776
A;Molecule type: DNA
A;Residues: 1-479 «KOP>
A;Cross-references: EMBL:X63473; NID:9296913; PIDN:CAA45071.1; PID:9296914
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphc
C;Superfamily: transmembrane #status predicted <TM1>
F;06-127/Domain: transmembrane #status predicted <TM2>
F;106-127/Domain: transmembrane #status predicted <TM3>
F;147-170/Domain: transmembrane #status predicted <TM5>
F;140-422/Domain: transmembrane #status predicted <TM5>
F;434-455/Domain: transmembrane #status predicted <TM5>
F;434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-479 < PER
A; Residues: 1-479 < PER
A; Residues: 1-479 < PER
A; Cross-rences. In In In Interpreted to the property of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   muscarinic acetylcholine receptor M3 - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 24-Nov-1999
C;Accession: 510127
R;Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.
EMBO J. 6, 3923-3929, 1987
A;Title: Distinct primary structures, ligand-binding properties and tissue-specific expr
A;Reference number: S04326; MUD:88166632; PMID:3443095
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Pred. No. 13;
4; Mismatches 0; Indels
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Pred. No. 13;
4; Mismatches 0; Indels
                                                           Indels
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Pred. No. 12;
4; Mismatches
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           63.68;
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Matches 7; Conservative
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Best Local Similarity 63.0.
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415 PYNVMVLVNTF 425
           Best Local Similarity 63.6
Matches 7; Conservative
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415 PYNVMVLVNTF 425
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414 PYNVMVLVNTF 424
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Genomics 18, 175-184, 1993

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1 APYNIVLLLNTFQ------
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25.6%;
                                                                                                                                                                                                                                                                                                                                           Query Match 39.0%;
Best Local Similarity 25.6%;
Matches 11; Conservative
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66.7%;
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Best Local Similarity 66.7*
Then 8; Conservative
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Best Local Similarity 25.6
Matches 11; Conservative
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iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Acetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekfyqueh, J.; Sakowska, A.; Seronakachi, M.; Tamakoshi, A.; Tanaka, T.; Tanaka, T.; Tosato, Y.; Uchiyama, A.; Authors: Yoshikawa, H.; Zamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A.; Authors: Yoshikawa, H.; Zumanetein, E.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Uchiyama, A.; Reference number: A69580; MulD:98044033; PMID:9384377
A.; Reference number: A69580; MulD:98044033; PMID:9384377
A.; Residues: L. 216 ckuy.
A.; Molecule type: DNA
A.; Mesidues: L. 216 ckuy.
A.; Resperimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            macrophage inflammatory protein-1 alpha receptor - mouse
C;Species: Mus musculus (house mouse)
C;Species: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: 149339
R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemoki
A;Reference number: 149339; MUID:95340546; PMID:7542241
A;Accession: 149339
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NyAlternate names: interleukin-8 receptor homolog; muBLR1 protein

Systeides: Mus musculus (house mouse)

Cyspecies: Mus musculus (house mouse)

Cyspecies: O7-Sep-1994 #sequence_revision 26-May-1995 #text_change 21-Jul-2000

CyAccession: S42628; C48809

Rikaiser, E.; Foerster, R.; Wolf, I.; Ebensperger, C.; Kuehl, W.M.; Lipp, M.

Bur J. Immunol. 23, 2532-2539, 1993

A;Title: The G protein-coupled receptor BLR1 is involved in murine B cell differentiatic

A;Reference number: S42628; MJID:9409211; PMID:8405054
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A;Cross-references: EMBL:X71788; NID:g2598563; PIDN:CAA50673.1; PID:g433947
R;Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Woore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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A,Residues: 1-355 <RES>
A,Cross-references: EMBL:U28404; NID:g881547; PIDN:AAAB9153.1; PID:g881548
C,Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.0%; Score 46; DB 2; Length 216; larity 64.7%; Pred. No. 8; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 39.0%; Score 46; DB 2; Best Local Similarity 35.0%; Pred. No. 13; Matches 7; Conservative 5; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: glnM
C,Superfamily: histidine permease protein M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 PYNLSVFVSAFQDVLFTNQC 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 PYNIVLLINTFQEFFGLNNC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIPLLITFVFYFGLPN 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 NIVLLLATFOEFFGLAN 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 35
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A,Title: Identification, chromosomal location, and genome organization of mammalian G-promaterence number: A48909, MUID:94116980, PMID:8288218
A,Accession: C48909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 36
$32785
Give the coupled receptor - rat
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cipate: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 24-Nov-1999
CiAccession: 332783 #sequence_revision 10-Nov-1995 #text_change 24-Nov-1999
Rikouba, M.; Vanetti, M.; Wang, X.; Schaefer, M.; Hoellt, V.
A; Kouba, M.; Vanetti, M.; Wang, X.; Schaefer, M.; Hoellt, V.
A; Kouse Cioning of a novel putative G-protein-coupled receptor (NLR) which is expressed A; Reference number: $32785; MUID:91238948; PMID:8386678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-374 < KOU>
A;Cross-references: 03:X71463; GB:S59748; NID:g599926; PIDN:CRA50582.1; PID:g599927
C;Superfamily: vertebrate-rhodopsin
C;Superfamily: vertebrate-rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F28A12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T28952
R;Sammons, L.; Murray, J.
R;Sammons, L.; Murray, J.
B;Sammons, L.; Murray, J.
B;Description: The sequence of C. elegans cosmid F28A12.
A;Reference number: 220547
A;Reference number: 220547
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Refidues: 1-613 cSAM>
A;Residues: 1-613 cSAM>
A;Cross-references: EMBL:U64851; PIDN:AAC47987.1; GSPDB:GN00023; CESP:F28A12.1
A;Experimental source: strain Bristol N2; clone F28A12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Nap position: 5
A,Introns: 41/1; 92/3; 159/1; 302/3; 358/1; 382/1; 433/2; 464/1; 512/3; 567/3
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                               A Status: preliminary; nucleic acid sequence not shown
A; Molecule type: mRNA
A; Molecule type: mLNA
A; Residues: 151-269 × MLL>
A; Cross-references: GB: 1220312; NID: 9438798; PIDN: AAA16852.1; PID: 9438799
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                           22;
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                                                                                                                                                                                                                                                                                                                                        Score 46; DB 2; Length 374; Pred. No. 14; 6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :||:||: ||: ||: || :| 275 SPYHIVIFLDTLERLKAVNSSCELSGYLSVAITLCEFLGLAHC 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .-----EFFGLNNC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----EFFGLNNC 21
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Pred. No. 14;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 46; DB 2;
Pred. No. 23;
2; Mismatches
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.; ;

Gaps

7

Length 354; 4; Indels

Score 45; DB 2; Pred. No. 19; 1; Mismatches

4'59 ILNTFNKIFGLN 470

g

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-354 <RES>
A;Cross-references: EMBL:U04808; NID:g2558635; PIDN:AAB87093.1; PID:g439861
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: September 28, 2004, 09:07:10 Job time : 13.075 secs
                                                                                                                                                                                                                                                                                                                                                                                                  247 PYNIVIFLETLKFYNFF 263
                                                                                                                                                                                                                                                                                                                                            2 PYNIVLLLNT--FQEFF 16
                                                                                                                                                                                                                    Match 38.1%;
Local Similarity 58.8%;
les 10; Conservative
                                                                                                                                                                                                                       Query Match
Best Local S:
Matches 10
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                                                                           RESULT 38

DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - spinach chloroplast

Cispecies: chloroplast Spinacia oleracea (spinach)

Cispecies: 15-bec-1988 #sequence_revision 15-bec-1988 #text_change 18-Jun-1999

CiAccession: C29959

R;Hudson, G.S.; Holton, T.A.; Whitfeld, P.R.; Bottomley, W.

A; Mol. Biol. 200, 639-654, 1988

A; Title: Spinach chloroplast rpoBC genes encode three subunits of the chloroplast RNA pc

A; Reference number: A29959; MUID:88316931; PMID:3045324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Harrison, J.K.; Barber, C.M.; Lynch, K.R.
Neurosci. Lett. 169, 85-89, 1994
A;Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and A;Reference number: 158186; MUD:94323113; PMID:8047298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein C04E6.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-061-1999 #sequence_revision 15-0c1-1999 #text_change 02-Jun-2000
C;Accession: T25510
R;Bentley, D.; Gattung, S.
Submitted to the EMBL Data Library, April 1997
A;Description: The sequence of C. elegans cosmid C04E6.
A;Reference number: 22043
A;Reference number: 22043
A;Reference number: 22043
A;Accession: T25510
A;Residues: 1-312 <BEN>
A;Greatus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-312 <BEN>
A;Gross-references: EMBL:U97012; PIDN:AAB52330.1; GSPDB:GN00023; CESP:C04E6.10
A;Reperimental source: strain Bristol N2; clone C04E6
C;Genetics:
A;Genetics:
A;Genetics:
A;Map position: 5
A;Introns: 68/2; 97/2; 148/3; 241/3; 263/1
C;Superfamily: Caenorhabditis hypothetical protein C49G7.2
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
C;Accession: IS8186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                            A/Accession: C29959
A/Molecule type: DNA
A/Residues: 1-1070 cHUD>
A/Fesidues: 1-1070 cHUD>
A/Cross-references: GB:MS5297; NID:g295119; PIDN:AAA84637.1; PID:g295121
C/Genetics:
A/Gene: rpoB
A/Gene: chloroplast
C/Superfamily: DNA-directed RNA polymerase beta chain
C/Keywords: chloroplast; nucleotidyltransferase; transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ب.
د
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 38.6%; Score 45.5; DB 2; Length 1070; 1 Similarity 45.8%; Pred. No. 50; 11; Conservative 3; Mismatches 7; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138.1%; Score 45; DB 2; Length 312; llarity 44.4%; Pred. No. 17; Conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          352 PQNLVTSTPLTTTFESFFGLHPLS 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 PYNIVL --- LLNTFQEFFGLNNCS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 IVLLINIFOEFFGLNNCS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 8; Conserv
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Best Local S
Matches 8
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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: September 28, 2004, 08:55:11; Search time 6.875 Seconds

(without alignments)

166.624 Million cell updates/sec

Perfect score: 118
Sequence: 1 APYNIVLLINTFOEFFGINNCS 22
```

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Listing first 45 summaries

141681 segs, 52070155 residues

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

P56492 cercopithec P56483 macaca mula P56483 macaca mula P56482 macaca mula 028255 archaeoglob P51678 mus musculu P30544 xenopus lae Q9erz3 mus musculu P08483 rattus norv P41984 bos taurus Q9n2a3 gorilla gor P20309 homo sapien
CKR3 CERAE CKR3 MACMU CKR1 MACMU ACM4 CHICK H182 ACCFU CKR3 MOUSE ACM3 MOUSE ACM3 DAT ACM3 GORGO ACM3 GORGO ACM3 GORGO
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444444444444 WWWG0000000 
512 100 100 100 100 100 100 100 100 100 1
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## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CKR5_CERTO STANDARD;
062743, 062744; 062745; 062746;
15-DEC-1998 [Rel. 37, Created)
15-DEC-1998 [Rel. 37, Last sequence update)
16-DEC-1998 [Rel. 37, Last sequence update)
16-OCT-2001 [Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
CCR5 OR CMMBRS.
   PRINTS; FROUZA; GFCARROCOUR.

PROSITE; PSO0223; G_PROTEIN RECEP_F1_1; 1.

PROSITE; PSO0262; G_PROTEIN RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

DOMAIN

1 30

EXTRACELULAR (POTENTIAL).

TRANSMEM 31 58 1 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                   6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                         SULFATION (BY SIMILARITY)
SULFATION (BY SIMILARITY)
SULFATION (BY SIMILARITY)
                                                                                                                                                                                     4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                  2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                               EF17D67CBCCC3DB0 CRC64;
                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                     3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 118; DB 1;
Pred. No. 4.7e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                 40558 MW;
GPCRRHODOPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                100.08;
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                                                                                                                                                                                                                                                                                                                                                                                               352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sest Local Similarity
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Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;
Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;
Mutations in CRS-coding sequences are not associated with SIV
carrier status in African nonhuman primates.",
AIDS Res. Hum. Retroviruses 15:931-939(1999).
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and cubsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IS-WAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCRS)
CCRS OR CWKBRS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cercopithecus pygerythrus (Vervet monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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                                                                                                                                                                                                                                                                                                                                                                               Length 352;
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CYTOPLASMIC (POTENTIAL).
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SULFATION (BY SIMILARITY).
                  CYTOPLASMIC (POTENTIAL).

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2 YRACELLULAR (POTENTIAL).

3 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
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                                                                                                           4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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Pred. No. 4.7e-11;
; Mismatches 0;
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                                                                                                     (POTENTIAL)
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                                                              40561 MW;
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CKR5_CERPY
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increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.

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MEDLINE=97268667; PubMed=9108095;

Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;

"Differential utilization of CCR5 by macrophage and T cell tropic
simian immunodeficiency virus strains.";

Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).

-: FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANIES and subsequently transduces a signal by
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EMBL; AF051902; AAC39830.1; -.
EMBL; AF051904; AAC39831.1; -.
EMBL; AF051904; AAC39831.1; -.
EMBL; AF051904; AAC39831.1; -.
InterPro; IPR00076; GPCR_Rhodpsn.
Pfam: PF00001; 7tm 1; 1.
PROSITE; PR00237; GPRATBIN RECEP F1 1; 1.
PROSITE; PS00237; GPROTEIN_RECEP_P1 2; 1.
PROSITE; PS00237; GPROTEIN_RECEP_P1 2; 1.
PROSITE; PS00240; GPROTEIN_RECEP_P1 3; 1.
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CRR-5) (CC-CKR-5) (CCR5).
CCR5 OR CMCRR5.
GOTILL gorilla gorilla (Lowland gorilla).
Bukaryota; Metazoa; Choqata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
NCBI_TAXID=9595;
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SULFATION (BY SIMILARITY).

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Y -> G (IN ISOLATE 087).

N -> G (IN ISOLATE 079).

L -> V (IN ISOLATE 079).

L -> V (IN ISOLATE 079).

Y -> G (IN ISOLATE 079).

Y -> I (IN ISOLATE 079).

Y -> I (IN ISOLATE 079).

Y -> I (IN ISOLATE 079).
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100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels
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EXTRACELULAR (POTENTIAL).

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EXTRACELLULAR (POTENTIAL).

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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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P51681; 014692; 014693; 014695; 014696; 014699; 014699; 014700; 014701; 014702; 014702; 014704; 014705; 014706; 014707; 014708; 015538; 0910A4.

01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last sequence update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR)
(HIV-1 fusion co-receptor) (CHEMR13) (CD195 antigen).
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CCR5 OR CMKBR5.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=96241590; PubMed=8639485;
Samson M., Labbe O., Mollereau C., Vassart G., Parmentier M.;
"Molecular cloning and functional expression of a new human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 100.0%; Score 118; DB 1; Length 352; Local Similarity 100.0%; Pred. No. 4.7e-11; es 22; Conservative 0; Mismatches 0; Indels
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CKRS_HUMAN
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"Majort C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F.; "Molecular cloning and functional characterization of a novel human CC chemokine receptor (CCR5) for RANTES, MIP-lbeta, and MIP-lalpha."; J. Biol. Chem. 271:17161-17166(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-38049523; PubMed-9388201;
Mummidi S., Ahuja S.K.;
Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;
Mummidi S., Chemokine Ecceptor 5 (CCR5) gene. Multiple transcripts with buman CC chemokinity, dual promoter usage, and evidence for polymorphisms within the regulatory regions and noncoding exons.";
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SEQUENCE FROM N.A.
MEDLINE=98001387; PubMed=9343222;
Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.;
Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.;
"Polymorphisms in the CCR5 genes of African green monkeys and mice implicate specific amino acids in infections by simian and human immunodeficiency viruses.";
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MEDLINE=98022612; PubMed=9359654;
Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism."; AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
                                                                                                                                                                                                                                                                                                                                                                                            Ϋ́.,
                                                                                                                                                                                                                         MEDILINE-96295970; PubMed-8699119; Combadiere C., Ahuja S.K., Tiffany H.L., Murphy P.M.; Combadiere C., Ahuja S.K., Tiffany H.L., Murphy P.M.; "Cloning and functional expression of CC CKR5, a human monocyte chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Σ.
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MEDLINE=96260017; PubMed=8649511;
Deng H., Liu R., Ellmeier W., Choe S., Unutmaz D., Burkhart M.,
di Marzio P., Marmon S., Sutton R.E., Hill C.M., Davis C.B.,
Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;
"Identification of a major co-receptor for primary isolates of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kopatz S.A., Aronstam R.S., Sharma S.V.; sincipal transduction "cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie CDNA resource center (www.cdna.org)."; submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                        McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson I Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E., Solinnsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D., Sagripanti J.L.; Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND VARIANT ARG-178.
Magierowska M., Barre-Sinoussi F., Issafras H., Theodorou I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chem. 272:30662-30671 (1997)
                                                                                                                                                                                                                                                                                                                               J. Leukoc. Biol. 60:147-152(1996).
                                                               SEQUENCE FROM N.A.
MEDLINE=96291862; PubMed=8663314;
    CC-chemokine receptor gene.";
Biochemistry 35:3362-3367(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Virol. 71:8642-8656(1997).
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SEQUENCE FROM N.A.
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Nagashima K.A., Cayanan C., Nadadon P.J., Koup R.A., Moore J.P.,
Nagashima K.A., Cayanan C., Nadadon P.J., Koup R.A., Moore J.P.,
Nagashima K.A., Cayanan C., Nadadon P.J., Koup R.A., Moore J.P.,
Nagashima K.A., Cayanan C., Nadadon P.J., Koup R.A., Moore J.P.,
Nagashima K.A., Cayanan C., Nadadon P.J., Koup R.A., Moore J.P.,
Nagashima K.A., Cayanan C., Nadadon P.J., Koup R.A., Moore J.P.,
Nagashima K.A., Cayanan C., Nadadon M.,
Nagashima K.A., Machanako T. Gadonki J.P., Watt R., Cayabyab M.,
Nagashima K., Nagashako T. Gadonki J.P., Watt R., Cayabyab M.,
Nagashima K., Nagashako T. Gadonki J.P., Watt R., Cayabyab M.,
Nagashima K., Nagashako T. Gadonki J.P., Watt R., Cayabyab M.,
Nagashima K., Nagashako T. Gadonki J. Galonki J. Galo
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the European Bioinformatics Institute. There are no restrictions on its
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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SULFATION (BY SIMILARITY)
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352 AA;
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EMBL; AF011533; AAB65733.1; -.

BRML; AF011535; AAB65733.1; -.

BRML; AF011536; AAB65735.1; -.

BRML; AF011536; AAB65735.1; -.

BRML; AF011536; AAB65735.1; -.

BRML; AF011537; AAB65737.1; -.

BRMC; GO:0005887; Cintegral to plasma membrane; TAS.

GO; GO:00016493; F:C-C chemokin activity; TAS.

GO; GO:0001505; F:C-C chemokin activity; TAS.

GO; GO:0007267; F:C-Ell-call signaling; TAS.

GO; GO:0007267; F:C-Ell-call signaling; TAS.

GO; GO:0007186; P:C-Protein coupled receptor protein signalin. .; TAS.

GO; GO:0007186; P:C-Protein coupled receptor protein signalin. .; TAS.

GO; GO:0007186; P:C-Protein coupled receptor protein signalin. .; TAS.

GO; GO:0007186; P:C-Protein coupled receptor protein; Sulfation;

FRML; PROGOZ1; GPROTEIN RECEP FIL; 1.

BROSITE; PSC5262; GPROTEIN RECEP FIL; 1.

BROSITE; PSC5262; GPROTEIN RECEP FIL; 1.

BROSITE; PSC5262; GPROTEIN RECEP FIL; 1.

BROWATN ATN.
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MEDLINE=99416438; PubMed=10486970;

MEDLINE=99416438; PubMed=10486970;

Mang Y.-W., Ryder O.A., Zhang Y.-P.;

"Sequence evolution of the CCR5 chemokine receptor gene in primates.";

Mol. Balol. Bvol. 16:1145-1154 (1999).

-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

MIP-1-beta and RANTES and subsequently transduces a signal by

increasing the intracellular calcium ions level. May play a role

in the control of granulocytic lineage proliferation or
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-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5)
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Wakaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hylobatidae; Hylobates.
YCBI_TaxID=61853;
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLUAR (POTENTIAL).
3 (POTENTIAL).
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CKR5_HYLLE
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Gaps

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AmbDLINES-99416436; PubMed=10486970;

Zhang Y.-W., Ryder O.A., Zhang Y.-P.;

Sequence evolution of the CCRS chemokine receptor gene in primates.";

Mol. Biol. Evol. 16:1145-1154(1999).

-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

MIP-1-beta and RANTES and subsequently transduces a signal by

increasing the intracellular calcium ions level. May play a role

in the control of granulocytic lineage proliferation or

differentiation. 15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last and cation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) -1- SUBCELLUIAR LOCATION: Integral membrane protein. -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors. Hylobaras moloch (Silvery gibbon).

Hylobarata; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates. 

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MEDLINE=97184592; PubMed=9032394; Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L., Newman W., Gerard N., Gerard C., Sodroski J.; The envelope "Utilization of C-C chemokine receptor 5 by the envelope glycoproteins of a pathogenic simian immunodeficiency virus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=M mulatta; STRAIN=Indian macaque;
MEDLINE=97213934; PubMed=9060623;
Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
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352 AA;
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Sequence evolution of the CCPS chemokine receptor gene in primates.";
Mol. Biol. Evol. 16:1145-1154(1999).
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium fons level. May play a role
in the control of granulocytic lineage proliferation or
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99NG5;
15-WAR-2004 (Rel. 43, Created)
15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5)
CCR5 OR CWKBR5.
                                                                                                                     EMBL; AF177899; AAK43382.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
PRAMPERS; PR00017; Trm_1; 1.
PROSITE; PS00237; GPCREHOOPSN.
PROSITE; PS05237; G_PROTEIN_RECEP_F1_1; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
DOMAIN.

EXTRACELULAR (POTENTIAL).
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-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Hylobatidae, Hylobates.
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CYTOPLAGNIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).

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Local Similarity 100.0%;
es 22; Conservative 0
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352 AA;
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CKR5_HYLSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCRS_MACMU STANDARD; PRT; 352 AA.

CCRS_MACMU STANDARD; PRT; 352 AA.

01-NOV-1997 (Rel. 35, Created)

01-NOV-1997 (Rel. 35, Last sequence update)

26-FBB-2003 (Rel. 41, Last annotation update)

26-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).

CCR5 OR CMKBR5.
                                                                                                                                      EMBL; AF177884; AAK43367.1; -.
InterPro; IPR00276; GPCR_Rhodpsn.
PRIMTS; PR00217; Tru_1; 1.
PRIMTS; PR00237; GPCRFHOOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
Macaca nemestrina (Pig-tailed macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          madaca ummestrina (rigy-distante macque).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0%; Score 118; DB 1; Length 352; 0%; Pred. No. 4.7e-11; 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                            1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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SULFATION (BY SIMILARITY)
SULFATION (BY SIMILARITY)
F4F64B3AD5AF65BA CRC64;
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
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ilarity 100.0%;
Conservative 0
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NCBI_TaxID=9544, 9541, 9545;
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Genetically divergent strains of simian immunodeficiency virus use CRS as a coreceptor for entry."; J. Virol. 71:2705-2714(1997).

DECENTABLE AND MACHES COLLETIS, and M. Nemestrina,
SPECIES M. M. Lascicularis, and M. Nemestrina,
MEDLINE 97268687; PubMed=9108095,
MEDLINE 97268687; PubMed=9108095,
Bedinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
Peiper S.C., Natlal utilization of CRSs by macrophage and T cell tropic
simian immunodeficiency virus strains.";
Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997)
- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or SPECIES=M.mulatta; MEDLINE=21354176; PubMed=11461684; Margulies B.J., Hauer D.A., Clements J.E.; "Identification and comparison of eleven rhesus macaque chemokine AIDS Res. Hum. Retroviruses 17:981-986 (2001) SEQUENCE FROM N.A. receptors." 

differentiation. SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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EMBL; U96762; AAC34132.1; -.
EMBL; AF005660; AAB62554.1; -.
EMBL; AF005661; AAB62555.1; -.
EMBL; AF005662; AAB62555.1; -.
InterPro; IPR000276; GPCR\_Rhodpsn.
Pfan; PF00001; 7tm 1; 1.
PROSITE; PS00237; GPCRHODPSN.
PROSITE; PS00237; GPCRHODPSN.
PROSITE; PS50262; G PROTEIN RECEP\_F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP\_F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation. EMBL, U77672; AACS1109.1; -. EMBL, U73739; AACS1158.1; -. EMBL; U96762; AAC34132.1; -.

TRANSMEM DOMAIN TRANSMEM

1 (POTENTIAL). CYTOPLASMIC (POTENTIAL). 2 (POTENTIAL). EXTRACELLULAR (POTENTIAL) 4 (POTENTIAL). EXTRACELLULAR (POTENTIAL) 5 (POTENTIAL). CYTOPLASMIC (POTENTIAL). 3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL). 6 (POTENTIAL) 301 352 178 DOMAIN TRANSMEM DOMAIN TRANSMEM FRANSMEM FRANSMEM **TRANSMEM** DOMAIN DOMAIN DOMAIN

(GLCNAC. . .) (POTENTIAL) 6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

BY SIMILARITY.

SULFATION (BY SIMILARITY).

SULFATION (BY SIMILARITY).

SULFATION (BY SIMILARITY).

SULFATION (BY SIMILARITY). 58B96C85909FACB2 CRC64; -> I (IN REF. 3) -> M (IN REF. 3) SULFATION SULFATION SULFATION N-LINKED (C M -> I (IN I -> M (IN 40507 MW; 241 292 352 AA; DOMAIN DISULFID CARBOHYD CONFLICT CONFLICT SEQUENCE RES RES

Gaps ö Length 352; Indels Query Match 100.0%; Score 118; DB 1; Best Local Similarity 100.0%; Pred. No. 4.7e-11; Matches 22; Conservative 0; Mismatches 0;

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RESULT 10

352 AA. PRT; STANDARD; PANTR

15-470, 002778; 15-471-1998 (Rel. 36, Created) 15-471-1998 (Rel. 36, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).

CCRS OR CMKERS.

CCRS OR CMKERS.

Pan troglodytes (Chimpanzee).

Eukaryota, Metazoa, Chordata; Craniata, Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primatee; Catarrhini; Hominidae; Pan.

SEQUENCE FROM N.A.

MEDDLINE=97268697. PubMed=9108095;

Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,

Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,

Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;

Pipfferential utilization of CCR5 by macrophage and T cell tropic

simian immunodeficiency virus strains.";

Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).

SEQUENCE FROM N.A.

Zimmerman P.A., Buckler-White A., Alkhatib G.,
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.

Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B., SEQUENCE FROM N.A. MEDLINE=98022612; PubMed=9359654; HO D.D.,

"HIV type 1 subtypes, coreceptor usage, and CCRS polymorphism."; AIDS Res. Hum. Retroviruses 13:1357-1366(1997). 

SEQUENCE FROM N.A.
MEDLINE-97426118; PubMed=9282822;
Zacharova V., Zachar V., Goustin A.S.;
"Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
HIV type 1 host.";

SEQUENCE FROM N.A.

AIDS Res. Hum. Retroviruses 13:1159-1161(1997).

MEDLINE=98090115; PubMed=9430250; Guillet J.-G., Butor C.; Pretet J.-L., Zerbib A., Girad M., Guillet J.-G., Butor C.; Chimpanze CKR4 and CKBs act as coreceptors for HIV type 1."; AIDS Res. Hum. Retroviruses 13:1583-1587

9

SEQUENCE FROM N.A. Zhang Y.; Zhang Y.; Sequence comparison of the CCR5 gene in primates and primate

phylogeny.";
Submitted (MUG-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (MUG-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or differentiation.

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9-1 1

Tue Sep 28 15:49:58 2004

MOD\_RES CARBOHYD

1 APYNIVLLINTFQEFFGLNNCS 22

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Matches
                                                                MEDLINE=97268687; PubMed=9108095;
Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
                                     SPECIES=P.hamadryas;
SEQUENCE FROM N.A.
```

nonhuman primates." SEQUENCE FROM N.A. use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch) ö EMBL; U89797; AAC03777.1; -.
EMBL; AF177894; AAK43377.1; -.
EMBL; AF177894; AAK43377.1; -.
EMBL; AF177894; AAK43377.1; -.
EMBL; AF177894; AAK43377.1; -.
PLINTERPROPOUGL; GPCRHODOPSN.
PROSITE; PS00237; GPCRHODOPSN.
PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.
PROSITE; PS0262; GPROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
DOMAIN

1 30 EXTRACELLULAR (POTENTIAL). SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL). ô Score 118; DB 1; Length 352; Pred. No. 4.7e-11; 0; Indels 5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY. 1 (POTENTIAL). CYTOPLASMIC (POTENTIAL). 2 (POTENTIAL). EXTRACELLULAR (POTENTIAL) -> S (IN REF. 1). 4A33E698B80FE34C CRC64; 4 (POTENTIAL). EXTRACELLULAR (POTENTIAL) 3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL). 0; Mismatches EMBL, U94329; AAB58446.1; -.
EMBL, AF0111542; AAB65742.1; -.
EMBL, U97666; AAC51670.1; -.
EMBL, AF011540; AAB65740.1; -. EMBL; AF005663; AAB62557.1; -. 40539 MW; 100.0%; 100.08; 22; Conservative 352 AA; Similarity DOMAIN TRANSMEM DOMAIN TRANSMEM TRANSMEM DOMAIN TRANSMEM *FRANSMEM* DISULFID SEQUENCE Query Match TRANSMEM TRANSMEM MOD\_RES MOD\_RES MOD\_RES MOD\_RES CARBOHYD Local DOMAIN DOMAIN DOMAIN Matches

Gaps

RESULT 11

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15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
16-COT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CRR-5) (CC-CRR-5) (CCRS OR CWKBRS. Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae, PRT; 352 AA. Papio hamadryas (Hamadryas baboon), and Papio anubis (Olive baboon). STANDARD; Cercopithecinae; Papio. NCBI\_TaxID=9557, 9555; PAPHA CKRS PA P56441; CKRS\_PAPHA PALD DE LA PALD DE LA

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Shearer M.H., Lee D.R., Kennedy R.C.;
Submitted (NOV-1997) to the Emal/Genbank/DDBJ databases.
-!-FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
-!- SUBCELLULAR LOCATION: Integral membrane protein. SEQUENCE FROM N.A.
SPECIES-P, handstyses,
REDLINE-99210133; PubMed=10195758;
Sakeena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.;
"Species-specific changes in the CCR5 gene from African and Asian EMBL; AF023452; AACOSOSTO, GPCR\_Rhodpsn.
Pfam; PF00001; 7tm 1, 1.
PRINGS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; GPROTEIN RECEP\_F1\_1; 1.
PROSITE; PS50262; GPROTEIN\_RECEP\_F1\_2; 1. "Differential utilization of CCR5 by macrophage and T cell tropic simian immunodeficiency virus strains."; Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997). 1 (POTENTIAL). CYTOPLASMIC (POTENTIAL). 2 (POTENTIAL). EXTRACELLULAR (POTENTIAL) 4 (POTENTIAL). EXTRACELLULAR (POTENTIAL) 5 (POTENTIAL). 6 (POTENTIAL). EXTRACELLULAR (POTENTIAL) 3 (POTENTIAL). CYTOPLASMIC (POTENTIAL). S (POTENTIAL). CYTOPLASMIC (POTENTIAL). 7 (POTENTIAL). CYTOPLASMIC (POTENTIAL). BY SIMILARITY. AIDS Res. Hum. Retroviruses 15:479-483(1999). EMBL; AF105287; AAD20556.1; -. EMBL; AF105289; AAD20557.1; -. EMBL; AF105289; AAD20558.1; -. EMBL; AF105290; AAD20559.1; -. DOMAIN TRANSMEM DOMAIN DOMAIN TRANSMEM DOMAIN TRANSMEM DOMAIN FRANSMEM RANSMEM DISULFID 'RANSMEM RES RES DOMAIN DOMAIN 

SULFATION (BY SIMILARITY)
SULFATION (BY SIMILARITY)
SULFATION (BY SIMILARITY)
SULFATION (BY SIMILARITY) N-LINKED (GLCNAC

Gaps SEISO4A9BAIFE8B2 CRC64; ; 0 100.0%; Score 118; DB 1; Length 352; 100.0%; Pred. No. 4.7e-11; vative 0; Mismatches 0; Indels 40489 MW; 268 ; 352 AA; Query Match Best Local Similarity SEQUENCE

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                                                                                                                                                                                                                                       MEDLINE=99416438; PubMed=10486970;
MEDLINE=99416438; PubMed=10486970;
Zhang Y.-W., Zhang Y.-P.;
Zhang Y.-V., Xyder O.A., Zhang Y.-P.;
Sequence evolution of the CCR5 chemokine receptor gene in primates.";
Mol. Biol. Evol. 16:1145-1154(1999).
-! FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
-! FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and bubsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AF075446; AAD19858.1; -.
InterPro; IFN000276; GPCR Rhodpsn.
PROMO01; Trm 1; 1.
PRINTS; PRO0237; GPCRRHODOPSN.
PROSITE; PS02237; GPROTEIN RECEP F1 1; 1.
PROSITE; PS02262; GPROTEIN RECEP F1 2; 1.
DOWAIN

TRANSMEM 31 58 I (POTENTIAL).
                                                           30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
28-FSB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5)
CCR5 OR OWGRS.
                                                                                                                                                                                                                                                                                                                                                                                                   differentiation.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                    Pongo pygmaeus (Orangutan).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pongo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

7 (POTENTIAL).

SYNTARCELLULAR (POTENTIAL).

SYNTARICH (POTENTIAL).
                               352 AA
                               PRT;
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                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10
14
15
352 AA;
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                               CKR5 PONPY 097881;
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TRANSMEM
              CKR5_PONPY
RESULT
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Gaps ö Score 118; DB 1; Length 352; Pred. No. 4.7e-11; Mismatches 0; Indels C 1 APYNIVLLINTFQEFFGLNNCS 22 . 0 100.0%; Query Match 100. Best Local Similarity 100. Matches 22; Conservative

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249 APYNIVLLINTFQEFFGLNNCS 270

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or send an email to ...

or send a
                                                                                                                                                                                                                                                                                                                                               MEDINE=99416438; PubMed=10486970;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Sequence evolution of the CCRS chemokine receptor gene in primates.";
MOD. Biol. Evol. 16:1145-1154(1999).
-I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
                                                                                                                                                                                           CCR5 OR CMKBR5.
Pygathix biezi Black Bub-nosed monkey) (Rhinopithecus bieti).
Pygathix betaio (Brordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine_receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CYTOPLASMIC (POTENTIAL).
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SULFATION (BY SIMILARITY).
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W, 4366F142730F938F CRC64;
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                            352 AA.
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Best Local Similarity 100.
Matches 22; Conservative
                                              STANDARD;
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                                         CKR5 PYGBI
097880;
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352 AA;
                               NCBI_TaxID=54133;
         CKR5 PYGNE 097882;
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Pfam; PRO0001; 7tm 1; 1.

PRINTS; PRO0237; G_PROTEIN REGEP F1 1; 1.

PROSITE; PS00262; G_PROTEIN_REGEP F1 2; 1.

AN G-procein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

PT CANSMEM 31 58 (POTENTIAL).

FT TRANSMEM 31 58 (CYPOLASNIC (POTENTIAL).

FT DOMAIN 59 68 (CYPOLASNIC (POTENTIAL).

FT CANSMEM 69 82 (POTENTIAL).

FT CANSMEM 69 68 (CYPOLASNIC).

FT CANSMEM 69 68 (CYPOLASNIC).

FT CANSMEM 69 68 (CYPOLASNIC).

FT CANSMEM 69 68 (CYPOLASNIC).
                                                                                                                                                                                                                                                                                                                    MEDLINE=99416438; PubMed=10486970;
ARDLINE=99416438; PubMed=10486970;
Alang Y.-W., Ryder O.A., Zhang Y.-P.;
Sequence evolution of the CCR5 chemokine receptor gene in primates.";
Mol. Biol. Evol. 16:1145-1154(1999).
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
                                                                                                                                                                                                                  Pygathrix nemaeus (Dove langur).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae, Colobinae,
Pygathrix.
                                                                                                                                     30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
38-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               differentiation.
SUBCELULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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FE4F9D9BD3B3E861 CRC64;
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1 Similarity 100.0%; Pred. No. 4.7e-11;
22; Conservative 0; Mismatches 0;
                                                                                                          352 AA.
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249 APYNIVLLINTFQEFFGLNNCS 270
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
"Sequence evolution of the CCR5 chemokine receptor gene in primates.";
Mol. Biol. Evol. 16:1145-1154(1999).
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
                                                                                                                                                                                                                                                                                                                                                       CCRS OR CMKBRS.
Trachypithecus francoisi (Francois' langur) (Indochinese langur).
Eukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
                                                                                                                                                                                                                                30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         differentiation.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0237; GFCRHODOPSN.
PROSITE; PS00237; G_PROTEIN RECEP_F1_2; 1.
PROSITE; PS50262; G_PROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
DOMAIN
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLUGAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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249 APYNIVLLINTFQEFFGLNNCS 270
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MEDLINE=99416438; PubMed=10486970;
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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Score 118; DB 1;
Pred. No. 4.7e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99416438; PubMed=10486970;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
"Sequence evolution of the CCR5 chemokine receptor gene in primates.";
Mol. Biol. Zvol. 16:1145-1154(1999)
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RAWIES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
                                                                                                                                                                                                                                                                                                                                                             Trachypithecus phayrei (Phayre's leaf monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae, Colobinae,
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EMBL; AF075443; AAD19855.1; -
INCLEPTO; IPR000275; GPCR_Rhodpsn.
PROSTITS; PR00237; GPCRRHODPSN.
PROSTITS; P800237; G_PROTEIN_RECRP_F1.1; 1.
PROSTITS; P850262; G_PROTEIN_RECRP_F1.2; 1.
G-protein coupled receptor; Transmem5rane; Glycoprotein; Sulfation.
                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
38-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCRS OR CMKBRS).
Trachypithecus phayrei (Phayre's leaf monkey).
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SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CYTOPLASMIC (F
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352 AA;
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Length 352;

Score 118; DB 1; Pred. No. 4.7e-11;

100.0%;

Best Local Similarity

Query Match

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Guo B., Kuno K., Harada A., Matsushima K.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RAYTES and subsequently transduces a signal by
increasing the intracellular calcium ions level.
-!- SUBCELULIAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
but not in nonhematopoietic cell lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chemoattractant protein 1) and murine macrophage inflammatory protein laipha receptors: evidence for two closely linked C-C chemokine receptors on chromosome 9.";
J. Biol. Chem. 271:7551-7558(1996).
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MEDLINE=97404635; PubMed=9261347;
Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H.,
Mang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.,
"Two distinct CCRS domains can mediate coreceptor usage by human
                                                                                                                                           CKR5_MOUSE STANDARD, PRT; 354 AA.
P51682; 035313; 035891; P97308; P97405; Q61867;
01-0CT-1996 (Rel. 34, Created)
15-UUL-1998 (Rel. 35, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CK-5) (MIP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tharo I.F.; Molecular cloning and functional expression of murine JE (monocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6, and NIH Swiss; TISSUE=Kidney, Liver, and Spleen; MEDLINE=98001387; PubMed=934322; Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.; Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.; Molymorphisms in the CCRS genes of African green monkeys and mice implicate specific amino acids in infections by simian and human immunodeficiency viruses."; J. Virol. 71:8642-8656(1997).
                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse),
Musaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-CSTBL/6 X. CBA; TISSUE=Thymus;

MEDIINE=96278910; PubMed=8662890;

Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;

Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;

Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;

Micloning and characterization of a novel murine macrophage
inflammatory protein-1 alpha receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boring L., Gosling J., Monteclaro F.S., Lusis A.J., Tsou C.-L.,
Charo I.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=129/Ola;
Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                           249 APYNIVLLLNTFOEFFGLNNCS 270
22
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=129/Svd; TISSUE=Spleen;
MEDLINE=96205938; PubMed=8631787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunodeficiency virus type 1.";
J. Virol. 71:6305-6314(1997).
  1 APYNIVLLINTFQEFFGLNNCS
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CCRS OR CMKBRS.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                            01-NOV-1997 (Rel. 35, Created)
1-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last amoutation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (MIP-1
                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Wistar; TISSUE-Brain;

BEDINES-89314064, Pubmed=9670089;

Spleiss O., Gourmala N. Boddeke H.W.G.M., Sauter A., Fiebich B.L.,
Berger M., Gebicke-Haerter P.J.;

Berger M., Gebicke-Haerter P.J.;

Eloning of rat HIV-1-chemokine coreceptor CKRS from microglia and
upregulation of its mRM in ischemic and endotoxinemic rat brain.";

J. Neurosci. Res. 53:16-28(1998).
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R EMBL; X12009; CAA12737.1; -.

R EMBL; V12009; CAA12737.1; -.

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3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                          NCBL_TaxID=10116;
                                                                                                                                                                 alpha receptor).
CCRS OR CMKBRS.
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                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation—the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                              EMBL; V047036; AACS2454.1; -

REMBL; X9411; CAA6386.1; -

REMBL; W08555; AAR37273.1; -

REMBL; U08327; AACS3386.1; -

REMBL; AF012972; AACS3389.1; -

REMBL; AF012972; AACS3389.1; -

REMBL; AF019772; AAAS1183.1; -

REMBL; AF019772; AAAS1183.1; -

REMBL; MG1:107182; CCr5.

ROJ GO:0016493; F:C-C chemokine receptor activity; IDA.

GO; GO:0016493; F:C-C chemokine receptor activity; IDA.

GO; GO:0016493; F:C-C chemokine receptor activity; IDA.

ROJ GO:
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   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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llarity 95.2%; Pred. No. 1.7e-09;
Conservative 0; Mismatches 1; Indels
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CYTOPLASMIC (POTENTIAL).
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Gaps ·. Score 105; DB 1; Length 354; Pred. No. 5.1e-09; 1; Mismatches 1; Indels 89.0%; Local Similarity 90.5 tes 19; Conservative Query Match Matches

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Length 360;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptors.";
AIDS Res. Hum. Retroviruses 17:981-986(2001).
-!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
Transduces a signal by increasing the intracellular calcium ions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF013958; AAD11572.1; -.
InterPro; IPR00276; GPCR_Rhodpsn.
PFROM; PR00237; GFCRRDODPSN.
PROSITE; PS0237; GFRRDEN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
AG_Protein coupled receptor; Transmembrane; Glycoprotein; Sulfation; Alternative splicing.
                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=A; ,
IsoId±018793-2; Sequence=Not described;
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE-1354176, PubMed=11461684,
Margulies B;J., Hauer D.A., Clements J.E.;
"Identification and comparison of eleven rhesus macaque chemokine
                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
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TYOPLANDER (POTENTIAL).
N-LINKED (GLUNAC. . .) (POTENTIAL).
SULPATION (BY SIMILARITY).
                                                                                                                                                                                                                                               (Monocyte chemoattractant protein 1 receptor) (MCP-1-R) CCR2 OR CMKBR2.
Macaca mulatta (Rhesus macaque).
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-!- ALTERNATIVE PRODUCTS:
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                                                                                                                                          360 AA
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Isold=D18793-1; Sequence=Displayed;
                                    252 PYNIVLLITFQEYFGLNNCS 272
             PYNIVLLLNTFQEFFGLANCS
                                                                                                                                          STANDARD;
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SULFATION OF TYR-26, AND N-GLYCOSYLATION.
MEDLINE=20501139, PubMed=11046064;
Preobrazhensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V., Chakravarty L., Kolattukudy P.E.;
"Monocyte chemotactic protein-1 receptor CCR2B is a glycoprotein that has tyrosine sulfation in a conserved extracellular N-terminal region.";
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MEDILTE_9715084; PubMed=8995400;
MEDILTE_9715084; PubMed=8995400;
MODIL L. M., Myers S.J., Tsou C.-L., Gosling J., Arai H., Charo I.F.;
"Organization and differential expression of the human monocyte
chemoattractant protein I receptor gene. Evidence for the role of the
carboxyl-terminal tail in receptor trafficking.";
J. Biol. Chem. 272:1038-1045(1997).
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=94195811; PubMed=8146186; Charo I.F., Myers S.J., Herman A., Franci C., Connolly A.J., Charo I.F., Myers S.J., Herman A., Franci C., Connolly A.J., Coughlin S.R.; "Molecular cloning and functional expression of two monocyte chemoattractant protein I receptors reveals alternative splicing of the carboxyl-terminal tails."; Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (MCP-1-R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ozuna M., Kuldanek S.A.,
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Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz J
Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J.,
Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang P
Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,
Solinnsky R.A., Desilva U., Diarz-Perez S., Zhou X., Yu Y.,
Watanabe M., Doggett N., Garcia D., Sagripanti J.L.,
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94324942; PubMed=8048929; Yamaka H., Endo N.; Yamagani S., Tokuda Y., Ishil K., Tamaka H., Endo N.; Vanagani S., Tokuda Y., Ishil K., Tamaka H., Endo N.; CDM, cloning and functional expression of a human monocyte chemoattractant protein 1 receptor."; Blochem. Blophys. Res. Commun. 202:1156-1162 (1994).
Query Match 87.3%; Score 103; DB 1; Length 36
Best Local Similarity 90.0%; Pred. No. 1.1e-08;
Matches 18; Conservative 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                             258 PYNIVILLNTFQEFFGLSNC 277
                                                                                                                                                                  2 PYNIVLLINTFORFFGLNNC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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macrophages.
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CKR2_RAT
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MIM; 601267; -.

MIM; 601267; -.

MIM; 601267; C: integral to plasma membrane; TAS.

GO; GO:0005867; C:soluble fraction; TAS.

GO; GO:0005696; P:achemokine receptor activity; TAS.

GO; GO:0005969; P:achemokine response; TAS.

GO; GO:0005969; P:achemotaxis; TAS.

GO; GO:000591; P:chemotaxis; TAS.

GO; GO:000591; P:chemotaxis; TAS.

GO; GO:000591; P:chemotaxis; TAS.

GO; GO:0005191; P:cytosolic calcium ion concentration elevation; TAS.

GO; GO:0007125; P:invasive growth; TAS.

GO; GO:0007125; P:invasive growth; TAS.

GO; GO:0007194; P:cytosolic calcium ion concentration elevation; TAS.

GO; GO:0007195; P:invasive growth; TAS.

GO; GO:0007194; P:cytosolic calcium ion concentration elevation; TAS.

GO; GO:0007125; P:invasive growth; TAS.

GO; GO:0007125; P:invasive growth; TAS.

GO; GO:0007129; P:invasive growth; TAS.

GO; GO:0007129; P:invasive growth; TAS.

GO; GO:0007129; P:invasive growth; TAS.

Fram; PROSITE; PS00227; GPCRRHODOPSN.

FRANSMEM 1; 1 (POTENTIAL).

FT TRANSMEM 115 136 3 (POTENTIAL).

FT TRANSMEM 115 136 3 (POTENTIAL).

FT TRANSMEM 115 136 3 (POTENTIAL).

FT TRANSMEM 115 136 GOTARTIAL).

FT TRANSMEM 117 220 6 (POTENTIAL).

FT TRANSMEM 127 224 (POTENTIAL).
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BY SIMILARITY.
SLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGR
             -!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.

Transduces a signal by increasing the intracellular calcium ions level. Alternative coreceptor with CD4 for HIV-1 infection.
-!- SUBSCELULAR LOGATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                              PTM: N-glycosylated. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
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EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                    IsoId=P41597-2; Sequence=VSP_001893;
                                                                                                                                                                                                                          Name=A;
IsoId=P41597-1; Sequence=Displayed;
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   J. Immunol. 165:5295-5303(2000)
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
C.C. chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR2).
CCR2 OR CMKBR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- INDUCTION: In animals in which experimental allergic encephalomyelitis (EAE) has been induced.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                     QCPVFYRETVDGVTSTNTPSTGEQEVSAGL (in
                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                     Score 103; DB 1; Length 374;
Pred. No. 1.1e-08;
                                                                                                                                                                                                                                                                       0; Indels
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                         /FIId=VSP_001893.
V -> I (in absNP:1799864).
/FIId=VAR_014339.
G -> E.
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InterPro; IPR000276; GPCR_Rhodpsn.
PFINTY; PR00037; TPM_1; -
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00242; G_PROTEIN_RECEP_F1_2; 1.
G_PPOLEIN COUPLE RECEP_F1_2; 1.
ENGSTER; PS50462; G_PROTEIN_RECEP_F1_2; 1.
ENGSTER; PS50462; G_PROTEIN_RECEP_F1_2; 1.
ENGSTER; PS50462; G_PROTEIN_RECEP_F1_2; 1.
ENTRACELLULAR (POTENTIAL).
                                                                                                                                                      7FTIG=VAR 014340.
374 AA; 41914 MW; F865BCD39E74CF0F CRC64;
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    GKGKSIGRAPEASLQDKEGA
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MEDLINE=98318173; PubMed=9655467;
                                                                                                                                                                                                                                                                                                                    2 PYNIVLLINIFOEFFGLNNC 21
                                                                                                                                                                                                                              87.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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81
112
128
149
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CKR1 HUMAN
P32246;
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MEDLINE=97026720; PubMed=8780240;

MEDLINE=97026720; PubMed=8780240;

MEDLINE=97026720; PubMed=8780240;

MEDLINE=97026720; PubMed=8780240;

MEDLINE=97026720; PubMed=8780240;

MEDLINE=97026720; PubMed=8780240;

MEDLINE=97026720; PubMed=987289;

MEDLINE=97026720; PubMed=9780240;

MEDLINE=97024720;

MEDLIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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PSIGE3, GG1172; S.4. Created)
O1 NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (C
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Cloning and functional expression of mCCR2, a murine receptor for
the C-C chemokines JE and FIC.";
J. Biol. Chem. 271:11603-11606(1996).
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boring L., Gosling J., Monteclaro F.S., Lusis A.J., Tsou C.-L., Charo I.F.,
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                            EXTRACELLULAR (POTENTIAL)
                                                                                                                               POTENTIAL.
EXTRACELLULAR (POTENTIAL)
POTENTIAL.
                                                                                                                                                                                                                                                              BY SIMILARITY.
2E7BB012F5D6FD09 CRC64;
                                                                                               CYTOPLASMIC (POTENTIAL).
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                                                                   POTENTIAL.
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MEDLINE=96216064; PubMed=8662823;
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MEDLINE=96205938; PubMed=8631787;
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                                                                                                                                                                                                                                                                                                  42763 MW;
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126
373 AA,
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Matches 15; Conserv
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DISULFID
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TRANSMEM
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TRANSMEM
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CKR2_MOUSE
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01-0CT-1993 (Rel. 27, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
C-C chemokine receptor type 1 (C-C CKR-1) (CC-CKR-1) (CCR (Macrophage inflammatory protein-1 alpha receptor) (MIP-lalpha-R) (RANTES-R) (HM145) (LD78 receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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MEDLINE=93161416; PubMed=7679328;
Neote K., Digregorio D., Mak J.Y., Horuk R., Schall T.J.;
"Molecular cloning, functional expression, and signaling characteristics of a C-C chemokine receptor.";
Cell 72:415-425(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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Y -> H (IN REF. 1).
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CYTOPLASMIC (POTENTIAL).
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FA012C10F4C9325A CRC64;
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CYTOPLASMIC (POTENTIAL).
modified and this statement is not removed.
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PRINTS; PR01237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

G-protein coupled receptor; Transmembrane.
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or send an email to license@isb-sib.ch).
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                                                                  EMBL; U47035; AAC52453.1; -. EMBL; U51717; AAC52557.1; -.
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Bust Local Similarity 70.00,
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Homo sapiens (Human).
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373 AA;
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Gaps

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Length 355; Indels

DB 1;

us-10-084-813-14.rsp

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BY SIMILARITY.
E -> D (IN REF. 3).
B2C100FFED275985 CRC64;
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Pred. No. 0.24;
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Pred. No. 1.2;
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Best Local Similarity 40.0%;
Matches 8; Conservative 6
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R GO; GO: 0005887; C:integral to plasma membrane; TAS.

R GO; GO: 0004950; F:chemokine receptor activity; TAS.

R GO; GO: 0007155; P:cell adhesion; TAS.

R GO; GO: 0007156; P:cell surface receptor linked signal transdu. .; TAS.

R GO; GO: 0007267; P:cell signaling; TAS.

R GO; GO: 00072794; P:cytosolic calcium ion concentration elevation; TAS.

R GO; GO: 00072794; P:cytosolic calcium ion concentration elevation; TAS.

R GO; GO: 0007595; P:immune response; TAS.

R GO; GO: 0007125; P:inflammatory response; TAS.

R GO; GO: 0007125; P:inflammatory response; TAS.

R GO; GO: 0007125; P:invasive growth; TAS.

R HALENDO: TRR000276; GPCR_Rhodpsn.

R Pfam; PR00001; Tut 1, 1.
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                                                                                                                                                                                                                                                        Nomera 1, Nielsen European (1978) Matsushima K.; Mondieular Cloning of CDNAs encoding a LD78 receptor and putative leukocyte chemotactic peptide receptors."; Int. Immunol. 5:1239-1249 (1993).

-i. FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1 delta, RANTES, and MCP-3 and, less efficiently, to MIP-1-beta or MCP-1 and subsequently transduces a signal by increasing the intracellular calcium ions level. Responsible for affecting stem cell proliferation.

-i. SUBCELLULAR LOCATION: Integral membrane protein.

-i. TISSUE SPECIFICITY: Widely expressed in different hematopoietic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
        [2]
SEQUENCE FROM N.A.
MEDINE=93240122; PubMed=7683036;
Gao J.-L., Kuhns D., Tiffany H.L., McDermott D., Li X., Francke
                                                                                                           "Structure and functional expression of the human macrophage inflammatory protein 1 alpha/RANTES receptor."; J. Exp. Med. 177:1421-1427 (1993).
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PROSITE; PS00237; G_PROTEIN RECEP_F1_1; 1.

PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein.

DOMAIN 134 EXTRACELLULAR (FOTENTIAL).
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CYTOPLAGNIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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MEDLINE=94092629; PubMed=7505609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L09230; AAA58408.1; -. EMBL; L10918; AAA3643.1; -. EMBL; L10925; BAA01723.1; -. PIR; A45177; A45177. Genew; HGNC:1602; CCR1.
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-!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1-SUBINIT: In chloroplasts, the RNA polymerase is composed of four subunits: alpha, beta, beta', and beta'.
-1-SUBICELLULAR LOCATION: Chloroplast.
-1-SIMILARITY: Belongs to the RNA polymerase beta chain family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + {RNA}(N).
                                                                                                                                                                              Chloroplast.
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Pinus.
NCBL_TaxID=3350;
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                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=95024047; PubMed=7937893;
Wakasugi_T., Tsudzuki J., Ito S., Nakashima K., Tsudzuki T.,
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
DNA-directed RNA polymerase beta chain (EC 2.7.7.6)
                                                                                                                                            Pinus thunbergii (Green pine) (Japanese black pine)
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VARIANT
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Imai T., Chantry D., Raport C.J., Wood C.L., Nishimura M., Godiska R.,
Yoshie O., Gray P.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION, TISSUE SPECIFICITY, AND PHOSPHORYLATION.
MEDLINE=20219238; PubMed=10754297;
Inngjerdingen M., Damaj B., Maghazachi A.A.;
"Human NK cells express CC chemokine receptors 4 and 8 and respond to thymus and activation-regulated chemokine, macrophage-derived chemokine, and I-309.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Campbell J.J., Haraldsen G., Pan J., Rottman J., Qin S., Ponath P., Andrew D.P., Warnke R., Ruffing N., Kassam N., Wu L., Butcher E.C.; "The chemokine receptor CCR4 in vascular recognition by cutaneous but not intestinal memory T cells.";
Nature 400:776-780 [1999].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Power C.A., Meyer A., Nemeth K., Bacon K.B., Hoogewerf A.J., Proudfoot A.E.I., Wells T.N.C.; "Molecular cloning and functional expression of a novel CC chemokine receptor cDNA from a human basophilic cell line."; J. Biol. Chem. 270:19495-19500(1995).
  Gaps
                                                                                                                                                       SEQUENCE FROM N.A., AND VARIANTS VAL-130 AND SER-178.
MEDLINE=21040311; PubMed=11196669;
MEDLINE=21040311; Tuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki Hirai K., Tokunaga K.;
Minai K., Tokunaga K.;
"New variations of human CC-chemokine receptors CCR3 and CCR4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97313486; PubMed=9169480;
Imai T., Baba M., Nishimura M., Kakizaki M., Takagi S., Yoshie O.;
The T cell-directed CC chemokine TARC is a highly specific
biological ligand for CC chemokine receptor 4.";
J. Biol. Chem. 272:15036-15042(1997).
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kopatz S.A., Aronstam R.S., Sharma S.V.; "cDMA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org)."; submitted (UUN-2003) to the EMBL/GenBank/DDBJ databases.
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2; Mismatches
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Biol. Chem. 273:1764-1768(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Spleen;
MEDLINE=95370289; PubMed=7642634;
                                                             355 PQNLVTSTLLKNTFQDFFG 373
                                       2 PYNIV---LLLNTFOEFFG 17
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  12; Conservative
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U. Immunol. 164:4048-4054(2000).

-I-FUNCTON: High affinity receptor for the C-C type chemokines TARC/SCTA17 and MUC/SCTA22. The activity of this receptor is mediated by G(i) proteins which activate a phosphatidylinositol-calcium second messenger system. Can function as a chemoatrzactant homing receptor on circulating memory lymphocytes and as a coreceptor for some primary HIV-2 isolates. In the CNS, could mediate hippocampal-neuron survival.

-I-SUBELLUIAR LOCATION: Integral membrane protein.

-I-TISSUB SPECIFICITY: Predominantly expressed in the thymus, in peripheral blood leukocytes, including T cells, mostly cd4+ cells, and in monocytes. Detected also in macrophages, IL-2-activated natural killer cells and skin-homing memory T cells, mostly the ones expressing the cutaneous lymphocyte antigen (CLA). Expressed in brain microvascular and coronary artery endochelial cells. PHOSPHORYLATION ON YET UNDERSIA BNOST PROBABLY BY BASHORYLATION ON YET UNDERSIA BNOST PROBABLY BY HELLEY, ADRERGIC RECEPTOR KINASES I AND 2.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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/FTId=VAR_010669.
C -> S.
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EMBL; AB002388; BAA86965.1; --
EMBL; AB002389; BAA86966.1; --
EMBL; AB0023891; BAA86967.1; --
EMBL; AB0023891; BAA869691; --
EMBL; AY32539; AAP84352.1; --
EMBL; AS7160; A57160.
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rare TATA-less promoter structure conserved between Drosophila
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EMBL, AB02387; BAA86964.1; --
EMBL, AF247361; ALUB5154.1; --
EMBL, AY221092; AAO65970.2; --
EMBL, BC033514; AAH33514.1; --
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                                          Genomics 80:86-95(2002).
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      a rare humans.
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Genew;
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Xiao L., Weiss S., Qari S., Rudolph D., Hodge T., Lal R.;

"Partial resistance to infection by syncytium-inducing primary HIV-1
in exposed uninfected individuals homozygous for CCR5 32bp deletion.";

Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=21040311; PubMed=11196669;
Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H.,
Hirai K., Tokhunaga K.;
"New variations of human CC-chemokine receptors CCR3 and CCR4.";
Genes Immun. 1:97-104(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Combadiere C., Ahuja S.K., Murphy P.M., Inman eosinophil CC chemokine receptor.";
                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96281895, PubMed=8676064, pont D., Gerard N.P., Onth P.D., Qin S., Post T.W., Mang J., Wu L., Gerard N.P., Newman W., Gerard C., Mackay C.R.; "Molecular cloning and characterization of a human ectaxin receptor
                                                                                                                                                                                                                                                                                                    CKR3 HUMAN STANDARD; Q9ULY8; 355 AA.

D1-05T-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-YAR-2004 (Rel. 43, Last annotation update)
C-C chemokine receptor 1999 3 (C-C CKR-3) (CCR-3) (CCR3)
(CKR3) (Bosinophil cotaxin receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIINE=96235044; PubMed=8642344; Demartino J.A., Malkowitz L., Buddherty B.L., Siciliano S.J., Demartino J.A., Malkowitz L., Sirotina A., Springer M.S., "Cloning, expression, and characterization of the human eosinophil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria; Primates, Catarrhini, Hominidae, Homo.
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MEDLINE-22074933; PubMed=12079287;
Vijh S., Dayhoff D.E., Wang C.E., Imam Z., Ehrenberg P.K.,
Michael N.L.;
                                                                   44.9%; Score 53; DB 1; Length 360; 52.4%; Pred. No. 0.71;
                                                                                                                8; Indels
    /FTId=VAR_010670.
S1EBE12AD1FAFABF CRC64;
                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expressed selectively on eosinophils."; J. Exp. Med. 183:2737-2748(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Combadiere C., Ahuja S.K., Murphy P.M.; J. Biol. Chem. 270:30235-30235(1995).
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                                                                                                                                                                                 257 PYNIVLFLETLVELEVLQDCT 277
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TISSUE=Monocytes;
MEDLINE=95348056; PubMed=7622448;
                                                                                                                                                         2 PYNIVLLINIFQEFFGLNNCS 22
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J. Exp. Med. 183:2349-2354(1996).
                             41402 MW;
                                                                 Query Match
Best Local Similarity 52.4%;
Matches 11; Conservative
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                               360 AA;
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                                                                                                                           TAS.
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GO; GO:0007155; P:cell adhesion; TAS.
GO; GO:0006956; P:cellular defense response; TAS.
GO; GO:00006935; P:chemotraxis; TAS.
GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
GO; GO:0007188; P:c-protein signaling, coupled to cAMP nucleo. .; TP
GO; GO:0007125; P:inflammatory response; TAS.
GO; GO:0007125; P:inflammatory response; TAS.
InterPro; IRF000276; GPCR_Rhodpsn.
PFfam; PR000201; 7tm 1; 1.
PRINTS; PR00137; GPCRRHODOSN.
Kopatz S.A., Aronstam R.S., Sharma S.V.; "cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org)."; Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
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360 AA
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INTERPO. INTEROCOZÓ, GPCR Rhodpsn.
PEdm., PF00001; Tum.1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSTITE, PS00237; GPCRRHODOPSN.
PROSTITE, PS00237; GPCRTRIN RECEP.F. 1; 1.
G-protein coupled receptor; Transmembrane.
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                                                                                                                                                                      EMBL; AF003954; AAC03337.1; -.
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nes 10; Conserv
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P51680;
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Matches
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STRAIN=Wistar; TISSUE=Spleen;
MEDLINE=98318173; PubMed=9655467;
Jiang Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
Defiebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
"Chemokine receptor expression in cultured glia and rat experimental
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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/FIGEVAR 010668.

S -> T (IN REF. 4 AND 5).
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30-WAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last amnotation update)
C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR-3)
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G_PROTEIN_RECEP_F1_1; 1.
G_PROTEIN_RECEP_F1_2; 1.
receptor; Transmembrane; Polymorphism.
34 EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                               5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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| PYNVAILLSSYQSILFGNDC 273
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J. Neuroimmunol. 86:1-12(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41043 MW;
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Rattus norvegicus (Rat).
                                                                                                                  276 355 AA;
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les 8; Conserv
                                 PROSITE; PS50262;
G-protein coupled
      PS00237;
                                                                                                                  CKR3_RAT
O54814; O55169;
                                                                                                               TRANSMEM
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CKR3_RAMT

CKR3_CANT

CKR4

SDT 30-19

CKR 30-19

SDT 30-19

CKR 3
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
MEDLINE=56136324; PubMed=8573157;
Hoogewerf A.J., Black D., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
Moolecular cloning of murine CC CKR-4 and high affinity binding of chemokines to murine and human CC CKR-4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ø
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01-0CT-1996 (Rel. 34, Last sequence update)
15-MXR-2004 (Rel. 43, Last annotation update)
C-C chemokine receptor type 4 (C-C CKR-4) (CC-CKR-4) (CCR-CKR-4) (CCR-CKR-4)
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STRAIN=C57BL/6; TISSUE=Cytotoxic T-cell;
MEDLINE=97335974; PubMed=9192765;
Youn B.-S., Kim S.-H., Lyu M.S., Kozak C.A., Taub D.D., Kwon B.S.;
"Molecular cloning and characterization of a cDNA, CHEMRI, encoding chemokine receptor with a homology to the human C-C chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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880F682984F501DA CRC64;
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MEDLINE=20273981; PubMed=10811868;

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                                                                                                                                                                                                      -!- DEVELOPMENTAL STAGE: Low expression at 7.5 dpc and 12.5 dpc in the
      Buser R., Conquet F., Proudfoot A.E.I., Wells T.N.C., Power C.A.; "A key role for CC chemokine receptor 4 in lipopolysaccharide-induced endotoxic shock.";
                                                  1. EXP. Med. 1911/755-1764 (2000).

-1- FUNCTION: High affinity receptor for the C-C type chemokines TARC/SCYA17 and MDC/SCYA20. The activity of this receptor is mediated by G(1) proteins which activate a phosphatidylinositolalipopolysaccharide (LPS)-induced endotoxic shock. In the CNS, could mediate hippocampal-neuron survival.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- TISSUE SPECIFICITY: Expressed in the thymus, macrophages and T-
                                                                                                                                                                                                                 yolk sac.
-!- PTH: IN NATURAL KILLER CELLS, SCYA22 BINDING INDUCES
PHOSPHORYLATION ON YET UNDEFINED SER/THR RESIDUES, MOST PROBABLY
BY BETA-ADRENERGIC RECEPTOR KINASES 1 AND 2 (BY SIMILARITY).
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEGN. PF000017 7tm 1; 1. PRINTS, PR00237; GPCRRHODOPSN. PROSITE; PS00237; GPROTEIN RECEP F1 1; 1. GPROTEIN COURSE F1 2; 1. G-protein coupled receptor; Transmembrane; Glycoprotein; Phosphorylation. 39 EXTRACELULAR (POTENTIAL).
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E -> Q (IN REF. 2).
E -> Q (IN REF. 2).
W -> C (IN REF. 2).
W -> C (IN REF. 2).
G -> A (IN REF. 2).
G -> A (IN REF. 2).
F -> S (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; JC4587; JC4587.
MGD; MGI:107824; Ccr4.
MGD; MGI:107824; Ccr4.
MGD; G0:0016493; F:C-C chemokine receptor activity; IMP.
GO; G0:0005935; P:Chemocaxis; IMP.
GO; G0:0005954; P:inflammatory response; IMP.
InterPro; IPR000276; GPCR_Rhodpsn.
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311
360 AA;
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                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AB041392; BAA94477.1;
InterPro; IPR000276; GPCR_Rhodpsn.
PRIMTS; PR0001; 7mm_1; 1.
PROSITE; PS00237; GPCREHOOPSN.
PROSITE; PS50237; GPROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; GPROTEIN RECEP_F1_2; 1.
Post synaptic membrans; Ionic Ananel; Glycoprotein; Transmembrane; Phosphorylation; Multigene family; G-protein coupled receptor.
                                                                                                                                                                                                     Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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        Length 360;
                             8; Indels
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PHOSPHORYLATION (POTENTIAL)
PHOSPHORYLATION (POTENTIAL)
12B0324E13D37DDF CRC64;
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EXTRACELLULAR (POTENTIAL).
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2 (POTENTIAL).
                                                                                                                                                 15-WAR-2004 (Rel. 43, Created)
15-WAR-2004 (Rel. 43, Last sequence update)
17-WAR-2004 (Rel. 43, Last annotation update)
Muscarinic acetylcholine receptor M2 (Fragment)
4; DB 1;
. 1;
                                                                                                                            440 AA
                             Mismatches
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        ilarity 47.6%; Pred. No. Conservative 3; Mismatc
                                                               257 PYNVVLFLETLVELEVLODCT 277
                                                  2 PYNIVLLINTFOEFFGLNNCS 22
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                   Similarity
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Genew; HGNC:1951; CHRM2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kitano T., Kobayakawa H., Saitou N.;
Submitted (ARR-2000) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: THE MUSCARINIC ACETYLCHOINE RECEPTOR MEDIATES VARIOUS
-! FUNCTION: THE MUSCARINIC ACETYLCHOINE RECEPTOR MEDIATES VARIOUS
-! REARAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS
THROUGH THE ACTION OF REATEINS. PRIMARY TRANSDUCING EFFECT IS
ADENVIATE CYCLASE INHIBITION.
-! SUBCELLULAR LOCATION: Integral membrane protein.
-! SINGLALITY: Belongs to family 1 of G-protein coupled receptors.
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=88166632; PubMed=3443095;
Peralta B.G., Ashkenazi A., Winslow J.W., Smith D.H.,
Ramachandran J., Capon D.J.;
"Distinct primary structures, ligand-binding properties and tissuespecific expression of four human muscarinic acetylcholine
                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDILINE=87263421; PubMed=3037705;
BONNEY T.I., Buckley N.J., Young A.C., Brann M.R.;
"Identification of a family of muscarinic acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Brain;
Puhl H.L. III, Ikeda S.R., Aronstam R.S.;
"cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org).";
Submitted (APR-2002) to the EMBL/GenBank/DD5J databases.
                                         .;
0
              Length 440;
                                         0; Indels
              Score 52; DB 1;
Pred. No. 1.2;
4; Mismatches (
                                                                                                                                                              ACM2_HUMAN STANDARD; PRT; 466 AA. P08172; Q9P1X9; 01-AUG-1988 (Rel. 08, Created) 01-AUG-1988 (Rel. 08, Last sequence update) 01-AUG-2004 (Rel. 43, Last annotation update) Muscarinic acetylcholine receptor M2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M16404; AAA51570.1; -.
EMBL; X15264; CAA33335.1; -.
EMBL; AF498916; AAM18939.1; -.
EMBL; AB041391; BAA94476.1; -.
PIR; S10126; S10126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptors.";
EMBO J. 6:3923-3929(1987).
                                                                                                                                                                                                                                                                                                                                                                                             Science 237:527-532(1987).
                                                                                  375 APYNVMVLINTF 386
  Ouery Match
Best Local Similarity 66...
and 8; Conservative
                                                                   APYNIVLLINTF 12
                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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MIX, 118493; ...
R MIX, 118493; ...
R GO; GO:0005887; C:integral to plasma membrane; TAS.
R GO; GO:0004981; F:muscarinic acetylcholine receptor activity; TAS.
R GO; GO:0007207; P:muscarinic acetyl choline receptor, phospho. ..; TAS.
R GO; GO:0007307; P:muscarinic acetyl choline receptor, phospho. ..; TAS.
R GO; GO:0007309; P:neurogenesis; TAS.
R GO; GO:0008016; P:requlation of heart rate; TAS.
R GO; GO:0008016; P:requlation of heart rate; TAS.
R FAM: PROMOTO Tem 1; 1.
R PROSITE; PSO0237; GPCRR.ROADSN.
R PROSITE; PSO0237; GPCRR.ROEDSN.
R PROSITE; PSO0237; GPCRENEIN RECEP FI. 1; 1.
R PROSITE; PSO0262; G PROTEIN RECEP FI. 2; 1.
R POSTER; PSO0262; G PROTEIN RECEP FI. 2; 1.
R POSTER; PSO0262; G PROTEIN RECEP FI. 2; 1.
R POSTER; PSO0262; G PROTEIN RECEP FI. 2; 1.
R POSTER; PSO0262; G PROTEIN RECEP FI. 2; 1.
R POSTER; PSO0262; G PROTEIN RECEP FI. 2; 1.
R POSTER; PSO0262; G PROTEIN RECEP FI. 2; 1.
R POSTER; PSO0262; G PROTEIN RECEP FI. 2; 1.
R POSTER; PSO0262; G PROTEIN RECEP FI. 2; 1.
R POSTER; PSO0262; G PROTEIN RECEP FI. 2; 1.
R POSTER; PSO0262; G PROTEIN RECEP FI. 2; 1.
R POSTER; PSO0262; G PROTEIN RECEP FI. 2; 1.
R POSTER; PSO0262; G PROTEIN RECEP FI. 2; 1.
R POSTER; PSO0262; G PROTEIN RECEP FI. 2; 1.
R POSTER; PSO0262; G PROTEIN RECEP FI. 2; 1.
R POSTER; PSO0262; G PROTEIN RECEP FI. 2; 1.
R POSTER; PSO0262; G PROTEIN RECEP FI. 2; 1.
R POSTER; PSO0262; G PROTEIN RECEP FI. 2; 1.
R POSTER; PSO0262; G PROTEIN RECEP FI. 2; 1.
R POSTER; PSO0262; G PROTEIN RECEP FI. 2; 1.
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R PROTEIN RECEP FI. 2; 1.
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Gomeza J., Wess J.;

Tsolation, sequence and functional expression of mouse muscarinic

scetylacholine receptor genes.";

Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

-:- FUNCTION: THE MUSCARINIC ACCTYLCHOLINE RECEPTOR MEDIATES VARIOUS

CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENTLARE CYCLASE,

BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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EXTRACELULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLUTAR (POTENTIAL)
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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66.78;
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465 4
466 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                              3D-structure.
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-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SUBCELLULAR LOCATION: Integral membrane protein coupled receptors.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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                                                                                                                                                                                                               EMBL; X04708; CAA28413.1; -.
EMBL; M16331; AAA30986.1; -.
PIR; A27386; A27386.
InterPro; IPR0002776; GPCR.
PROSITE; P800237; GFCRHODOPSN.
PROSITE; P800237; GFORENTN RECEP. FT. 1; 1.
PROSITE; P850026; G PROTEIN RECEP. FT. 2; 1.
PROSITE; P850026; G PROTEIN RECEP. FT. 2; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane; Phosphorylation; Multigene family; G protein coupled receptor.

ENTRACELLULAR (POTENTIAL).
                                                                                                 [2]
SEQUENCE FROM N.A.
MEDLINE=87206169; PubMed=3107123;
Peralta E.G., Winslow J.W., Peterson G.L., Smith D.H.,
Ashkenazi A., Ramachandran J., Schimerlik M.I., Capon D.J.;
"Primary structure and biochemical properties of an M2 muscarinic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
T., Haga K., Ichiyama A., Kangawa K., Matsuo H., Hirose T.,
S.;
                                    "Primary structure of porcine cardiac muscarinic acetylcholine receptor deduced from the cDNA sequence."; FEBS Lett. 209:367-372(1986).
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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53D089F179789CD9 CRC64;
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EXTRACELLULAR (POTENTIAL)
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401 APYNVMVLINTF 412
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                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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      THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS ADENTIATE CYCLASE INHIBITION.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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INTERPO: JPR000276; GPCR_Rhodpsn.
PEAM; PF00001; 7tm 1; Jr.
PRINTS; PR00237; GPCRHODOPSN.
PROSITE; PS00262; G_PROTEIN RECEP_F1_2; 1.
PROSITE; PS50262; G_PROTEIN RECEP_F1_2; 1.
POSTSYNAPTION; Multigene family; G-protein coupled receptor.
DOMAIN

1 22 EXTRACELLULAR (POTENTIAL).
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Kubo T., Maeda A., Sugimoto K., Akiba I., Mikami A., Takahashi H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Nezzoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9623;
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL)
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PHOSPHORYLATION (POTENTIAL)
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CYTOPLASHIC (POTENTIAL).
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EXTRACELLURAR (POTENTIAL).
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CYTOPLASHIC (POTENTIAL).
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EXTRACELLULAR. (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Best Local Similarity 66.,
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SEQUENCE FROM N.A.
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 CCR3 OR CMKBR3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Furtuta M., Ohya S., Imaicuri Y., Watanabe M.;

"Molecular cloning of m3 muscarinic acetylcholine receptor in rat
iris."

"Molecular cloning of m3 muscarinic acetylcholine receptor in rat
iris."

"Smooth Muscle Res. 34:111-122(1998).

-!- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
CELLULAR RESPONSES, INCLUDING INHIBITION OF ADERYLATE CYCLASE,
BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS
THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS
ADENYLATE CYCLASE INHIBITION.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                       "Primary structure of rat cardiac beta-adrenergic and muscarinic cholinergic receptors obtained by automated DNA sequence analysis: further evidence for a multigene family."; Proc. Natl. Acad. Sci. U.S.A. 84:8296-8300(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELULAR (POTENTIAL).
7 (POTENTIAL).
7 (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                               MEDINE=88066581; PubMed=2825184;
Gocayne J.D., Robinson D.A., Fitzgerald M.G., Chung F.-Z.,
Kerlavage A.R., Lentes K.-U., Lai J., Wang C.-D., Fraser C.M.,
                                         P10980; 092221;
01-JUL-1989 (Rel. 11, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
CHRM2 OR CHRM-2.
                              466 AA
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99138467; PubMed=9972520;
                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22428 1111128444
22428 2121128444
220022428
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
TRANSMEM
DOMAIN
TRANSMEM
DOMAIN
CARBOHYD
                                RAT
             ACM2 RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created).
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAX-2000 (Rel. 39, Last annotation update)
C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3) (CCR3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
(GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                   Score 52; DB 1; Length 466;
Pred. No. 1.3;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Y13775; CAA74106.1; -.

InterPro; IPR000276; GPCR_Rhodpsn.

FEAN; PR000237; GPROTEIN RECEP_F1_1; 1.

RROSITE; PS50262; G_PROTEIN RECEP_F1_2; 1.

RPOSITE; PS50262; G_PROTEIN RECEP_F1_2; 1.

G_Protein coupled receptor; Transmembrane.

G_Protein coupled receptor; Transmembrane.

G_Protein coupled receptor; Transmembrane.

FTRANSMEM 35 62 I(POTENTIAL).

FTRANSMEM 35 72 CYTOPLASMIC (POTENTIAL).

FTRANSMEM 33 2 (POTENTIAL).

FTRANSMEM 33 2 (POTENTIAL).

FORMAIN 94 107 EXTRACELLULAR (POTENTIAL).
                          N-LINKED (GLCNAC. . .) (POT
BY SIMILARITY.
PHOSPHORYLATION (POTENTIAL)
                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                        70ECCD86366A676B CRC64;
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
                                                                                                PHOSPHORYLATION (POTENT PHOSPHORYLATION (POTENT N -> 5 (IN REF. 1).

VS -> 5A (IN REF. 1).

G -> D (IN REF. 1).

C -> Y (IN REF. 1).

C -> Y (IN REF. 1).

I -> V (IN REF. 1).

I -> V (IN REF. 1).
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                                                                                                                                                                                                                                                                                                                                                             51539 MW;
                                                                                                                                                                                                                                                                                                                                                                                                           44.1%;
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70,44

us-10-084-813-14.rsp

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73
1094
1130
1130
1147
1147
1224
224
2265
282
306
1180
355 AA,
                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCR1 OR CMKBR1.
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DOMAIN
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DISULFID
CONFLICT
                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CKR1 MAC P56482;
                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                  ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98118446; PubMed=9454694;
Sol N., Treboute C., Gomas E., Ferchal F., Shacklett B., Alizon M.;
"The rhesus macaque CCR3 chemokine receptor is a cell entry cofactor
for HIV-2, but not for HIV-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virology 240:213-220(1999).

-!- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin, MCP-3, MCP-4 and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level.

-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
28-FEB-2003 (Rel. 36, Last sequence update)
C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR-3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIINE=21354176; PubMed=11461684;
Margulies B.J., Hauer D.A., Clements J.E.;
"Identification and comparison of eleven rhesus macaque chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                  ;
                                                                                                                                                                            Score 51.5; DB 1; Length 355;
Pred. No. 1.2;
5; Mismatches 3; Indels 1
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                 EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
                                                                                                                                          44F7A5EFEEB978FF CRC64;
                                                                                             CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AIDS Res. Hum. Retroviruses 17:981-986(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF017283; AAB70527.1; -
EMBL; Y13776; CAA4107.1; -
Interpro; IPR002076; GPCR Rhodpsn.
FEAM; PR00011; 7tm 1; 1.
RRINTS; PR00237; GFCRHODOPSN.
PROSITE; PS00237; GFROTEIN RECEP F1.1; 1.
GFORTEL; PS50262; GFROTEIN RECEP F1.2; 1.
G-protein coupled receptor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                              355 AA.
                                                                                                                                                                                                                                                                      |||::|:|:|
254 PYNVAILISTYQSILFGLD 272
                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCR3 OR CMKBR3.
Macaca mulatta (Rhesus macaque)
                                                                                                                                            40830 MW;
                                                                                                                                                                                43.68;
                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cercopithecinae; Macaca.
 203
223
223
264
281
355
183
                                                                                                                                            355 AA;
                                                                                                                                                                                               Local Similarity
les 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptors.";
                                                                                                                                                                                                                                                                                                                                                                              CKR3 MACMU
P56483;
                                    DOMAIN
TRANSMEM
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TRANSMEM
DOMAIN
DOMAIN
TRANSMEM
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DISULFID
SEQUENCE
                                                                                         TRANSMEM
                                                                                                                                                                                Query Match
                                                                      DOMAIN
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptors.";
AIDS Res. Hum. Retroviruses 17:981-986 (2001).
-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-AND
SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING STEM CELL
PROLIFERATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 1 (C-C CKR-1) (CC-CKR-1) (CCR-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Macaca mulatta (Rhesus macaque).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Margulies B.J., Hauer D.A., Clements J.E.; Identification and comparison of eleven rhesus macaque chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 51.5; DB 1; Length 355;
Pred. No. 1.2;
6; Mismatches 3; Indels 1
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
                                                                                                                                    G (POTENTIAL).
CYTOPLASNIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELULAR (POTENTIAL).
7 (POTENTIAL).
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-> R (IN REF. 2).
E271F1E694970D9F CRC64;
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL) . BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 355 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=21354176; PubMed=11461684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         254 PYNVAILISTYQSVLFGLD 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 PYNIVLLLNTFQE-FFGLN 19
                                                                                                                                                                                                                                                                                                                                                                                                         40805 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF017282; AAB70526.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cercopithecinae; Macaca.
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**UB-IO-084-813-14.18D** 

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol. Chem. 265:2828-2834(1990).

-!- FUNCTION: The muscarinic acetylcholine receptor mediates various cellular responses, including inhibition of adenylate cyclase, breakdown of phosphoinositides and modulation of potassium channels through the action of G proteins. Primary transducing effect is inhibition of adenylate cyclase. May couple to multiple functional responses in cell lines.
-!- SUBCELLULAR LOGATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            omatus garino (unicosm).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                     7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIINE=90153912; PubMed=2154460;
Tietje K.M., Goldman P.S., Nathanson N.M.;
"Cloning and functional analysis of a gene encoding a novel
muscarinic acetylcholine receptor expressed in chick heart and
                                                                                                                                                                                                                          Query Match
43.2%; Score 51; DB 1; Length 355;
Best Local Similarity 45.0%; Pred. No. 1.4;
Matches 9; Conservative 4; Mismatches 7; Indels
                                                   4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                 SIMILARITY.
41CAEA7CC19D23D4 CRC64;
    2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Muscarinic deetylcholine receptor M4.
                                                                                                                                                                                                                                                                                                                                                                                     PRT; 490 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP, P02699; IBOJ.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7rm_1; 1.
PRINTS; PR000237; GPCRHODOPSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; GPROTEIN_RECEP_F1_2; 1.
2 (POTENTIAL)
                                                                                                                                                                                                                                                                                                      254 PYNLTELISVPQEFLFTHLC 273
                                                                                                                                                                                                                                                                                     2 PYNIVLLLNTPOEFFGLNNC 21
                                                                                                                                                                                    BY
                                                                                                                                                                                                  41198 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; JO5218; AAA48563.1; -. PIR; A35546; A35546.
                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken)
183
                                                                                                                                                                     5
106
355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9031;
 65
92
1108
1147
1147
1148
224
224
224
2265
306
                                                                                                                                                                                                                                                                                                                                                                         ACM4_CHICK
ID ACM4_CHICK
AC P17200;
                                        DOMAIN
TRANSMEM
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TRANSMEM
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DISULFID
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SEQUENCE FROM N.A.

SERAIN-VC-16 / DSM 4304 / ATCC 49558;

MIDLINE-98049343; Pubmed-9389475;

WIDLINE-98049343; Pubmed-9389475;

MIDLINE-98049343; Pubmed-9389475;

MIDLINE-98049343; Pubmed-9389475;

MIDLINE-98049343; Pubmed-9389475;

MICHARYON D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

MILLE SER, Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

MILLE SER, Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

Corton M.D., Sprigges T., Artiach P., Kaine B.P., Sykes S.M.,

Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
Nature 390:1364-370 (1397).
-!- CATALYTIC ACTIVITY: L-histidinol-phosphate + 2-oxoglutarate = 3-
(imidazol-4-yl)-2-oxopropyl phosphate + L-glutamate.
-!- COPACTOR: Pyridoxal phosphate (By similarity).
-!- COPACTOR: Pyridoxal phosphate (By similarity).
-!- PATHWAY: Histidine biosynthesis; seventh step.
-!- STMILARITY: Belongs to class:II of pyridoxal-phosphate-dependent
--- SIMILARITY: Belongs to class:II of pyridoxal-phosphate aminotransferases
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
N-LINKED (GLORAC. .) (POTENTIAL).
N-LORDBSFA7D2298E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           028255;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
41stidinol-phosphate aminotransferase 2 (EC 2.6.1.9) (Imidazole acetol-phosphate transaminase 2).
                                                                                                                                                                                                                                                                                                                                                                                           ö
                 receptor
                                                                                                                                                                                                                                                                                                                                                           Score 50; DB 1; Length 490;
Pred. No. 2.8;
4; Mismatches 1; Indels
                                                                                                    3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                           6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
               Phosphorylation, Multigene family, G-protein coupled re
DOMAIN 1 42 EXTRACELLULAR (FOTENTIAL)
                                                       CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archaea; Buryarchãeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               342 AA
membrane; Ionic channel;
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                                                                                                                                                                                                                                                                                                                                 54937 MW;
                                                                                                                                                                                                                                                                                                                                                               42.4%;
61.5%;
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426 PYNVMVLINTFCE 438
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 61...
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          2 PYNIVLLLNTFOE 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaeoglobus fulgidus.
                                                                                                                                                                                             433
447
467
490
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20
25
115
490 AA;
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                                              subfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 38
HI82 ARCFU
ID HI82 ARCFU
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DISULFID
SEQUENCE
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CARBOHYD
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BY SIMILARITY
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MEDLINE=95010703; PubMed=7925970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 PYNIVLLINTFQEFFGLNNC 21
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г
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                                                                                                                                                                                                       EMBL; U29677; AAA86118.1; -.
EMBL; U28406; AAA89155.1; -.
MGD; MGI:104616; Ccr3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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ACM4_XENLA
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01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3) (CCR-3)
(CCR3) (CKR3) (Macrophage inflammatory protein-1 alpha receptor-like
2) (MIP-1 alpha RL2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular characterization of two murine eosinophil beta chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                   InterPro; IRR004839; Aminotrans I/II.
InterPro; IRR004839; Aminotrans II.
InterPro; IRR004839; Aminotrans II.
InterPro; IRR001817; Aminotrans II.
InterPro; IRR005861; Hige aminotrans.
PROSITE; PRO0155; aminotran I 2; 1.
IIGREAMS; TICR01141; hisc; 1.
IIGREAMS; TICR01141; hisc; 1.
IIGREAMS; TICR01141; Transferase; Aminotransferase;
Histidine biosynthesis; Transferase; Aminotransferase;
Pyridoxal phosphate; Complete proteome.
BINDING 206 206 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SEQUENCE 342 AA; 38941 MW; F71DA0FD66191D80 CRC64;
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Post T.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 48; DB 1; Length 342;
Pred. No. 4.1;
5; Mismatches 3; Indels
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MEDLINE=95340546; PubMed=7542241;
Gao J.-L., Murphy P.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunol. 155:5299-5305(1995),
                                                                                                                                                                                  EMBL; AE000963; AAB89229.1; -. PIR; G69502; G69502.
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                                                                                                                                                                                                                                                                       HAMAP; MF_01023; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                          HSSP; P06986; 1FG7.
TIGR; AF2024; -.
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STRAIN=129/Sv;
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P51678;
    SPTE WEEN PRESENTATION OF THE PRESENTATION OF
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"Cloning of a Kenopus laevis muscarinic receptor encoded by an intronless gene.", Macopus laevis muscarinic receptor encoded by an FEBS Lett. 352:175-179(1994).
-!- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE, BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                             MGD; MGI:10461b; ucrs.
GO; GO:0016493; F:C-C chemokine receptor activity; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0006935; P:chemotaxis; IDA.
InterPro; IPR000276; GPCR_Rhodpsn.
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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AC11ED66E283CEAF CRC64;
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Pred. No. 4.3;
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01-APR-1993 (Rel. 25, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Muscarinio acetylcholine receptor M4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ed. No. 4.3;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G PROTBIN RECEP F1 1; 1.

PROSITE; PS50262; G PROTBIN RECEP F1 2; 1.

G-protein coupled receptor; Transmembrane.

DOMAIN
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THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS INHIBITION OF ADENYLATE CYCLAGES. SUBCELLULAR LOCATION. Integral membrane protein. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.7%; Score 48; DB 1; Length 484; 63.6%; Pred. No. 5.8; 0; Indels ive 4; Mismatches 0; Indels
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Best Local Similarity 63.6
Matches 7; Conservative
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Search completed: September 28, 2004, 09:04:07 Job time : 7.875 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                          US-10-084-813-14
118
1 APYNIVLLIATFQEFFGLNNCS 22
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Maximum Match 100%
Listing first 45 summaries
                                                                           OM protein - protein search, using sw model
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3: sp_bacteria:*
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5: sp_invertebrate:*
6: sp_mammal:*
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10: sp_phage:*
11: sp_organelle:*
9: sp_phage:*
11: sp_virus:*
12: sp_virus:*
13: sp_virus:*
14: sp_unclassified:*
15: sp_brinclassified:*
16: sp_bacteriap:*
17: sp_princlassified:*
18: sp_brinclassified:*
16: sp_bacteriap:*
17: sp_archeap:*
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	O14694 homo sapien	Q9tuq7 erythrocebu		Q9un26 homo sapien	Q9un23 homo sapien	Q9ubj7 homo sapien	homod			Q9tqw0 hylobates c		Q9tuu9 cercopithec	Q9tuw8 gorilla gor	Q9tut4 macaca neme	Q9tuw9 hylobates c	Q9tsq1 cercopithec
SUMMARIES	ΩI	014694	COLLO	Q9UN24	Q9UN26	Q9UN23	Q9UBJ7	Q9UN25	Q9UN27	Q9UBT9	OMOIGO	Q9TUX1	QUITCO	Q9TUW8	Q9TUT4	O9TUW9	Q9TSQ1
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6 Q9TUU8			6 Q9TQU7																					6 Q9TUR3					
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ated)  st sequence update)  st annotation update)  traniata; Vertebrata; Eu  atarrhini; Hominidae; H  ", Huang Y., Cao Y., Wa  age, and CCR5 polymorph  "o(1997).  "embrane; IEA.  "oty; IEA.  "embrane; IEA.  "ty; IEA.  "EPF! I; I.  EPF! I; I.  ERFERAO7A67863AEB CRC64:	DB 4; 1e-10; 0;
MBLrel. 05, Created) MBLrel. 05, Last sequence up MBLrel. 24, Last annotation ragment).  man).  can Chordata; Craniata; Vert ia; Primates; Catarrhini; Ho A.  co-receptor usage, and CCR5 etroviruses 0:0-0(1997).  C:integral to membrane; IEA. F:receptor activity; IEA. F:receptor	Score 118; DB 4; Pred. No. 2.1e-10; Mismatches 0;
MELLEL. 05, Created) MBLEEL. 05, Last sequence MBLEEL. 24, Last annotati ragment).  And Chordata, Craniata, V ia; Primates; Catarrhini; A.  Co-receptor usage, and C etrovituses 0.0-0(1997).  Cintegral to membrane; I E:receptor activity; IEA.  F:receptor activity; IEA.  Cintegral to membrane; I F:receptor activity; IEA.  G-PROTEIN RECEP FIL2; I  G-RROTEIN RECEP FIL2; I  33374 MM: ARFRAGTAG7A67	υн
LIMINARY;  EWBLrel. 05, Las EWBLrel. 05, Las EWBLrel. 24, Las Las Cas Coas Convolruses 0;  Co-receptor us certoviruses 0;  A. A. Co-receptor us Co-receptor us Co-receptor us Co-receptor us Co-receptor us Co-receptor act Firedopsin-lip P:G-protein con 275, G-protein con 275, G-protein con 275, G-protein Co-receptor act Firedopsin-lip P:G-protein con 275, G-protein Co-receptor act Firedopsin-lip P:G-protein Co-receptor act Firedopsin-lip Firedo	.04;
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1 1 0.14694 PRELIM 0.14694; 0.1-5AN-1998 (TEME 0.1-5AN-1998 (TEME 0.1-5AN-1998 (TEME 0.1-5AN-1998 (TEME 0.1-5AN-1998 (TEME 0.1-5AN-1998 (TEME CCRS receptor (Teme CCRS	ch 1 Simi 22;
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230 APYNIVLLLNTFQEFFGLNNCS 251

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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor protein signalin. . ; IEA.
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF162049; AAD47804.1;
GO; GO:0016801; C:integral to membrane; IEA.
GO; GO:0001881; F:receptor activity; IEA.
GO; GO:0001886; F:receptor activity; IEA.
GO; GO:0001886; P:rhodopsin-like receptor protein signalin. . .; IEA.
InterPro; IPR000276; GPCR_Rhodopsn.
Prim; PF00001; Tum_1; 1.
PRINTS; PR00237; GGCRHODPSN.
PROSITE; PS00237; GFRATEIN_RECEP_F1_2; 1.
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K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCRS genes from diverse simian and prosimian
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                        Erythrocebus patas (Red guenon) (Hussar).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Erythrocebus.
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                         334 AA
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                                                         PRT;
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22; Conservative 0
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; "Sequences of the CCR5 genes from diverse simian and prosimian
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                                                                                                                      / Match 100.0%; Score 118; DB 4; Length 339; Local Similarity 100.0%; Pred. No. 2.1e-10; nes 22; Conservative 0; Mismatches 0; Indels
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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339 339
339 AA; 39162 MW; AS6369FE0529F4AB CRC64;
                                                                                               339 AA; 39066 MW; 8BAF02E19423BF79 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
11-UJN-2003 (TrEMBLrel. 24, Last annotation update)
C-C Chemokine receptor 5 (Fragment).
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100.0%; Pred. No. 2.1e-10;
ative 0; Mismatches 0;
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           Pfam; PF00001; 7tm i; 1.
PRO131; GPCRADOPSN.
PRO51TE; PS00237; GPROTEIN RECEP F1 1; 1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
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                                                                                                                                                                                                   242 APYNIVLLINIFQEFFGLNNCS 263
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InterPro; IPR000276; GPCR_Rhodpsn.
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Matches 22; Conservative
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Homo sapiens (Human).

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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF161921; AAD47678.1;
EMBL; AF161921; AAD47678.1;
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:000186; F:receptor activity; IEA.
GO; GO:000186; F:receptor activity; IEA.
GO; GO:000186; P:rhodopsin.like receptor activity; IEA.
GO; GO:000186; P:rhodopsin.like receptor activity; IEA.
FEAN; PRO001; 7tm 1; 1.
PRINTS; PR00237; GPCR.RhodopsN.
PROSITE; PS00237; GPRCHODOPSN.
PROSITE; PS00237; GPRCHIN_RECEP_F1_1; 1.
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

A Sequence S., Voder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;

R Sequence of the CORS genes from diverse simian and prosimian

T Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AFIG1920; AAD4767.1; -.

R GO; GO:0016021; C:integral to membrane; IBA.

GO; GO:001684; F:roceptor activity; IEA.

GO; GO:0001884; F:roceptor activity; IEA.

GO; GO:0001884; F:roceptor activity; IEA.

R GO; GO:0001884; F:roceptor activity; IEA.

R GO; GO:0001885; F:roceptor activity; IEA.

R GO; GO:0001886; P:G-protein coupled receptor protein signalin. .;

R PFINTS; PRO0237; GPCRRHODOPSN.

R PFINTS; PS00237; GPCRRHODOPSN.

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R PROSITE; PS00237; GPROTEIN_RECEP_F1_2; I.

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1 SSQUENCE 339 AA; 39115 MM; 3C6369F922C91AA7 CRC64;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 118; DB 4; Length 339; 100.0%; Pred. No. 2.1e-10; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1
339 339
339 AA; 39115 MW; 3C6369F922C91AA7 CRC64;
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339 339
339 AA, 39128 MW, 9C3369FFFIF2F27A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Best Local Similarity
Matches 22; Conserv
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094937
10 09493
11 09493
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11 01-M
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; Species."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF161918; AAD47675.1; Rembrane; IEA.

GO; GO:001621; C:integral to membrane; IEA.

GO; GO:00184; P:receptor activity; IEA.

GO; GO:00184; P:rhodopsin-like receptor protein signalin. .; InterPro; IPR00276; GPCR_Rhodpsn.

R GO; GO:0001786; PG-protein coupled receptor protein signalin. .; INTERPROSER: PROO237; GPROTEIN RECEP_F1_; I.

R PRINTS; PROO237; GPROTEIN RECEP_F1_; I.
                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID=9606;
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCR5 genes from diverse simian and prosimian
species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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100.0%; Score 118; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels C
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339 339
339 AA; 39146 MW; 10FE05FE5371D4B3 CRC64;
                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
CCC chemokine receptor 5 (Fragment).
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01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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                                                                                                                                                                                      Hylobates concolor (crested gibbon)
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       DDT THE READ OCCOOR OF THE PRINCE OCCOOR OCC
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### Species.";

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-Potein cupled receptor protein signalin. . .; IEA.
InterPro; IPR000276; PFOR_Rhodysn.
Pfam; PF00001; 7tm_1; 1.
PRIMTS; PR00237; GPCR-RHODOPSN.
PRIMTS; PR00317; GPROTEIN RECEP F1 1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Kunstman K., Chan Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinksy S.; "Sequences of the CCRS genes from diverse simian and prosimian
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 118; DB 4; Length 339; Best Local Similarity 100.0%; Pred. No. 2.1e-10; Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                   1 1
339 339
339 AA, 39086 MW; 88ADBB44E2CB4EC2 CRC64;
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339 339
339 AA, 39114 MW; 3C6369F92C29F4A7 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 APYNIVLLINTFQEFFGLNNCS 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 APYNIVLLINTFOEFFGLNNCS 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 APYNIVLLINTFOEFFGLNNCS 22
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les 22; Conservative (
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                                                                                                                                                                                                                                                                Receptor.
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Best Local &
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RESULT 10 Q9TQW0

Matches

Q9UBT9

RESULT 9 Q9UBT9

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Kunsteman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinksy S.; Shibata R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinksy S.; Sequences of the CRS genes from diverse simian and prosimian species."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AFIGHSR; AAAP46441.; -

REBL; AFIGHSR; AAAP4641.; -

RO; GO:001681; Fraceptor activity; IEA.

GO; GO:001584; Fraceptor activity; IEA.

GO; GO:001584; Fraceptor activity; IEA.

RO; GO:0001584; Fraceptor activity; IEA.

RO; GO:0001017 FR. Findopsin-like receptor protein signalin. .; IEA.

InterPro: PROMOST; GERRHODOPSN.

PRINTS; PROMOST; GERRHODOPSN.

ROSITE; PSO0237; G_PROTEIN_RECEP_FI_1; 1.

REMSITE; PSO02237; G_PROTEIN_RECEP_FI_2; 1.
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EMBL, AF162024; AAD47779.1; --
EMBL, AF161889; AAD47779.1; --
EMBL, AF161889; AAD477646.1; --
EMBL, AF161889; AAD47646.1; --
EMBL, AF161889; AAD4779.1; --
EQO, GO:0016021; F:receptor activity; IEA.
GO; GO:0001284; F:rhodopsin-like receptor protein signalin. ..; IEA.
InterPro; IRR000276; GFCR_Rhodopsn.
PROMING; FRO0237; GFCR_Rhodopsn.
PROSITE; PS50262; GFROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; GFROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                     SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCR5 genes from diverse simian and prosimian
species.",
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hylobatidae, Hylobates.
NCBI_TaxID=29089;
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
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339 AA; 39036 MW; 5555FEAF2614D35C CRC64;
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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Gaps

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Length 339; Indels

Q9TUU9

RESULT 12
09TUU9
10 09TUU
AC 09TUU
DT 01-MA
DT 0

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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibate R., Toder A., Fillai S., Kuiken C., Marx P., Wolinksy S.;
Shibate R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCR5 genes from diverse simian and prosimian
species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
GO, GO:0001621; C:integral to membrane; IEA.
GO, GO:0001527; F:receptor activity; IEA.
GO, GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO, GO:0001585; F:Profeein coupled receptor protein signalin. ..; IEA.
InterPro; IPRO00276; GPCR_Rhodpsn.
                                                Species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

B. Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

R. GO; GO:0016021; C:integral to membrane; IEA.

R. GO; GO:0001881; F:receptor activity; IEA.

R. GO; GO:0001884; F:rbodopsin-like receptor activity; IEA.

R. GO; GO:000188; F:rbodopsin-like receptor activity; IEA.

R. InterPro; IPR000275; GPCR_Rhodpsn.

R. PFfam; PF00001; 7tm 1; 1.

R. PRINTS; PR00237; GPCRHODOPSN.

R. PROSITE; PS00237; GPCRHODOPSN.

R. PROSITE; PS00237; GPCREIN_RECEP_F1_1; 1.

R. PROSITE; PS00262; GPROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macaca nemestrina (Pig-tailed macaque).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Emamalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecines, Macaca.
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy & "Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 118; DB 6; Length 339; 100.0%; Pred. No. 2.1e-10; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   339 339 34, 39092 MW, 84B51B9548E0703C CRC64;
                                                                                                                                                                                                                                                                                                                                                      339 339 34, 39079 MW; A4A79753DA2F7AAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 118; DB 6;
100.0%; Pred. No. 2.1e-10;
Live 0; Mismatches 0;
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PRINTS; PR00237; GPCRHOODSN.
PROSITE; PS00237; G PROTEIN RECEP_F1_1; 1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
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les 22; Conservative
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hes 22; Conserv
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Submitted (qui-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161948; AAD4704.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001186; F:G-protein coupled receptor protein signalin. . .; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
PF00001; 7rm_1; 1.
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gorilla gorilla gorilla (Lowland gorilla).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Cercopithecus diana (Diana monkey).
Cercopithecus diana (Diana monkey).
Bukaryota; Netzezoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
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K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCRS genes from diverse simian and prosimian
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
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                                                                       Length 339;
                                                                       Query Match 100.0%; Score 118; DB 6; Length 3
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     339 339 339 MW; 6D1A91546270F70D CRC64;
             339 339
339 AA; 39075 MW; 09257FBFB834C4AE CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
C-C Chemokine receptor 5 (Fragment).
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OFIUS,
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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PRINTS; PRODO237; GPCRRHODOPSN.
PROSITE; PSO0237; G PROTEIN RECEP_F1_1; 1.
PROSITE; PSSO262; G_PROTEIN_RECEP_F1_2; 1.
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22; Conservative
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
Receptor. 1 1
NOW_TER 339 339
SEQUENCE 339 AA; 39216 MW; 847E935FA40
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Best Local Similarity 100.0%;
Matches 22; Conservative 0
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Q9TQW4
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Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161890; AAD47647.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:001632; E:receptor activity; IEA.
GO; GO:000184; F:rhodopsin-like receptor activity; IEA.
GO; GO:000186; F:rhodopsin-like receptor protein signalin. .; IEA.
Interpro; IPR000276; GPCR_Rhodpsn.
PRIMTS; PR000237; GPCRHHODOSN.
PROSITE; PS00237; GPRHHODOSN.
PROSITE; PS00237; GPRCHHODOSN.
PROSITE; PS00237; GPRCHHODOSN.
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Submitted (ULL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF162023; AAD47778.1;
GO, GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001894; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001896; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001896; F:rhodopsin-like receptor protein signalin. . ; IEA.
InterPro; IPR000276; GPCR Ehodpsin-PPGDSN.
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                                                                                                                                                                                                                                                                                                                                                              Hylobates concolor (crested gibbon).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hylobatidae, Hylobates.
NCBL_TaxID=29089;
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K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCRS genes from diverse simian and prosimian
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.
"Sequences of the CCRS genes from diverse simian and prosimian
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                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161949; AAD4705.1; ...
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:001884; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001884; F:rhodopsin-like receptor protein signalin. .; IEA.
InterPro; IPR000276; GPCR_Rhodopsn.
PROSITE; PS00037; GPCRHHODOSN.
PROSITE; PS00037; GPCRHHODOSN.
PROSITE; PS00237; GPCRHHODOSN.
PROSITE; PS00237; GPCRHHODOSN.
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mammalia; Eutheria; Primates; Cararrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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                                                     Length 339;
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339 AA; 39216 MW; 847E935FA403E52D CRC64;
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339 339
339 AA; 39049 MW; 6D1A93F66270F3ED CRC64;
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01-MAX-2000 (TEMBLEEL. 13, Created)
01-MAY-2000 (TEMBLEEL. 13, Last sequence update)
01-UNN-2003 (TEMBLEEL. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                     100.0%; Score 118; DB 6;
100.0%; Pred. No. 2.1e-10;
iive 0; Mismatches 0;
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; Pred. No. 2.1e-10;
0; Mismatches 0;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-UUN-2003 (TrEMBLrel. 24, Last ann
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                1 APYNIVLLINTFQEFFGLNNCS 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cercopithecus diana (Diana monkey)
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242 APYNIVLLINTFQEFFGLNNCS 263

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SEQUENCE FROM N.A. Kunber B., Oprondek J., Stanton J., Agy M., Kunstman K., Chen Z., Korber B., Kuiken C., Marx P., Wolinksy S., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCRS genes from diverse simian and prosimian

1 APYNIVLLINTFOEFFGLNNCS

NCBI\_TaxID=9598;

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EQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Anibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
Sequences of the CCR5 genes from diverse simian and prosimian

RT Sequences J.
Sequences J. Molecule CCR5 genes from diverse simian and prosimian

REL, ARIC2041, AAD47802.1; -.

REL, AFI62042, AAD47792.1; -.

REMBL, AFI62042, AAD47799.1; -.

ROS, GO:0016021, C:integral to membrane, IEA.

GO; GO:0016021, C:integral to membrane, IEA.

GO; GO:000184; F:receptor activity, IEA.

GO; GO:0001884; F:receptor activity, IEA.

GO; GO:0001884; F:receptor activity, IEA.

ROS; GO:0001884; F:receptor activity, IEA.

ROS:REL, PROSIZE; PSOSO27; GFRRHODOPSN.

RECEPTOR ROSIZE; PSOSO237; GFRRHODOPSN.

ROSIZE; ROSIZE; PSOSO237; GFRRHODOPSN.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Bummalia, Eutheria, Primates, Catarrhini, Cercopithecidae,

Cercopithecinae, Erythrocebus.
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K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Sthattan R., Chen Z., Fillai S., Kuiken C., Marx P., Wolinksy S., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vettebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Cercopithecus.
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339 339
339 AA; 39150 MW; 847D5F92BB03E6E2 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TYEMBLrel. 13, Created)
01-MAY-2000 (TYEMBLrel. 13, Last sequence update)
01-UJN-2003 (TYEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cercopithecus nictitans (white-nosed guenon)
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nes 22; Conservative
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                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                         Q9TQU7
Q9TQU7;
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Q9TUQ5
                                                                                                                                                                                               RESULT 20
Q9TQU7
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                                                                                                                                                                                                       species..;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161901; AAD47662.1;
EMBL; AF161901; AAD47652.1;
EMBL; AF161901; AAD47658.1;
EMBL; AF161901; AAD47662.1;
EMBL; AF161904; AAD47661.1;
EMBL; AF161904; AAD47661.1;
EMBL; AF161901; AAD47661.1;
EMBL; AAD47661.1;
EMBL
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EMBL, AF161903; AAD47660.1; Che EMBL/GenBank/DDBJ databases.

EMBL, AF161903; AAD47660.1; Che membrane; IEA.

GO; GO:0001584; P:receptor activity; IEA.

R GO; GO:0001586; P:receptor activity; IEA.

R GO; GO:000186; P:receptor activity; IEA.

R FROMONI; PROMONI; PROMONI
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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339 AA; 39159 MW; 8E699E882BAC0E84 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
0-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 118; DB 6; 100.0%; Pred. No. 2.1e-10;
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Best Local Similarity
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EMBL; AFFEL972; AAA47727.1; EMBL; Pentanny Debt Garabases.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0004827; F:receptor activity; IEA.

GO; GO:000186; F:rhodopsin-like receptor activity; IEA.

GO; GO:0007186; F:rhodopsin-like receptor protein signalin. . .; IEA.

InterPro; IPRO0276; GPCR_Rhodpsn.

PRINTS; PRO0237; GPCRRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_FI_1; 1.
                                                                                                            Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
mamalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinksy S.; "Sequences of the CCR5 genes from diverse simian and prosimian species.";
                                                                                                                                                                                                                                                                                                                                          Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161954; AAD47710.1; --
EMBL; AF161950; AAD47700.1; --
EMBL; AF161950; AAD47700.1; --
EMBL; AF161952; AAD47700.1; --
GO; GO:0001687; F:receptor activity; IEA.
GO; GO:000186; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
FF00001; 7rm 1; --
PRINTS; PR00237; GFCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Macaca mulatta (Rhesus macaque).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 118; DB 6; Length 339; 100.0%; Pred. No. 2.1e-10; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            339 339 339 339 339 AW; C576E7AA492D7080 CRC64;
           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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tes 22; Conservative (
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NCBI_TaxID=9544;
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

BNBL; AR162054; AAD47809.1; -.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001186; F:rhodopsin-like receptor protein signalin. .; IEA.

InterPro; IRP000276; GPCR.Rhodpsn.

PRIMTS; PR000237; GGCR.RHODPSN.

PROSITE; PS00237; GGRRHODPSN.

PROSITE; PS00237; GGRRHODPSN.

PROSITE; PS00237; GFROTEIN_RECEP_F1_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Platyrrhini, Callitrichidae, Saguinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        r species..;
Submitted (UTL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF16,2015; AAD47770.1;
R GO; GO:0016021; C:integral to membrane; IEA.
R GO; GO:00168472; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
R GO; GO:0007186; P:G-protein coupled receptor protein signalin. ..;
R InterPro; IPR000276; GPCR_Rhodpsn.
R Pfam; PF00001; 7mm 1; 1.
R Pfam; PF00001; 7mm 1; 1.
R PRINTS; PR00237; GPCRRHODOPSN.
R PROSITE; PS00237; GPROTEIN_RECEP_F1 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                        'Match 100.0%; Score 118; DB 6; Length 339; Local Similarity 100.0%; Pred. No. 2.1e-10; es 22; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 339;
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                                                                                                                                                                                                                                                                          339 339
339 AA; 39048 MW; 1A2E19E3A6A5A52A CRC64;
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339 339
339 AA; 39063 MW; 78BCE7A84B877085 CRC64;
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Pred. No. 2.1e-10;
Mismatches 0;
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Best Local Similarity 100.0%;
Matches 22; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                    Receptor.
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Q9TQT0
ID Q9TQT0
AC Q9TQT0;
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339 AA.

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MCBI_TaxID=100936;
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Q9TQV6
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161953; AAD47709.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0001894; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001894; F:rhodopsin-like receptor protein signalin. .; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR00017; 7tm 1; 1.
PRINTS; PR00197; GPCRRHODOPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cercopithecus aethiops vervet.

Bukaryota, Metazoa, Chordata; Craniata, Vertebrata, Buteleostomi, Mammalia; Butheria, Primates; Catarrhini, Cercopithecidae, Cercopithecuse, Cercopithecuse, Cercopithecus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCR5.

Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Bukaryota; Netazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalla; Butheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Macaca.

NCBI_TaxID=9541;
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                                                                                                                            Length 339;
                                                                                                                                                                 Indels
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339 339
339 AA, 39137 MW, 9E626ED3288607C1 CRC64,
                                                                                     SBFCBC5BA96C2F9E CRC64;
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01-WAY-2000 (TrEMBirel. 13, Created)
01-WAY-2000 (TrEMBirel. 13, Last sequence update)
01-UJW-2003 (TrEMBirel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment);
                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                        Match 100.0%; Score 118; DB 6; Local Similarity 100.0%; Pred. No. 2.1e-10; les 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                         339 AA
    PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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                                           1 1
339 339
339 AA; 39067 MW;
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DT 01-MA
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DE C-C C
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EMBL; AF1620005; AAD47750.1; -...
EMBL; AF1620001; AAD47755.1; -...
EMBL; AF162001; AAD47755.1; -...
EMBL; AF162001; AAD47757.1; -...
EMBL; AF162001; AAD47758.1; -...
EMBL; AF162001; AAD47758.1; -...
EMBL; AF162001; AAD47758.1; -...
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:000188; F:rhodopsin-like receptor activity; IEA.
GO; GO:000188; F:rhodopsin-like receptor protein signalin. ..; IEA.
InterPro; IPR000276; GPCR Rhodpsn.
FFERM; PP00001; 77m_1; 1...
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
SEQUENCE FROM N.A. Korber B., Oprondek J., Stanton J., Agy M., Kunstman K., Chen Z., Korber B., Chrostan R., Wolinksy S.; Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; "Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                    species.; Submitted (JUL.1999) to the EMBL/GenBank/DDBJ databases. Submitted (JUL.1999) to the EMBL/GenBank/DDBJ databases. Submitted (JUL.1999) to the EMBL/GenBank/DDBJ databases. GO; GO:0016621; C:integral to membrane; IEA. GO; GO:0014872; F:receptor activity; IEA. GO; GO:000186; P:GProtein coupled receptor activity; IEA. InterPro; IPR000276; GPCR_Rhodpsn. InterPro; IPR000276; GPCR_Rhodpsn. PRINTS; PR000217; Thu 1; 1. PRINTS; PR000217; GPCRHODDPSN. PROSITE; PS000237; GPROTEIN RECEP_F1_1; 1. PROSITE; PS500262; G_PROTEIN_RECEP_F1_2; 1.
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M. Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S. Shibata R., Yoder G.C., Marx P., Wolinksy S. Sequences of the CCRS genes from diverse simian and prosimian species.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 118; DB 6; Length 339; 100.0%; Pred. No. 2.1e-10; cive 0; Mismatches 0; Indels (
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339
39178 MW; 9DF2A6F446C55AED CRC64;
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339 AA; 39168 MW; 6A4BF72FEBFF566F CRC64;
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01-VAY-2000 (TrEMBLrel. 13, Created)
01-VAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      339 AA
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PROSITE; PS00237; G PROTEIN RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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SEQUENCE 339 AA; 3
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NCBI_TaxID=33548;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae, Cercopithecinae, Macaca.
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kulken C., Marx P., Wolinksy S.,
"Sequences of the CCR5 genes from diverse simian and prosimian
    species.";
Submitted (UTL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF161951; AAD47707.1; -
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0016872; F:receptor activity; IEA.
GO, GO:000186; P:GProtein coupled receptor protein signalin.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR000276; GPCR_Rhodpsn.
PRGMTS: PR00037; GPCRHODOPSN.
PROSITE; PS00237; GPCRHODOPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 118; DB 6; Length 339; 100.0%; Pred. No. 2.1e-10; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         339 AA; 39098 MW; F0132E8BC44EF829 CRC64;
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Q9TUU7,
Q9TUU7,
Q1-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 APYNIVLLINIFOEFFGLNNCS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macaca fuscata (Japanese macaque)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
Les 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor.
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Matches
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Q9TQV0
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota, Meteazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
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            Length 339;
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100.0%; Score 118; DB 6; Length 3
100.0%; Pred. No. 2.1e-10;
iive 0; Mismatches 0; Indels
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339 339
339 AA; 39019 MW; 7176F940AF11F3ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     339 AA
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                                                                                                                                                                                                                  242 APYNIVLLLNTFOEFFGLNNCS 263
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                                                                                                                                                                1 APYNIVLLLNTFOEFFGLNNCS 22
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Query Match 100.
Best Local Similarity 100.
Matches 22; Conservative
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Q9TUQ9
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Gaps
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                                                                                                             Pfam, PF00001, 7tm 1; 1.
PRINTS, PR00237, GPCRHODOPSN.
PROSITE, PS00237, G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
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Gaps
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Papio papio (Guinea baboon).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Papio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCR5 genes from diverse simian and prosimian
species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AF161995, AAD47750.1; --
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0014872; F:receptor activity; IEA.
GO; GO:0001584; F:receptor activity; IEA.
GO; GO:0001186; P:receptor activity; IEA.
GO; GO:0007186; P:receptor coupled receptor protein signalin.
PFG0001; 7rm 1; IRA
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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339 339 339 WW, 847F8F936B00E6E2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QTUS7;
01-WAY-2000 (TYEMBLrel. 13, Created)
01-WAY-2000 (TYEMBLrel. 13, Last sequence update)
01-JUN-2003 (TYEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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                                                                                                                                                                                                        100.0%; Score 118; DB 6; 100.0%; Pred. No. 2.1e-10;
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                         PROSITE; PS00237; G PROTEIN RECEP F1 1; 1. PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
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                                                                                                                                                                                                                                                                                                             1 APYNIVLLLNTFOEFFGLNNCS 22
  PRINTS; PR00237; GPCRRHODOPSN
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Best Local Similarity 100.
Matches 22; Conservative
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les 22; Conservative
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                                                                           Receptor.
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O9TUW7
DD O9TUW AC 09TUW DT 01-MA'DT 01-MA'DT 01-MA'DT 01-MA'DT 01-MA'DT 0CR5.
GN CCC CG GN CCR5.
OC BURAT
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Q9TUS7
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EMBL; AF162046; AADA7801.1; -

EMBL; AF162043; AADA780.1; -

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:00018872; F:receptor activity; IEA.

GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.

GO; GO:000186; P:G-protein coupled receptor protein signalin. .; IEA.
                                                                                                                                                                                                                                                                                                                                EQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
A Shibara R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;

"Sequences of the CCR5 genes from diverse simian and prosimian

"Sequences of the CCR5 genes from diverse simian and prosimian

"Sequences of the CCR5 genes from diverse simian and prosimian

"Sequences of the CCR5 genes from diverse simian and prosimian

"Secies.";

"Secies.";

"Mady7744.1;

"Rembi, AF161989; AAD47743.1;

"Rembi, AF161989; AAD47743.1;

"Rembi, AF161989; AAD47743.1;

"Rembi, AF161989; AAD47743.1;

"Responsive to the EMBL/GenBank/DDBJ databases.

"Responsive to the EMBL/GenBank/GenBank/DDBJ databases.

"Responsive to the EMBL/GenBank/Gen
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Eukaryota, Metacoa; Chordata; Craniata; Verrebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., Sequences of the CCRS genes from diverse simian and prosimian species.",
                                                                                                                                                                                                Eukaryota, Metazom; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Papio.
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                         Q9TQV0;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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100.0%; Pred. No. 2.1e-10;
tive 0; Mismatches 0;
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  339 AA
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PRT;
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                                                                                                                                                                                       Papio papio (Guinea baboon)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
les 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
  PRELIMINARY;
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Pfam; PF00001; 7tm_1; 1.
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  Q9TQV0
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RESULT 32

8 원 ô

242 APYNIVLLINTFQEFFGLNNCS 263

NCBI\_TaxID=9598;

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species.; submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AF161997; AADJ-7752.1; c. the EMBL/GenBank/DDBJ databases. EMBL, AF161997; AADJ-7752.1; c. membrane; IEA. GO; GO:0016201; C:integral to membrane; IEA. GO; GO:001584; F:rhodopsin-like receptor activity; IEA. GO; GO:0007186; F:rhodopsin-like receptor protein signalin. .; IEA. InterPro; IFR000276; GPCR_Rhodops. InterPro; IFR00037; GPCR_Rhodops. FEMI, FR00237; GPCRRHODPSN. PROSITE; PS00237; GPROTEIN_RECEP_F1.1; 1. PROSITE; PS50262; G_PROTEIN_RECEP_F1.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macaca mulatta (Rhesus macaque).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECURICE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A.P. Pillai S., Kuiken C., Marx P., Wolinksy S.,
Sequences of the CCR5 genes from diverse simian and prosimian
species.",
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF161970; AAD47725.1;
EMBL, AF161970; Cintegral to membrane, IEA.

GO, GO:0106021; C:integral to membrane, IEA.

GO, GO:010612; F:receptor activity; IEA.

GO, GO:0101884; F:rhodopsin-like receptor activity; IEA.
                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 339;
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                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 100.0%; Score 118; DB 6; 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   339 AA.
                                                             339 AA
                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 APYNIVLLINTFQEFFGLNNCS 22
                                                                                                                                                                                                     Papio papio (Guinea baboon)
                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                     Cercopithecinae; Papio.
                                                                                                                                                                                                                                                                                       NCBI_TaxID=100937;
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SEQUENCE FROM N.A.
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                   RESULT 36
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161908; AAD47665.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016842; F:receptor activity; IEA.
GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001186; P:Grotein coupled receptor protein signalin. . .; IEA.
InterPro; IFR000276; GPCR_Rhodopsn.
Pfam: PF00001; 7tm_1; 1.
                                                                                   species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161899; AAD47656.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:001884; F:rreceptor activity; IEA.
GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001886; F:rbocotein outpled receptor protein signalin. .; IEA.
InterPro; IRR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_l; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
        Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; "Sequences of the CCR5 genes from diverse simian and prosimian species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinkey S.,
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pongo pygmaeus (Orangutan).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
NCBI_TaxID=9600;
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0
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; Pred. No. 2.1e-10;
0; Mismatches 0; Indels 0
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339 339
339 AA; 39157 MW; 4A9EBAD183E8E72D CRC64;
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339 AA; 39103 MW; 4350C4625FB0657C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
                                                                                                                                                                                                                                               Pfam; PF00001; 7tm 1; 1. —
PRINTS; PR00237; GPCRHODDSN.
PROSITE; PS00337; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
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1 Similarity 100.0%;
22; Conservative 0
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SEQUENCE FROM N.A.
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Receptor. NON\_TER NON\_TER SEQUENCE

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Query Match

Local

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Q9TUW3

RESULT 35 Q9TUW3

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Cercopithecus mona.
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Best Local Similarity
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SEQUENCE
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Q9TUQ8
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCRS genes from diverse simian and prosimian species.";
                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia! Butheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Papio.

WCBI_TaxID=100937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF161993; AAD47748.1; -.

EMBL; AF161997; AAD47745.1; -.

EMBL; AF161991; AAD47745.1; -.

EMBL; AF161991; AAD47745.1; -.

EMBL; AF161991; C:integral to membrane; IEA.

GO; GO:0016015; F:receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor protein signalin. .

PERML; AF00001; Jrm 1: 1.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
InterPro; IPR00276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GFCRHODDSEN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
Receptor.
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                                                                                                                                          100.0%; Score 118; DB 6; Length 339; 100.0%; Pred. No. 2.1e-10;
                                                                                                                                                                   Indels
                                                                                            31 31 31
339 AA, 39155 MW; 3D1B5039B9E24C82 CRC64;
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                                                                                                                                                                                                                                                                                                      CJ-NAY-2000 (TrEMBLrel. 13, Created)
01-NAY-2000 (TrEMBLrel. 13, Last sequence update)
01-NAY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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PRNTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                         APYNIVLLINTFQEFFGLNNCS 263
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                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                           1 APYNIVLLINTFQEFFGLNNCS 22
                                                                                                                                                                                                                                                                                                                                                                          Papio papio (Guinea baboon)
                                                                                                                                                     Local Similarity 100.
tes 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           339
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SEQUENCE
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                                                                                                                                          Query Match
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Q9TQV3
ID Q9TQV:
AC Q9TQV:
DT 01-MA
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SEQUENCE FROM N.A.

KINSTANDARY STANTON J., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wollnksy S.;
T sequences of the CCRS genes from diverse simian and prosimian

T species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF162040; AAD47795.1;
T SPECIES AF162040; AAD47793.1;
T SPECIES AF162040; AAD47793.1;
T GO; GO: 0016021; C :integral to membrane; IEA.

GO; GO: 0016021; C :integral to membrane; IEA.

GO; GO: 0016021; C :integral to membrane; IEA.

GO; GO: 0010186; P: G-protein coupled receptor protein signalin. .; II]

INTERPRO, JEN00276; GPCRRADODEN.

PROSITE; PRO0237; GPCRRADODEN.

PROSITE; PSS00237; GPCRRADODEN.

PROSITE; PSS00262; G_PROTEIN_RECEP_F1_2; 1.
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Mamalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Cercopithecus.
NCBI_TaxID=36226,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cercopithecus nictitans (white-nosed guenon).
Wakaryota, Metazoa; Chordara, Craniata; Verrebrata, Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M. Skunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M. Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S. Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S. Sequences of the CCR5 genes from diverse simian and prosimian species.";

Species.";

Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AFIG5045, AAD47800.1, -.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:000188; F:rhodopsin-like receptor activity; IEA.

GO; GO:000188; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001286; F:Rhodopsin-like receptor protein signalin.
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339 339
339 AA, 39079 MW, 7176E3EAOE00F3ED CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 118; DB 6;
100.0%; Pred. No. 2.1e-10;
iive 0; Mismatches 0;
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 APYNIVLLINTFQEFFGLNNCS 263
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us-10-084-813-14.rspt

Search completed: September 28, 2004, 09:06:20 Job time : 36.2 secs

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Query Match 100.0%; Score 118; DB 6; Length 339; Best Local Similarity 100.0%; Pred. No. 2.1e-10; Matches 22; Conservative 0; Mismatches 0; Indels 0

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NON TER 139 339 NON TER 139 339 SEQUENCE 339 AA, 39148 MW, 0CA289CDDEEDE831 CRC64;

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                 Copyright
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OM protein - protein search, using sw model

September 28, 2004, 08:51:21; Search time 42.975 Seconds (without alignments) 118.345 Million cell updates/sec Run on:

US-10-084-813-15 95

1 YAFVGEKFRNYLLVFFQK 18 Title: Perfect score: Sequence:

Scoring table:

1586107 segs, 282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

geneseq11980s: geneseqp2000s: geneseqp2001s: geneseqp2001s: geneseqp2003s: geneseqp2003ss: geneseqp2003bs: geneseqp2003bs: A\_Geneseq\_29Jan04:\* 1: genesecn1980c.t Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

ption	Aab88982 HIV qp120	7 HIV		Aae14756 Human CCR	Aae14759 Human CCR	Aae14755 Human CCR	Adc10142 Human NOV	Adc10144 Human NOV	Aaw26766 Human che	407	Aaw27123 Human che	Aaw27125 Macaque c	Aaw07602 Human G-p	Aaw23835 Human CC	Aaw88232 HIV-1 co-	Human H	9 Amino	Human	Aae07048 Human G-p	Aag80111 Human CCR	Aae04321 Human che	Aae07037 Human G-p	Aae07039 Human G-p	Aab46858 Human HDG	Abb56342 Non-endog
ΙD	AAB88982	AAB88997	AAE14757	AAE14756	AAE14759	AAE14755	ADC10142	ADC10144	AAW26766	AAW27407	AAW27123	AAW27125	AAW07602	AAW23835	AAW88232	AAY80128	AAG79089	AAE07046	AAE07048	AAG80111	AAE04321	AAE07037	AAE07039	AAB46858	ABB56342
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1 YAFVGEKFRNYLLVFFQK 18

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Aab83354 Aab82948 Aau971550 Aau971550 Aam52828 Abg92883 Abg92883 Abg92883 Abg92883 Abb932883 Abb9375540 Abb977528 Abb97758	1
AAB83354 AAB82948 AAU97150 AAU97150 AAM52828 AAM52828 ABG22883 ABG22880 AAE25808 AAE25808 AAE25811 ABB1054 AAE25808 AAAE25814 AAB81054 AAB81054 AAB81054 AAB81054 AAB91933	1
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## ALIGNMENTS

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The present invention describes a number of peptides which are able to bind to HIV glycoprotein 120 (gp120). These are similar to the human chemokine receptors CCRS, CXCR4 and STR13, as well as CD4. These are useful in the treatment of HIV, as they prevent replication of the virus. The present sequence is an example of a peptide of the invention
                                                                                                                                                          Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
replication; CCR5; CXCR4; CD4; STRL33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gpl20 under physiological conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 95; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 8e-09;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                          HIV gp120 protein binding peptide #75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 37; 114pp; English.
                                AAB88982 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                      25-AUG-2000; 2000WO-US023505.
                                                                                                                                                                                                                                                                                                                                        99US-0151270P.
                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-244398/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18 AA;
                                                                                                                                                                                                                                          WO200116182-A2.
                                                                                                                                                                                                                                                                                                                                        27-AUG-1999;
                                                                                                                                                                                                          Homo sapiens.
                                                                                             23-MAY-2001
                                                                                                                                                                                                                                                                         08-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                       Saxinger C;
                                                              AAB88982;
RESULT 1
                 AAB88982
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Tue Sep 28 15:49:58 2004

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The present invention describes a number of peptides which are able to bind to HIV glycoprotein 120 (gpl20). These are similar to the human chemokine receptors CRS. CXCR and STRLJ3, as well as CP4. These are useful in the treatment of HIV, as they prevent replication of the virus. The present sequence is an example of a peptide of the invention
                                                                                                                           Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist; replication; CCR5; CXCR4; CTR133.
                                                                                                                                                                                                                                                                                                                                                                                     have homology to CXCR4 and STRL33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human CCR5 chemokine receptor deletion mutant fragment (aa 295-321).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chemokine receptor CCR5; P2 protein; HIV infection; AIDS; human immunodeficiency virus; gene therapy; human; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                    Novel polypeptides useful for treating HIV infection, regions of domains of human chemokine receptors CCR5, and binds to HIV gpl20 under physiological conditions.
                                                                                                                                                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                    HIV gp120 protein binding peptide #90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE14757 standard; peptide; 27 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 21, Page 38; 114pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 YAFVGEKFRNYLLVFFOK 18
                        AAB88997 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 YAFVGEKFRNYLLVFFOK 18
                                                                                                                                                                                                                                                   25-AUG-2000; 2000WO-US023505.
                                                                                                                                                                                                                                                                               99US-0151270P
                                                                            (first entry)
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Best Local Similarity 100.
Marches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-244398/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18 AA;
                                                                                                                                                                                                 WO200116182-A2
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Synthetic.
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                                                                           23-MAY-2001
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                                                   AAB88997
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Gaps

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The invention relates to nucleic acid encoding a protein which interacts with the carboxy terminus of the chemokine receptor CCR5 or of other chemokine receptor family members. Molecules of the invention are used to detect, prevent and treat HIV infection and progression to AIDS. Any CCR5 derived peptides, or compounds derived from the protein of the invention of the invention of the invention would block HIV infection. The present sequence is human chemokine receptor CCR5 C-terminal fragment deletion mutant which is incapable of interacting with the protein of the invention
                                                                                                                                                                                                                                Nucleic acid encoding a protein which interacts with the carboxy terminus of the chemokine receptor CCRS isolated from a human B cell cDNA library is useful to detect, treat and prevent HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human CCRS chemokine receptor deletion mutant fragment (aa 295-337).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chemokine receptor CCR5; P2 protein; HIV infection; AIDS; human immunodeficiency virus; gene therapy; human; mutant; mutein.
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Misc-difference 27 /note= "Wild-type Cys replaced by Glx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Wild-type Ser replaced by Glx"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE14756 standard; peptide; 43 AA.
                                                                                                                                                                                                                                                                                           Example 2; Fig 2A; 28pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YAFVGEKFRNYLLVFFQK 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-NOV-2000; 2000EP-00125052.
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                                                                                                                         16-NOV-2000; 2000EP-00125052.
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                                                                                                                                                                                                        WPI; 2002-437464/47.
                                                                                                                                                    (MOEL/) MOELLING K.
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Best Local Similarity
Matches 18; Conserv
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Synthetic.
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                                       EP1207202-A1
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                                                                                                                                                                               Moelling K,
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                                                                    22-MAY-2002
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(MOEL/) MOELLING

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The invention relates to nucleic acid encoding a protein which interacts with the carboxy terminus of the chemokine receptor CCR5 or of other deneokine receptor family members. Molecules of the invention are used to detect, prevent and treat HIV infection and progression to AIDS. Any CCR5 derived peptides, or compounds derived from the protein of the invention (e.g. antagonist or mutants) that disrupt binding of CCR5 to the protein of the invention would block HIV infection. The present sequence is human chemokine receptor CCR5 C-terminal fragment deletion mutant which is incapable of interacting with the protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid encoding a protein which interacts with the carboxy terminus of the chemokine receptor CCRS isolated from a human B cell cDNA library is useful to detect, treat and prevent HIV infection.
                                                                      Nucleic acid encoding a protein which interacts with the carboxy terminus of the chemokine receptor CCR5 isolated from a human B cell cDNA library is useful to detect, treat and prevent HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to nucleic acid encoding a protein which interacts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human CCR5 chemokine receptor C-terminal mutant fragment (aa 295-352)
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                                                                                                                                  Example 2; Fig 2A; 28pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE14759 standard; peptide; 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-NOV-2000; 2000EP-00125052
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Best Local 18; Conservative
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Misc-difference
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             Moelling K,
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with the carboxy terminus of the chemokine receptor CCRS or of other chemokine receptor family members. Molecules of the invention are used to detect, prevent and treat HIV infection and progression to AIDS. Any CCRS-derived peptides, or compounds derived from the protein of the invention (e.g. antagonist or mutants) that disrupt binding of CCRS to the protein of the invention would block HIV infection. The present sequence is human chemokine receptor CCRS C-terminal mutant fragment which is incapable of interacting with the protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to nucleic acid encoding a protein which interacts with the carboxy terminus of the chemokine receptor CCR5 or of other chemokine receptor family members. Molecules of the invention are used to detect, prevent and treat HIV infection and progression to AIDS. Any CCR5 derived peptides, or compounds derived from the protein of the invention and thock HIV infection. The present sequence is human chemokine receptor CCR5 C-terminal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human CCRS chemokine receptor C-terminal fragment (residues 295-352).
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                                                                                                                                                                                         Length 58;
                                                                                                                                                                                                                            0; Indels
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                                                                                                                                                                                       ch 100.0%; Score 95; DB 5; I Similarity 100.0%; Pred. No. 2.8e-08; 18; Conservative 0; Mismatches 0;
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Pred. No. 2.8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
58
                                                                                                                                                                                                                                                                                                                                                                                  AAE14755 standard; peptide; 58 AA.
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                                                                                                                                                                                                                                                               1 YAFVGEKFRNYLLVFFOK 18
                                                                                                                                                                                                                                                                                              20
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                                                                                                                                                                                                                                                                                 YAFVGEKFRNYLLVFFQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schweneker M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOEL/) MOELLING K.
                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                          Sequence 58 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP1207202-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-OCT-2002
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213 YAFVGEKFRNYLLVFFQK 230
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04-JUN-2001; 2001US-029561P.
06-JUN-2001; 2001US-0296404P.
07-JUN-2001; 2001US-0296418P.
07-JUN-2001; 2001US-0297414P.
11-JUN-2001; 2001US-0297414P.
12-JUN-2001; 2001US-0297567P.
14-JUN-2001; 2001US-0298288P.
15-JUN-2001; 2001US-0298288P.
18-JUN-2001; 2001US-029818P.
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ses 18; Conservative
                                                                                                                  Lepley DM;
                                                                                                                                                                                 WPI; 2003-210149/20.
N-PSDB; ADC10141.
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                                                                                                                            Burgess CE,
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   Gaps
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Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;
Gerlach VL, Gorman L, Guo X, Herrmann JL, Hjalt T, Ji W,
   Indels
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0
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human NOVX polypeptide SEQ ID NO: 162.
                                                                                                                                                                                                                                                                                          ADC10142 standard; protein; 268 AA.
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                                                               1 YAFVGEKFRNYLLVFFOK 18
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2001US-0308890P.
2001US-0324669P.
2001US-0324669P.
2001US-037477P.
2001US-0341562P.
2002US-0358656P.
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2002US-0359035P.
2002US-0359121P.
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2002US-0360858P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-JUN-2002; 2002WO-US017443
                                                                                                                  3 YAFVGEKFRNYLLVFFQK
                                                                                                                                                                                                                                                                                                                                                                                                                  18-DEC-2003 (first entry)
      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-JUN-2001;
15-JUN-2001;
18-JUN-2001;
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22-FEB-2002;
27-FEB-2002;
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28-JUN-2001;
28-JUN-2001;
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21-JUN-2001;
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14-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-JAN-2003
      18;
                                                                                                                                                                                                                                                                                                                                                   ADC10142;
      Matches
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ADC10142

XXX

XXX

XXX

ADC10142

ADC11

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The invention relates to novel isolated polypeptides, mature form of the polypeptide, a sequence that is 95% identical to the polypeptide or the polypeptide comprising one or more conservative substitutions. The NOVX polypeptide is useful for treating or preventing a pathology associated with the polypeptide e.g. disorders associated with aberrant expression or activity of the polypeptide, such as cancer, diabetes, obesity, and endocrine, CNS and inflammatory disorders. They can also be used in various detection and screening assays, chromosome mapping, tissue typing and predictive medicine. This sequence corresponds to one of the polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated NOVX polypeptides and nucleic acid molecules useful for treating, preventing and diagnosing pathological conditions with NOVX-associated disorders, such as cancer, obesity, diabetes and inflammatory or CNS diseases.
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Khramtsov NV, Li Liu X, Malyankar UM, Miller CE, Millet I; Ort T, Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK; Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G, Spaderna SK; Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 162; 772pp; English.
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Mammalian mixed lymphocyte receptor; chemokine receptor; MMLR-CCR; human, monocyte; macrophage; chemotaxis; haematopoiesis; infection; inflammation; proliferative disease; cardiovascular disease; tumour; rheumatiod arthritis; alveolitis; atherosclerosis; chronic granulomatous disease, asthma; myasthenia gravis; diabetes; inflammatory bowel disease; toxic shock syndrome; septic shock; Chediak-Higashi syndrome; therapy; diagnosis.

Human chemokine receptor MMLR-CCR.

(first entry)

21-MAY-1998

AAW26766;

/note= "a claimed polypeptide has isoleucine at residue 121"  $\,$ 

107. .128 /note= "conserved peptide" 121

Misc-difference

Peptide

Location/Qualifiers

Homo sapiens.

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The invention relates to novel isolated polypeptides, mature form of the polypeptide, a sequence that is 95% identical to the polypeptide or the polypeptide compirising one or more conservative substitutions. The NOVX polypeptide is useful for treating or preventing a pathology associated with the polypeptide e.g. disorders associated with aberrant expression or activity of the polypeptide, such as cancer, diabetes, obesity, and endocrine, CNS and infilamatory disorders. They can also be used in various detection and screening assay, chromosome mapping, itseue typing and predictive medicine. This sequence corresponds to one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dipippo VA, Edinger SR, Eisen A, Ellerman K, Catterton E, Gerlach VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA; Gerlach VL, Gorman L, Guo K, Herrmann JL, Hjalt T, Ji W, Kekuda R, Khramtsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I; Rotramtsov NV, Ei E, Esturajan W, Pena CEA, Rastelli L, Rieger DK; Rothenberg ME, Shenoy SG, Shimkets RA, Shithson G, Spaderna SK; Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP; Burgess CE, Lepley DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated NOVX polypeptides and nucleic acid molecules useful for treating, preventing and diagnosing pathological conditions with NOVX-associated disorders, such as cancer, obesity, diabetes and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 95; DB 7; Length 268; 100.0%; Pred. No. 1.4e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 164; 772pp; English.
19-JUN-2001; 2001US-0299230P.
22-JUN-2001; 2001US-029949P.
22-JUN-2001; 2001US-029949P.
26-JUN-2001; 2001US-0301530P.
28-JUN-2001; 2001US-0301530P.
28-JUN-2001; 2001US-0301530P.
31-JUL-2001; 2001US-0301550P.
31-JUL-2001; 2001US-0301550P.
31-JUL-2001; 2001US-0324669P.
31-JUN-2001; 2001US-0324669P.
31-FEB-2001; 2001US-035967P.
31-FEB-2002; 2002US-035903P.
32-FEB-2002; 2002US-035903P.
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CURA-) CURAGEN CORP.
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N-PSDB; ADC10143.
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This protein comprises human WMLR-CCR, a novel C-C chemokine receptor associated with monocyte/macrophage infiltration and chemotaxis and haematopolesis. The amino acid sequence was deduced from a cDNA clone (see AAT99542) obtained from a cDNA library made from monomuclear cells collected on day 2 of a mixed lymphocyte culture, i.e. cells associated with inflammation and immunomodulation. Another novel chemokine receptor, MHG-CCR (see AAN36767), is also claimed. MALR-CCR contains 7 transmembrane spanning segments connected by a serives of intracellular and sextracellular loops. MMLR-CCR and be used to study, diagnose and treat disease states in which normal leukocyte function is perturbed by normal leukopoiesis or inappropriate activation via proliferative disease, tumourigenesis, autoimmune disease, abnormal cell proliferation, solid tumours, cardiovascular disease, abnormal cell arthmis, anyasthenia gravis, diabetes, inflammatory bowel disease, toxic shock syndrome, septic shock and Chediak-Higashi syndrome
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100.0%; Pred. No. 1.7e-07;
trive 0; Mismatches 0;
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Gaps ö

AAW26766 standard; protein; 332 AA

RESULT 9
AAW26766
ID AAW20

213

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1 YAFVGEKFRNYLLVFFOK 18

Polynucleotide encoding MMLR-CCR or MPHG-CCR chemokine receptor - useful to study, diagnose and treat, e.g. infection, inflammation, solid tumour and proliferative and cardiovascular disease.

Wilde CG;

Coleman R,

Bandman O,

Au-Young J,

WPI; 1997-549729/50. N-PSDB; AAT99542

(INCY-) INCYTE PHARM INC

97WO-US006993 96US-00638081

25-APR-1997; 26-APR-1996;

WO9741225-A2

06-NOV-1997.

asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy; diagnosis; leukocyte trafficking; G protein coupled receptor; ligand; modulator; antibody; human.

56. .67 /label= Intracellular\_domain

Location/Qualifiers

Homo sapiens

Key Domain Domain Domain Domain Domain Domain Domain Domain

25. 145 label= Intracellular\_domain 9. .112 |abel= Extracellular\_domain

Extracellular\_domain Intracellular\_domain Extracellular\_domain

11 191 /label= F

301, .352
/label= Intracellular\_domain

WO9722698-A2

26-JUN-1997

/label= Ext 213. .235 /label= In

96WO-US020759 95US-00575967 96US-00661393

20-DEC-1996; 20-DEC-1995; 07-JUN-1996;

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The present sequence is human CC (Cys-Cys) chemokine receptor 5 (CCR5), which is stimulated by MIP-1 alpha, MIP-1 beta or RAWIES chemokines, but not by monocyte chemoattractant protein 1 (MCP-1), MCP-2, MCP-3, interleukin-8 (IL-8) or growth related gene product alpha (GRO alpha) chemokines, Active CCR-5 is also a receptor of human immundeficiency virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can used to diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid psoriasis, viral infections, asthma, idiopathic pulmonary fibrosis and autoimmune disorders
                                                                                                                                                      Human Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention; inflammatory disease; rheumatorid arthritis; glomerulonephritis; asthma: idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer; atherosclerosis; autoimmune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Active and inactive forms of human CC chemokine receptor CCR-5 - useful to diagnose, prevent and/or treat inflammatory disorders, autoimmune disease and viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 95; DB 2; Length 352; 100.0%; Pred. No. 1.9e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Libert F;
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                            AAW27407 standard; protein; 352 AA.
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                                                                                                                                                                                                                                                                                                                                                97WO-BE000023.
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                                                                                                                                                                                                                                                                                                                                                                                             96EP-00870102
                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Samson M, Parmentier M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
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N-PSDB; AAT90117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 352 AA;
                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                              28-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                            01-MAR-1996;
06-AUG-1996;
                                                                                                                                                                                                                                                                                  WO9732019-A2
                                                                                          14-APR-1998
                                                                                                                                                                                                                                                                                                                04-SEP-1997,
                                                                                                                          Human CCR5
                                                            AAW27407;
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Matches
RESULT 10
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This polypeptide sequence comprises novel human chemokine receptor 88C, a grotein coupled receptor that is involved in leukocyre trafficking. Its amno sequence was deduced from a cDNA clone (AAT85161) isolated from a macrophage library. It shows 62% identity to CCCKR1. Chemokine receptor and their polypeptide fragments can be produced in transformed host cells. The receptors, peptides comprising one or more of the extracellular or intracellular domains, and anti-receptor antibodies can be brotein binding, and are potentially posentially useful in the treatment of atherent acceptor activities, particularly ligand and G protein binding, and are potentially posentially useful in the treatment of atherents; rheumatoid arthritis, tumours, asthmaty viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infection, AIDS, inflammatory conditions, pathological immune response,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               abnormal haematopoietic processes etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 16; Page 47-48; 65pp; English
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Gaps

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New nucleic acid encoding chemokine receptors 88-2B and 88C - used modulate leukocyte trafficking, e.g. for treatment of inflammation, tumours, viral infections, auto-immune diseases, etc.

Raport CJ;

Gray PW, Schweickart VL,

(ICOS-) ICOS CORP.

WPI; 1997-341689/31.

N-PSDB; AAT85161

297 YAFVGEKFRNYLLVFFQK 314 셤

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RESULT 12 AAW27125

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Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;

Human chemokine receptor 88C.

14-DEC-1997 (first entry)

AAW27123;

AAW27123
ID AAW2
XX
XX
AC AAW2
XX

AAW27123 standard; protein; 352 AA.

RESULT 11

us-10-084-813-15.rag

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Novel human mature G-protein chemokine receptor HDGNR10 (AAW07602) is a 7-transmembrane protein involved in signal transduction. Its amino acid sequence was deduced from a cDNA clone (AAM44042) isolated from a human moncoyte library. Isolation of the cDNA allows prodn. of recombinant HDGNR10 in host, e.g. E. coli, COS or Sf9, cells. The recombinant sceptor can be used to identify agonists or antagonists of the receptor; such cpds. can be used to treat conditions related to the under- and over-expression of G-protein chemokine receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC chemokine receptor 5; CCR5; G-protein coupled receptor; human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.
haematopoiesis; leukaemia; inflammation; rheumatoid arthritis; diagnosis;
                                                                                                                                                                                                                                                                                                         Human G-protein chemokine receptor, HDGNR10 - useful to identify (ant)agonists, for treatment of haematopoiesis, leukaemia, chronic and acute inflammation, rheumatoid arthritis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="extracellular loop-1 (Claim 19)"
143. 171
14bb=1 IV
/note="transmembrane domain"
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100.0%; Pred. No. 1.9e-07;
ive 0; Mismatches 0;
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104. .126
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                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 44-46; 61pp; English
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                                                                                                                                       95WO-US007173.
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                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
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/label= I
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                             WPI; 1997-043072/04.
N-PSDB; AAT44042.
                                                                                                                                                                                                                                   Li Y, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 352 AA;
                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                            WO9639437-A1
                                                                                                                                       06-JUN-1995;
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                                                                                                            12-DEC-1996.
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                     therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This polypeptide sequence comprises macaque chemokine receptor 88C, a G protein coupled receptor that is involved in leukocyte trafficking. Its amino sequence was deduced from a 88C DNA (AAT85163) isolated by PCR amplification. It shows 97% identity to human 88C (AAW27123). 88C receptors and their polypeptide fragments can be produced in transformed host cells. The receptors, peptides comprising one or more of the extracellular or intracellular domains, and anti-receptor antibodies can be used to modulate receptor activities, particularly ligand and grotein binding, and are potentially potentially useful in the treatment of atheroslerosis, rheumatoid arthritis, tumours, asthma, viral infection, AIDS, inflammatory conditions, pathological immune response, abnormal haematopoietic processes etc. A hybridoma that produces an antibody that specifically binds to macaque 88C is claimed
                                                                                                                          Chemokine réceptor 88C; atherosclerosis; rheumatoid arthritis; tumour; sathma, viral infection; AIDS; inflammation; autoimmune disease; therapy; disquosis; leukocyte trafficking; G protein coupled receptor; ligand; modulator; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding chemokine receptors 88-2B and 88C - used to modulate leukocyte trafficking, e.g. for treatment of inflammation, tumours, viral infections, auto-immune diseases, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human G-protein chemokine receptor HDGNR10.
                                                                                                                                                                                                                                                                                                                                                                                                          Raport CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 36; Page 57-58; 65pp; English.
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   AAW27125 standard; protein; 352 AA
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96US-00661393
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                                                                 (first entry)
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Best Local Similarity 100."
Matches 18; Conservative
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                                                               14-DEC-1997,
                                                                                                                                                                                                                                   WO9722698-A2
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07-JUN-1996;
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                                                                                                                                                                                                                                                                  26-JUN-1997
                                                                                                                                                                                                       Macaca sp.
                                  AAW27125;
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AAW07602
ID AAW0
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AC AAW0
XX
DT 26-F
DE HUMB
XX
KW G-PF
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Gaps

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Length 352; 0; Indels "transmembrane domain 1"

"transmembrane domain 6"

.301

.167

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New CCRS variant protein of the HIV-1 co-receptor - useful in developing resistance of CCRS-expressing cells to {
m HIV-1} infection.
                                                                                                    /note= "corresponds to TGT (Cys) in wild-type CCR5, TGA (Stop) in CCr5m303"
103-.124
/note= "transmembrane domain 3"
                                                                                                                                                               /note= "transmembrane domain 4"
200. .223
                                                                                'note= "transmembrane domain 2"
                                                                                                                                                                                                                                    /note= "transmembrane domain 7"
                                                                                                                                                                                       'note= "transmembrane domain 5"
                                                                                                                                                                                                                                                                                                                                                                               Beretta A, Quillent C, Arenzana Siesdedos F,
                                                                                                                                                                                                                                                                                                                                                        (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 34-35; 55pp; English
                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                           98WO-EP003437
                                                                                                                                                                                            /note= "++
                                               32. .56
/note= "
                                                                   . .87
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-059835/05.
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                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 352 AA;
             Homo sapiens
                                                                                                                                                                                                                                                                                                                                  30-MAY-1997;
                                                                                                                                                                                                                                                              WO9854317-A1
                                                                                                                                                                                                                                                                                                           29-MAY-1998;
                                                                                                                                                                                                                                                                                    03-DEC-1998
                                    Key
Domain
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                                                                                                                                                                                                                                                                                                                                                                                                              This protein sequence comprises of a novel human macrophage-selective CC demonitor receptor that has been designated CCR5. The sequence was deduced from an isolated cDNA clone (see AAT76920). An Ala127Leu variant (see W238340 of CCR5 was also identified. The susceptibility of human macrophages to HIV infection depends on cell surface expression of CD4 and CCR5. CCR5 is a member of the 7-transmebrane superfamily of G-protein coupled cell surface molecules. It plays an essential role in the membrane fusion step of infection by some HIV isolates. The establishment of stable, non-human cell lines and transgenic mammals having cells that coexpress human CD4 and CCR5 provides valuable tools for research of HIV infection. Antibodies that bind to CCR5. CCRS variants, and CCR5-binding agents capable of blocking membrane fusion between HIV and target cells represent potential anti-HIV therapeutics for macrophage tropic strains
                                                                                                                                                                                                                                                                                                                                                        CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 95; DB 2; Length 352; 100.0%; Pred. No. 1.9e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                   Murphy PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
 .87. .210
note= "extracellular loop-2 (Claim 19)"
                                                                                                       'note= "extracellular loop-3 (Claim 19)"
                                                                                                                                                                                                                                                                                   Berger EA, Alkhatib G,
                                              'note= "transmembrane domain"
                                                                       /note= "transmembrane domain"
?61. .276
                                                                                                                                         'note= "transmembrane domain'
                                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW88232 standard; protein; 352 AA
                                                                                                                                                                                                                                                                                                                                                                                          Claim 68; Fig 1C; 70pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YAFVGEKFRNYLLVFFQK 18
                                                                                                                                                                                                                                                                                                                                                                     between HIV and a target cell
                                                                                                                                                                                                               97WO-US009586
                                                                                                                                                                                                                                       96US-0018508P
                                                                                                                 277. .300
/label= VII
                     194. .219
/label= V
                                                        .258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Conservative
                                                                      label=
                                                                                                                                                                                                                                                                                   Combadiere C, Feng Y,
Broder CC, Kennedy PE;
                                                                                                                                                                                                                                                                                                                     WPI; 1998-032650/03.
N-PSDB; AAT76920.
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Best Local Similarity
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 Region
                      Domain
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AAW88232
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Braun J;

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a co-receptor for infection by macrophage-tropic (M-tropic) strains of HIV-1. The invention relates to the identification of a CCRS variant (see AAM89231), designated CCRS, one relates to the identification of a CCRS variant (see AAM89231), designated CCRS, one relation to the relation that the relation of the cCRS allele shows a presence of the CCRS 30 variant with the wild type CCRS allele shows a positive correlation with resistance to infection with M-tropic HIV-1 strains, and may indicate slower progression of the disease. The detection of CCRS variants may be used to identify individuals at lower risk of infection relative to the general population who, if infected, may exhibit slower progression to AIDS. Probes and primers (see AAV84127-36) are provided for use in diagnostic methods for detecting the presence of such variants. A method is provided for inhibiting HIV-1 infection of a cell expressing the CCRS receptor. This involves introducing a nucleic acid encoding a CCRS variant into the cell, thereby reducing the number
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This is the amino acid sequence of wild-type human CCR5, which serves as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 95; DB 2; Length 352; 100.0%; Pred. No. 1.9e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acid encoding a CCR5 variant into the cell, thereby redu
of functional CCR5 molecules present on the cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297 YAFVGEKFRNYLLVFFQK 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YAFVGEKFRNYLLVFFQK 18
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Best Local Similarity 100.0
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AAY80128
ID AAY80:
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AAY80128 standard; protein; 352 AA.

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HIV-1, CCR5, CCR5m303; co-receptor; infection; diagnosis; AIDS; gene therapy; human.

HIV-1 co-receptor CCR5

15-MAR-1999

AAW88232;

dendritic cell; T lymphocyte; HIV; gpl20; entry; T cell; macrophage; HIV infection; CCR5.

Amino acid sequence of human CCRS protein.

receptor; DC-SIGN; lectin; ICAM3; HIV

Human; 2-type

(first entry)

10-DEC-2001

28-FEB-2001; 2001WO-US006322. 32-MAR-2000; 2000US-00517605. (UYNY ) UNIV NEW YORK STATE

WO200164752-A2 Homo sapiens.

37-SEP-2001

UYNI-) UNIV NIJMEGEN

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designated HDGNRIO. HDGNRIONS a numerical content of the properties of the propertie
                                                                                                                                                                                                      receptor; G-protein chemokine receptor; HDGNR10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acid encoding human G-protein chemokine receptor usefu
for diagnostic assays, scientific research and screening for compounds
which bind to and activate or inhibit activation of the receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polynucleotides are also useful for in vitro purposes related to scientific research, synthesis of DNA and manufacture of DNA vectors
                                                                                                                                                                                                                            diagnosis; haematopolesis; wound healing; coagulation; angiogenesis; tumour; infection; leukaemia; psoriasis; allergy; T-cell mediated autorimmune disease; atherogenesis; anaphylaxis; inflammation; allergic reaction; silicosis; sarcoidosis; rheumatoid arthritis; hyper-eosinophilia syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present sequence represents a human G-protein chemokine
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                                                                                                                                          Human G-protein chemokine receptor HDGNR10 SEQ ID NO:2.
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100.0%; Score 95; DB 3; 1
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 18; Conservative 0; Mismatches 0;
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                                                                                     (first entry)
                                                                                                                                                                                                      coupled
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N-PSDB; AAZ91481.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUN-1995;
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                                                                                     19-MAY-2000
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                         AAY80128;
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Gaps
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                                                                                            Human G-protein chemokine receptor (CCR5) HDGNR10 protein #1.
Indels
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 Mismatches
                                                        AAE07046 standard; protein; 352 AA
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                    1 YAFVGEKFRNYLLVFFOK 18
                                                                                 (first entry)
                                                                                 16-OCT-2001
                                                                     AAE07046;
                                            RESULT 18
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Gaps

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0; Indels

AAG79089 standard; protein; 352 AA.

RESULT 17 AAG79089 AAG79089;

297 YAFVGEKFRNYLLVFFQK 314

1 YAFVGEKFRNYLLVFFQK 18

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV; human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; cytostatic; immunosuppressive; nootropic; neuroperotective; gene therapy; neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary, adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         An antibody for the treatment or prevention of HIV-infection comprises a gpl20 portion which binds to DC-SIGN or is exposed upon gpl20 binding of DC-SIGN due to concomitant conformational change.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 95; DB 4; Length 352; 100.0%; Pred. No. 1.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Geijtenbeek T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 118-119; 131pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                functions in HIV-1 entry into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Van Kooyk Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-602565/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Littman DR,
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calls, HIV infection (such as Pneumocystis carini pheumonia or Kaposi's carcoma) or defective or aberrant Treell antigen presenting cell interaction. The disease or disorder may also be an infectious disease (e.g. a viral infection, such as an early stage HIV infection, a issease (e.g. a viral infection, or a poxvirus infection, an autoimmune disease (e.g. theumatoid arthritis) or a neurodegenerative disorder. The disease or disorder may be associated with aberrant CGRS expression, lack of CGRS infection, aberrant CRS ilgand expression, or lack of CGRS ligand function. CGRS HIDGRALD protein is used as a food additive or preservative to increase or decrease storage capabilities. CGR HIDGRALD DNA, protein, antibodies, agonists and antagonists are also useful in the disorders, agonists and antagonists are also useful in the disposits, treatment and prevention of cancer (breast, overy, adrenal urogenital); immune disorders (Adisson's disease, allergies, autoimmune thyroiditis, diabetes mellitus, Crohn's is disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular disorders (myocacdial ischaemias) and wound healing. The present sequence is human CCRS HDGRNIO protein

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Isolated nucleic acid encoding a human G-protein chemokine receptor (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human G-protein chemokine receptor (CCR5) HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are useful for treating, preventing or ameliorating a disease or disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 102; Fig 1; 518pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                           09-FEB-2000; 2000US-0181258P.
09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurodegenerative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen CA, Roschke V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-488966/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diseases e.g.
                       Homo sapiens
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                                       Key
Domain
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multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia.
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                                                                                   1. .36
/label= Extracellular_domain
                                                                                                                                         7. .58
label= Transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136. .260
|Tabel= Transmembrane_domain
|note= "Segment 6"
                                                                                                                             Transmembrane domain
                                                                                                                                                                                  9. .67
label= Intracellular_loop_1
                                                                                                                                                                                                                                                                                     .03. .124
|Tabel= Transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        287. .305
/label= Transmembrane_domain
/note= "Segment 7"
                                                                                                                                                                                                                                                                     Extracellular_loop_1
                                                                                                                                                                                                                                                                                                                                           Intracellular_loop_2
                                                                                                                                                                                                                                                                                                                                                          42. .166
label= Transmembrane_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane_domain
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                                                                       Location/Qualifiers
                                                                                                                                                                        "Segment 1"
                                                                                                                                                                                                                                                                                                                note= "Segment 3"
                                                                                                                                                                                                                                                                                                                                                                                  note= "Segment 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Segment 5'
                                                                                                                                                                                                                                                      89. .102
/label= E:
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                                                                                                                                                                                                                                                                                                                                                                                                     .195
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/label= E
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/label= T
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Gaps

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Query Match 100.0%; Score 95; DB 4; Length 352; Best Local Similarity 100.0%; Pred. No. 1.9e-07; Matches 18; Conservative 0; Mismatches 0; Indels

Sequence 352 AA;

AAE07048 standard, protein; 352 AA.

RESULT 19

AAE07048

(first entry)

16-OCT-2001

AAE07048;

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Isolated nucleic acid encoding a human G-protein chemokine receptor (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune
                                                                                                            Human, G-protein chemokine receptor; CCR5, HDGNR10, inflammation; HIV; human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; cytostatic; immunosuppressive; noctropic, neuroprotective; gene therapy; neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia.
                                                                               Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                      09-FEB-2000; 2000US-0181258P.
09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
                                                                                                                                                                                                                                                                                                                                                                                         09-FEB-2001; 2001WO-US004153.
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N-PSDB; AAD13299.
                                                                                                                                                                                                                                                                                                                      WO200158916-A2.
                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                        16-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen CA,
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Li Y, Ruben SM;

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diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders.
        Example 40; Page 504-505; 518pp; English.
                                                                             Sequence 352 AA;
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 100.0%; Score 95; DB 4; Length 352; 100.0%; Pred. No. 1.9e-07;
                        0; Indels
                        Mismatches
                          ó
                                                             297 YAFVGEKFRNYLLVFFQK 314
                                                 1 YAPVGEKFRNYLLVFFOK 18
       l Similarity 100.
18; Conservative
Query Match
Best Local Si
Matches 18
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AAG80111 standard; protein; 352 AA 17-JAN-2002 (first entry) Human CCR5 protein. AAG80111; 

Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection; inflammation; autoimmune disease; metastasis; bronchial asthma; lupus; chronic bowel inflammation; rheumatoid arthritis; cytostatic; antiinflammatory; antiasthmatic; immunosuppressive; dermatological; antirheumatic; antiarthritic.

WO200172830-A2 Homo sapiens.

04-OCT-2001.

02-APR-2001; 2001WO-EP003708,

31-MAR-2000; 2000DE-01016013

(IPFP-) IPF PHARM GMBH. (FORS/) FORSSMANN U.

Spodsberg N; Heitland A, Forssmann W, Adermann K,

WPI; 2001-626256/72.

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or prostatio), organ rejection, inflammation and autoimmune diseases.

Also inhibitors of (I) are used therapeutically against tumors (and their metastases), inflammation (particularly bronchial asthma or chronic bowel inflammation), or autoimmune diseases (rheumatoid arthritis or lupus), where the (cardio) vascular, lymphatic, respiratory, nervous, digestive, endocrine, motor or urogenital systems or skin are affected, and bone marrow diseases. The products of the invention are chemokine derivatives which have cytostatic, antiinflammatory, antiasthmatic, immunosuppressive, dermatological, antiirheumatic, antiarthritic. Chemokines act on specific tumor and inflammatory cells through a constellation of chemokine receptors (CR), which control migration and proliferation of these cells. AG88045-AA680128 represent human chemokine fragments used to illustrate the method of the invention
Diagnostic agent containing two or more receptor-specific ligands, useful for detecting tumors, inflammation etc., also therapeutic use of ligand inhibitors.
                                                                                                                                                                     This invention describes a novel diagnostic agent (A) comprising at least two different ligands (I) for receptors (II) that are implicated in disease. (A) are used for the diagnosis of tumors (especially colorectal
                                                                                                                   Disclosure; Page 10; 26pp; German.
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Sequence 352 AA;

ö Gaps ó, Length 352; 0; Indels 100.0%; Score 95; DB 4; I 100.0%; Pred. No. 1.9e-07; ive 0; Mismatches 0; 297 YAFVGEKFRNYLLVFFOK 314 1 YAFVGEKFRNYLLVFFOK 18 Cuery Match
Best Local Similarity 100.0

ઠે 셤 RESULT 21 AAE04321

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Gaps

AAE04321 standard; protein; 352 AA 04-SEP-2001 (first entry) AAE04321;

Human chemokine receptor (CKR), CC-CKR-5 related protein #2. 

Human, transformed mammalian cell; CD4; reporter gene; translocation; human immuno deficiency virus; HIV; long terminal repeat; LTR; therapy; chemokine receptor; CKR; cellular dysfunction; HIV infection; cofactor; CC-CKR-5; envelope glycoprotein; anti-HIV.

Homo sapiens.

US6258527-B1.

10-JUL-2001.

96US-0017157P. 97US-00861105. 21-MAY-1997; 20-MAY-1996; 19-JUN-1996;

96US-0020043P. 19-MAY-1997; (AARO-) AARON DIAMOND AIDS RES CENT. (UXNY ) UNIV NEW YORK STATE.

Deng H, Ellmeier W, Landau NR, Liu Littman DR,

3

WPI; 2001-417127/44.

N-PSDB; AAD08577.

mammalian cell (I) that contains a  ${\rm CD4}$  gene, reporter gene for identification of drugs and antibodies for treatment of Transformed nand HIV LTR 1

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The present invention relates to a transformed mammalian cell that contains a gene encoding CD4, a construct encoding a reporter gene under the regulation of an human immuno deficiency virus (HIV) long terminal repeat (LTR) and that has been transduced with a vector encoding a human chemokine receptor (CKR) where the CD4 and the CKR are present on the cell surface of transformed mammalian cell. The invention is useful for identifying drugs or antibodies that interfere with the translocation of HIV into transformed mammalian cell or for identifying a human chemokine receptor that facilitates the infection of a particular HIV strain into the transformed mammalian cell. Compounds identified can be used to treat cellular dysfunction and to prevent or combat HIV infection. The present cellular dysfunction has receptor (CKR), CC-CKR-5 related protein. CC-CKR-5 is the prinary macrophage-tropic strains of HIV-1
Disclosure; Col 47-50; 37pp; English
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# Sequence 352 AA;

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Gaps
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Length 352;
                          0; Indels
 100.0%; Score 95; DB 4; L
100.0%; Pred. No. 1.9e-07;
ive 0; Mismatches 0;
                                                                        297 YAFVGEKFRNYLLVFFQK 314
                                                     1 YAFVGEKFRNYLLVFFOK 18
Query Match
Best Local Similarity 100.
Matches 18; Conservative
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AAE07037 standard; protein; 352 AA. AAE07037;

(first entry) 16-OCT-2001 Human G-protein chemokine receptor (CCR5) HDGNR10 protein #1.

Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV; human immunodeficiency virus; antimicrobial; vasodilator; vulnerary; cytostatic; immunosuppressive; nootropic, neuroprotective; gene therapy; neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia.

## Homo sapiens

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142. .166
/label= Transmembrane_domain
/note= "Segment 4"
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| label = Transmembrane_domain
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/label= Transmembrane_domain
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/label= Transmembrane_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37. .305
/label= T
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/label=
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RESULT 22
AABO7037
XX
AAC AAE07
XX
AAC AAE07
XX
XX
XX
Human
XX
Hum
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Extracellular loop 2
      196. .223
/label= Transmembrane_domain
                       236. .260
/label= Transmembrane_domain
                                           'label= Transmembrane_domain
                24. 235 _
label= Intracellular_loop_3
                                    Extracellular_loop_3
            "Segment 5"
                             note= "Segment
167. .195
'label= Ex
                                 .274
                                 261. .27
/label=
              note=
                                                            WO200158915-A2
                                                  Domain
Domain
       Domain
                 Domain
                        Domain
                                  Domain
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16-AUG-2001.

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09-FEB-2001; 2001WO-US004152

09-FEB-2000; 2000US-0181258P. 09-MAR-2000; 2000US-0187999P. 22-SEP-2000; 2000US-0234336P.

(HUMA-) HUMAN GENOME SCI INC

Li Y, Ruben SM; Rosen CA,

WPI; 2001-488965/53. N-PSDB; AAD13181. Isolated nucleic acid encoding a human G-protein chemokine receptor (CCRS) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheunatoid arthritis, hyperproliferative disorders and neurodegenerative disorders.

# Claim 102; Fig 1; 495pp; English

The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10 protein. CCR5 HDGNR10 cDNA is included in ATCC Deposit No: 97183. CCR5 HDGNR10 antibodies are useful for treating, preventing or ameliorating a disease or disorder associated with inflammation, defective or aberrant chemotaxis of immune cells. HIV infection (such as Pneumocystis carini commonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen presenting cell interaction. The disease or disorder may also be an infection, a cytomegalovirus infection such as an early stage HIV infection, a cytomegalovirus infection, or a poxvirus infection), an infection, a cytomegalovirus infection, or a poxvirus infection), an infection, a cytomegalovirus infection, or a poxvirus infection), and catoline assets or disorder may be associated with aberrant CCR5 catoline and independent in the disease or disorder may be associated with aberrant CCR5 capters in a lack of CCR5 function, aberrant CCR5 ligand expression, or additive or preservative to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA, protein, antibodies, agonists and antagonists are also useful in the diagnosis, treatment and prevention of cancer (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract, liver, lung, urogenital); immune disorders (Addison's disease, allegias, autoimmune thyroidisis, diabetes mellitus, collin's disease, multiple solerosis, rheumatoid arthritis and ulcerative collin's is cardiovascular disorders (Myocardial ischaemias) and wound

## Sequence 352 AA;

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Gaps
                                                             ..
Query March
100.0%; Score 95; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
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Domain

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297 YAFVGEKFRNYLLVFFQK 314

AAE07039 standard; protein; 352 AA 

AAE07039;

(first entry) 16-OCT-2001

Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.

Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV; human immunodeficiency virus; antimicrobial; vascaliator; vulnerary; cytostatic; immunosuppressive; nootropic; neuroprotective; gene therapy; neurodegenerative disorder; Kaposi's sarcoma; autoimmune disoase; rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow; gastrointestinal tract; lung; liver; immune disorder; Addison's disease; haemolytic antenna; autoimmune thyroiditis; diabetes mellitus; allergy; multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing; cardiovascular disorder; myocardial ischaemia.

Homo sapiens.

WO200158915-A2.

16-AUG-2001.

09-FEB-2001; 2001WO-US004152.

09-FEB-2000; 2000US-0181258P. 09-MAR-2000; 2000US-0187999P. 22-SEP-2000; 2000US-0234336P.

(HUMA-) HUMAN GENOME SCI INC

Li Y, Ruben SM; Rosen CA, Roschke V,

WPI; 2001-488965/53. N-PSDB; AAD13198.

Isolated nucleic acid encoding a human G-protein chemokine receptor (CCRS) HDGNR10 polypeptide, useful for preventing or treating autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders and neurodegenerative disorders.

Example 40; Page 486-487; 495pp; English.

The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10

protein. CCR5 HDGNR10 antibodies are useful for treating, preventing or
ameliotaring a disease or disorder associated with inflammation,
defective or aberrant chemotastic fairmune cells, HIV infection (such as
considerating addisorder associated with inflammation,
defective or aberrant chemotastic fairmune cells, HIV infection (such as
aberrant T-cell antigaen presenting cell interaction. The disease or
disorder may also be an infection, a disorder with a infection, or a
considerative infection, an autoimmune disease (e.g. rheumatoid arthritis) or
a neurodegenerative disorder. The disease or disorder may be associated
with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5
is used as a food additive or preservative to increase or decrease
consideration and in gene therapy. CCR5 HDGNR10 DNA, protein,
contibodies, agonists and antagonists are also useful for chromosome
contibodies, agonists and antagonists are also useful in the diagnosis,
creatment and prevention of cancer (breast, ovary, adrenal gland, bone,
contibodies, agonists and antagonists, autoimmune haemolytic anaemia,
disorders (Adisaor's disease, allergies, autoimmune haemolytic anaemia,
autoimmune thyroiditis, diabetes mellitus, cardiovascular
content and prevential ischaemias) and wound healing

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                            Gaps
                            ;
 Length 352;
                           0; Indels
100.0%; Score 95; DB 4; L
100.0%; Pred. No. 1.9e-07;
ive 0; Mismatches 0;
Query Match 100.
Best Local Similarity 100.
Matches 18; Conservative
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Sequence 352 AA;

RESULT 24 AAB46858

AAB46858 standard; protein; 352 AA

AAB46858;

(first entry) (revised) 16-AUG-2001 04-MAY-2001

Human HDGNR10 protein.

HDGNR10; human; G-protein chemokine receptor; antiinflammatory; immunomodulatory; antioparaitic; antiparaitic; vasotropic; gene therapy; haematopoiesis; wound healing; coagulatic; angiogenesis; solid tumour; infection; leukemia; growth factor activity; T-cell mediated autoimmune disease; psoriasis; allergy; atherogenesis; anaphylaxis; malipanacy; inflammation; histamine; IGE; silicosis; shock; immunoglobulin B-mediated allergic reaction; rheumatoid arthritis; prossaglandin-independent fever; bone marrow failure; sarcoidosis; hyper-eosinophilic syndrome; vulnerary.

Homo sapiens.

US2001000241-A1.

12-APR-2001

29-NOV-2000; 2000US-00725285

95US-00466343. 98US-00195662. 99US-00339912. 06-JUN-1995; 18-NOV-1998; 25-JUN-1999;

(LIYY/) LI Y. (RUBE/) RUBEN S M.

Li Y, Ruben SM;

WPI; 2001-226317/23. N-PSDB; AAF26390 New human G-protein chemokine receptor polypeptides and polynucleotides, useful for identifying (ant)agonists to the G-protein chemokine receptor

Claim la; Page 15; 22pp; English.

This invention describes a novel receptor polypeptide (I) selected from filly defined 329 amino acid sequence (II) fully disclosed in the specification; and (ii) a polypeptide encoded by the CDNA contained in a plasmid, and fragments, analogs and derivatives of the polypeptide. The products of the invention have antiinflammatory, immunomodulatory, anticoagulant, antiallergic, immunosuppressive, vulnerary, cytostatic, antiparastic, antiparastic, antipheumatic, antiarchritic and vasotropic activity and can be used for gene therapy. The G-protein chemckine receptors, HDGNR10, (I) are useful for screening for compounds which activate or inhibit activation of (I). The products of the invention can also be used for stimulating haemacopoiesis, wound healing, coagulation, angiogenesis, treating solid tumours, chronic infections, leukemia, T-cell mediated autoimmune diseases, parastitic infections, psoriasis, and stimulating growth factor activity. HDGNR10 is useful for treating

RESULT 26

4AB8335

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying agonists of G protein-coupled receptors (GPCRs) for use in disease treatment, comprises contacting candidate compounds with versions of GPCRs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to G protein-coupled receptors (GPCRs) for which the endogenous ligand has been identified. Non-endogenous constitutively activated versions of known GPCRs are used in the invention for the direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists. Such agonists are useful as therapeutic agents for diseases or disorders associated with GPCRs. The present sequence is a non-endogenous version of a known human GPCR
allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation, histamine and immunoglobulin E (IgE)-mediated allergic reactions, prostaglandin-independent fever, bone marrow failure, silicosis, sarcoidosis, rheumatoid arthritis, shock and hyperecionaphilic syndrome. (N.B. This record was resubmitted to correct errors in the keyword formatting)
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, G protein-coupled receptor; GPCR; non-endogenous; mutant;
constitutively activated GPCR; agonist; disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 95; DB 4; Length 352; 100.0%; Pred. No. 1.9e-07; cive 0; Mismatches 0; Indels
                                                                                                                                                     Length 352;
                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    Non-endogenous human GPCR protein, SEQ ID NO: 477
                                                                                                                                                   100.0%; Score 95; DB 4; L
100.0%; Pred. No. 1.9e-07;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 277-278; 394pp; English.
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                                                                                                                                                                                                                                                                                                                                       ABB56342 standard; protein; 352
                                                                                                                                                                                                                                                  297 YAFVGEKFRNYLLVFFOK 314
                                                                                                                                                                                                                     1 YAFVGEKFRNYLLVFFOK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lehmann-Bruinsma K, Liaw CW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-APR-2000; 2000US-0195747P
                                                                                                                                                                                                                                                                                                                                                                                                      18-FEB-2002 (first entry)
                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-648759/74.
N-PSDB; ABI97978.
                                                                                                                                                                   Local Similarity
es 18, Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 352 AA;
                                                                                                                       Sequence 352 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                       ABB56342;
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                                                                                                                                                       Query Match
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Matches
                                                                                                                                                                                                                                                                                                     RESULT 25
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This sequence represents the human CCRS protein sequence. The invention relates to a method for determining whether an agent is capable of modulating the interaction of chemotractic chemokine receptor 5 (CCRS) with gpl20, comprising incubating the agent with CCRS and gpl20 and determining whether the agent modulates the interaction, where gpl20 is associated with CDA, and where the interaction is a low affinity binding. The method is used to identify an agent capable of modulating the interaction of CCRS with gpl20, an agent capable of modulating the interaction of CCRS with gpl20, an agent capable of modulating the confittion associated with CCRS and gpl20 interaction, to treat a subject with a disease or condition associated with CCRS and gpl20 interaction, to treat a subject with a disease or condition associated with CCRS and gpl20 interaction, and for preparing a pharmaceutical for treating human immunodeficiency virus (HIV). It can also be treat anti-inflammatory diseases. The method is commercially useful, amenable to high throughput screening, and cetects interaction of gpl20 with cells expressing only CCRS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determining if an agent can modulate CCRS-gp120 interaction, comprises incubating the agent with CCRS and gp120 and determining if the agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                       Chemotactic chemokine receptor 5; gpl20; CD4; therapy; HIV; CCR5; human immunodeficiency virus; anti-inflammatory disease; human.
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100.0%; Pred. No. 1.9e-07;
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AAB83354 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB82948 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 110; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rickett GA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    297 YAFVGEKFRNYLLVFFQK 314
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                                                                                                                                                                                                                                                                                                             03-JAN-2001; 2001EP-00300020.
                                                                                                                                                                                                                                                                                                                                              12-JAN-2000; 2000GB-00000659.
12-JAN-2000; 2000GB-00000661.
12-JAN-2000; 2000GB-00000663.
                                                                                                          Human CCR5 protein sequence
                                                                     09-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modulates the interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dobbs S, Perros M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-477088/52
N-PSDB; AAF87099.
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Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                     (PFIZ ) PFIZER LTD (PFIZ ) PFIZER INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 352 AA;
                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                      25-JUL-2001.
                                    AAB83354;
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AAB82948;

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Gaps

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297 YAFVGEKFRNYLLVFFQK 314

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1 YAFVGEKFRNYLLVFFOK 18

Conservative

Local Similarity les 18; Conser

Best Loca Matches

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Human, G-protein chemokine receptor; CCR5; HDGNR10; inflammation; fimune ed.l chemotaxis; autroimmine disease; rheumatoid arthritis; neurodegeneration; viral infection; Kaposi sarcoma; cancer; hyperproliferative disease; neurological disease; receptor.
           Human G-protein chemokine receptor (CCR5) HDGNR10 #1.
                                                                                                                         US2002048786-A1
                                                                                                  Homo sapiens.
                                                                                                                                                   25-APR-2002.
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ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is that of human HIV-1 co-receptor CCR5. Amino acids 2-18 in the N-terminal region of CCR5 comprise an HIV-1 gp120-binding site that determines the specificity of the interaction between CCR5 and HIV-1 gp120. Post-translational sulfation of the tyrosine residues in the CCR5 N-terminus is required for gp120 binding and may critically modulate the susceptibility of target cells to HIV-1 infection in vivo. The invention provides claimed sulfated peptides (see AAB82947) that are based on the CCR5 N-terminal region and which are effective for inhibiting HIV-1 binding to CCR5. These peptides are used in claimed methods of inhibiting HIV infection of CO4+ cells, of preventing CD4+ cells are infected with HIV, and of identifying an agent which inhibits binding of a CCR5 receptor. The methods may be carried cout in a subject, especially a human, infected (therapeutic method), not infected with HIV (prophylactic method), or in a subject who is not infected with, but has been exposed to, HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                               CCR5; chemokine; co-receptor; human immunodeficiency virus type 1; HIV-1; infection; therapy; vaccine; anti-HIV-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                       Novel compounds comprising specific amino acids within CCRS (HIV 1 ccreceptor) amino terminal domain including negatively charged and two sulfated tyrosine residues is useful for treating HIV infection in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 95; DB 4; Length 352; 100.0%; Pred. No. 1.9e-07; tive 0; Mismatches 0; Indels
                                                                                                                           2. .18
/note= "binds to HIV-1 gp120"
                                                                                                                                                                                                                                                                                       (PROG-) PROGENICS PHARM INC.
(AARO-) AARON DIAMOND AIDS RES CENT.
                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 30; 163pp; English
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                                                                                                                                                                                                                                      29-FEB-2000; 2000US-0185657P.
19-MAY-2000; 2000US-0205839P.
07-FEB-2001; 2001US-0267231P.
                                                                                                                                                                                                                 28-FEB-2001; 2001WO-US006699.
                         Human HIV-1 co-receptor CCR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Best Local Similarity
Local 18; Conserve
                                                                                                                                                                                                                                                                                                                             Olson WC;
                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-611273/70.
N-PSDB; AAH26903.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 352 AA;
                                                                                                                                                               WO200164710-A2
                                                                                       Homo sapiens
                                                                                                               Key
Binding-site
                                                                                                                                                                                       07-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-2002
21-DEC-2001
                                                                                                                                                                                                                                                                                                                             Dragic T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU97150;
                                                                                                                                                                                                                                                                                                                                                                                                                                   humans.
                                                  CCR5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU97150
ID AAU9
XX AAU9
AC AAU9
XX I3-A
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The present invention relates to the isolation of a novel human G-protein chemokine receptor (CCRS) designated HDGNR10, and polynucleotide chemokine receptor (CCRS) designated HDGNR10 and polynucleotide corporates encoding it. The invention also describes antibodies that bind chuman G-protein chemokine receptor (CCRS) HDGNR10 and polynucleotide corporates inflammation, defective or aberrant chemotaxis of immune corporations (especially arthritis, neurodegeneration, viral inflammation, defective or aberrant chemotaxis of immune colls and T-cell/attigen-presenting cell interactions, infections and autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral infections (expecially early-stage human immune deficiency virus (H1V), cytcmegalovirus or pox virus infections, Kaposi sarcoma, or conditions associated with aberrant or deficient expression of the CCRS receptor or its ligands. The antibodies are also useful to determine CCRS expression, e.g. for diagnosis, prognosis and monitoring of cancer and other chyperproliferative diseases. The polynucleotide sequences encoding human CG-protein chemokine receptor (CCRS) HDGNR10 can be used to produce the receptor and in the treatment of a wide range of diseases such as infectious diseases (e.g. influenza) neurological diseases (e.g. HDGNR10 #HDGNR10 #HDGNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding an antibody specific for the G-protein chemokine receptor CCRS, useful for treatment and diagnosis of e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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100.0%; Pred. No. 1.9e-07;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU97152 standard; protein; 352 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 61; Fig 1; 180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297 YAFVGEKFRNYLLVFFQK 314
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                                                                                  09-FEB-2000; 2000US-0181258P.
09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Li Y,
09-FEB-2001; 2001US-00779879.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosen CA, Roschke V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-434754/46.
N-PSDB; ABK51853.
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Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                (ROSE/) ROSEN C A. (ROSC/) ROSCHKE V.
                                                                                                                                                                                                                                                                                                                                                                            (LIYY/) LI Y.
(RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammation.
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CCR5; CC chemokine receptor 5; human; HIV infection; human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome; drug screening; identification; variant.

(first entry)

22-FEB-2002

AAM52829;

Human CCR5 Gln 55 variant

'note= "Glu replaces wild-type Leu; encoded by CTG'

Location/Qualifiers

Key Misc-difference Misc-difference

Homo sapiens,

/note= "Encoded by AGC"

WO200171346-A2

27-SEP-2001

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New nucleic acid encoding an antibody specific for the G-protein chemokine receptor CCR5, useful for treatment and diagnosis of e.g.
                                                  immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;
neurodegeneration; viral infection; Kaposi sarcoma; cancer;
hyperproliferative disease; neurological disease; receptor.
                                           G-protein chemokine receptor; CCRS; HDGNR10; inflammation;
                          Human G-protein chemokine receptor (CCR5) HDGNR10 #2.
                                                                                                                                                                                                                                                                                                                         Disclosure, Page 165-166; 180pp; English.
                                                                                                                                                                                                                                            Ruben SM;
                                                                                                                                                                                                                                            Li Y,
                                                                                                                                                           09-FEB-2000; 2000US-0181258P.
09-MAR-2000; 2000US-0187999P.
22-SEP-2000; 2000US-0234336P.
                                                                                                                                           09-FEB-2001; 2001US-00779879.
        13-AUG-2002 (first entry)
                                                                                                                                                                                                                                            Roschke V,
                                                                                                                                                                                                                                                             WPI; 2002-434754/46.
N-PSDB; ABK51870.
                                                                                                                                                                                                ROSEN C A.
                                                                                                                                                                                                                         RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 352 AA;
                                                                                                         US2002048786-A1.
                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                         inflammation
                                                                                                                          25-APR-2002
                                                                                                                                                                                                                                            Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HDGNR10 #2
                                                                                                                                                                                                                (LIYY/)
(RUBE/)
                                                                                                                                                                                                ROSE/)
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The present invention relates to the isolation of a movel human G-protein chemokine receptor (CCR5) designated HDGNR10, and polymucleotide sequences encoding it. The invention also describes antibodies that bind human G-protein chemokine receptor (CCR5) HDGNR10 and polymucleotide sequences encoding the antibodies. The antibodies are useful for treating or preventing inflammation, defective or aberrant chemotaxis of immune cells and T-cell/antigen-presenting cell interactions, infections and autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral infections (especially early-stage human immune deficiency virus (HIV), cytomegallovitus or pox virus infections, Kaposi sarcoma, or conditions associated with aberrant or deficient expression of the CCR5 receptor or its ligands. The antibodies are also useful to determine CCR5 expression, e.g. for diagnosis, prognosis, and monitoring of cancer and other hyperproliferative diseases. The polymucleotide sequences encoding human G-protein chemokine receptor (CCR5) HDGNR10 can be used to produce the receptors, and in the treatment of a wide range of diseases such as infectious diseases (e.g. cancer). The Horman as the expression of the seases (e.g. present sequence represents human G-protein chemokine receptor (CCR5) HDGNR10 can be used to produce the receptors and hyperproliferative disorders (e.g. cancer). The Horman and Amendal Amendal diseases (e.g. encoments) and hyperproliferative disorders (e.g. cancer). The Horman Amendal Amendal diseases and Horman Amendal Amendal diseases.
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                                      Gaps
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 100.0%; Score 95; DB 5; Length 352; 100.0%; Pred. No. 1.9e-07; ative 0; Mismatches 0; Indels
                                                                      1 YAFVGEKFRNYLLVFFQK 18
Query Match
Best Local Similarity 100.
Matches 18; Conservative
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                                                                                there is a glutamine, rather than a leucine, at position 55
                                                                                      Length 352;
                                                                                   Sequence 352 AA;
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The invention relates to a method for identifying a binding compound for a chemokine receptor 5 (CCR5). The method involves screening a library of test molecules (particularly peptides) with immobilised CCR5, and then central those molecules which be invention also relates to constitute those molecules which bind. The invention also relates to construct the consensus motifs for CCR5-binding peptides, a transfer vector encoding tagged CCR5, a computer-aided method for identifying consensus motifs for CCR5-binding peptides, a computer aided drug screening assay that utilises the three-dimensional a computer aided drug screening assay that utilises the three-dimensional structure of CCR5. Compounds identified using the methods for the invention are useful for treating or preventing the methods of the invention are useful for treating or preventing HTM (human immunodeficiency virus) infection or AIDS (acquired immunodeficiency syndrome) in a patient. The methods of the invention may also be used to sidentify agonists or antagonists of the interaction of CCR5 with its natural ligand, and to determine a binding motif for CCR5. The present sequence represents a naturally occurring variant of human CCR5 in which

Identifying CC chemokine receptor 5 binding compound for treating AIDS, comprises binding a molecule from library to a molecule having binding property corresponding to CCRS and identifying bound molecule.

Example 3; Fig 4B; 50pp; English.

Tan Hehir CA;

See RH,

Nestor JJ, Wilson CJ, WPI; 2002-010610/01.

N-PSDB; ABA02318.

(CONS-) CONSENSUS PHARM INC.

21-WAR-2000; 2000US-0190996P. 21-WAR-2000; 2000US-0191299P. 20-WAR-2001; 2001US-00813448. 20-WAR-2001; 2001US-00813653.

21-MAR-2000; 21-MAR-2000;

21-MAR-2001; 2001WO-US009155

Gaps ; 0 Indels 100.0%; Score 95; DB 5; I 100.0%; Pred. No. 1.9e-07; tive 0; Mismatches 0; 297 YAFVGEKFRNYLLVFFQK 314 1 YAFVGEKFRNYLLVFFOK 18 Conservative Query Match Best Local Similarity Matches 18; Conserv ઠે Б

( ) · ; ; \*

AAM52829 standard, protein; 352 AA.

RESULT 30 AAM52829 ID AAM5

297 YAFVGEKFRNYLLVFFQK 314

Human, G-protein chemokine receptor; HDGNR10; CCR5 receptor; haematopoiesis; wound healing; coagulation; angiogenesis; solid tumour; chronic infection; betwaemia; T-cell mediated autoimmune disease; parasitic infection; psoriasis; growth factor activity; allergy; atherogenesis; anaphylaxis; malignancy; inflammation; histamine; immunoalboulin. B; IgE-mediated allergic reaction; sarcoidosis; prostaglandin-independent fever; bone marrow failure; shock; rheumatoid arthritis; hyper-eosinophilic syndrome; cytostatic; infinanceuppressive; antiparasitic; antipsoriatic; antiallergic; antiaticic; antiaticic; antiaticic; antiaticic; antiaticic; antiaticic;

Human G-protein chemokine receptor, HDGNR10.

(first entry)

03-DEC-2002 ABG70597;

ABG70597 standard; protein; 352 AA.

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The invention relates to a method for identifying a binding compound for CC chemokine receptor 5 (CCR5). The method involves screening a library of test molecules (particularly peptides) with immobilised CCR5, and then identifying those molecules which bind. The invention also relates to cCR5-binding molecules identified using the method of the invention. The invention also relates to cCR5-binding molecules identified using the method of the invention, methods for identifying consensus motifs for CCR5-binding peptides, a transfer vector encoding tagged CCR5, a computer-aided methods for determining the relative binding assay that utilises the three-dimensional a computer aided drug screening assay that utilises the three-dimensional structure of CCR5. Compounds identified using the methods of the invention are useful for treating or preventing HIV (human immunodeficiency virus) infection or AIDS (acquired immunodeficiency syndrome) in a patient. The methods of the invention may also be used to sidentify agonists or antagonists of the interaction of CCR5. The present sequence represents human CCR5.
                                                                                                                                                                                  CCR5; CC chemokine receptor 5; human; HIV infection; human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome; drug screening; identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying CC chemokine receptor 5 binding compound for treating AIDS, comprises binding a molecule from library to a molecule having binding property corresponding to CCR5 and identifying bound molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 95; DB 5; Length 352; 100.0%; Pred. No. 1.9e-07; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tan Hehir CA;
                                                                                                                                                   Human CC chemokine receptor 5 (CCR5)
                                AAM52828 standard; protein; 352 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 See RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2000; 2000US-0190996P.
21-MAR-2000; 2000US-0191299P.
20-MAR-2001; 2001US-00813448.
20-MAR-2001; 2001US-00813651.
20-MAR-2001; 2001US-00813653.
                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2001; 2001WO-US009155
                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2000; 2000US-0190946P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CONS-) CONSENSUS PHARM INC.
                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nestor JJ, Wilson CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-010610/01.
N-PSDB; ABA02317.
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                                                                                                                                                                                                                                                                                                        WO200171346-A2.
                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                            22-FEB-2002
                                                                                                                                                                                                                                                                                                                                             27-SEP-2001.
                                                                         AAM52828;
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RESULT 31
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The present invention relates to the isolation of human G-protein chemokine receptor, HDGNR10 (CCRS receptor), and the polymucleotide sequences are conciding it. HDGNR10 polymetide and polymucleotide sequences are or useful for diagnosing a disease or a susceptibility to a disease related to underexpression of HDGNR10. They are useful for identifying modulators for stimulating haematopolesis, wound healing, coaqulation, angiogenesis, to treat solid tumours, chronic infections, psoriasis, or for stimulating growth factor activity. The sequences are also useful for preventing and/or treating allargy, atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation, histamine and immunoglobulin B (IgB)-mediated allargic reactions, prostaglandin-independent fever, bone marrow failure, sarcoidosis, rheumatoid arthritis, shock and hypercessinophilic syndrome. Polymucleotide sequences encoding HDGNR10 can be used in gene therapy to treat conditions related to underexpression of HDGNR10. The present sequence represents human G-protein chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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1es 18; Conservative
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Matches
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297 YAFVGEKFRNYLLVFFQK 314

RESULT 32 ABG70597

1 YAFVGEKFRNYLLVFFOK 18

Conservative

Best\_Local Similarity Matches 18; Conserv

Novel human G-protein chemokine receptor polypeptide useful for identifying modulators for stimulating hematopoiesis, wound healing, leukemia, for treating allergy, rheumatoid arthritis, shock and as

WPI; 2002-690494/74. N-PSDB; ABS54272.

RUBE/) RUBEN S M.

Li Y, Ruben SM;

99US-00339912. 95US-00466343

25-JUN-1999; 06-JUN-1995; (LIYY/) LI Y

25-JUL-2002.

JS2002099176-A1.

Homo sapiens.

Claim 7; Fig 1; 22pp; English.

leukemia, for tr research agents.

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Immunoglobulin, variable heavy chain, variable light chain, human, G-protein chemokine receptor; CCR5, HDGNR10; cancer; inflammation; mimunologic deficiency syndrome; blood protein disorder; nephritis; ataxia telangiectasia; endoctoxin lethality; inflammatory bowel disease; histiocytosis; chemotaxis; infectious disease; autoimmune disease; hadison's disease; dermatitis; rheumatoid arthritis; allergy; neurodegenerative disorder; viral infection; poxvirus infection; human immunodeficiency virus; cytomegalovirus; Raposi's sarcoma; pheumocystis carnii infection; cardiovascular disorder; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human G-protein Chemokine Receptor gene (HDGNR10) useful for treating, preventing, ameliorating or monitoring diseases or disorders associated with aberrant expression of HDGNR10 e.g. cancer.
                                                                                               Human immunoglobulin variable heavy domain #1.
                       ABG92883 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 55; Fig 4; 562pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                             08-AUG-2001; 2001US-0310458P.
12-OCT-2001; 2001US-0328447P.
21-DEC-2001; 2001US-0341725P.
                                                                                                                                                                                                                                                                                                                                                                      2001WO-US004153.
                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                    08-FEB-2002; 2002WO-US003634
                                                                                                                                                                                                                                                                                                                                                           2001US-00779880
                                                                      19-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Roschke V, Rosen CA,
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N-PSDB; ABS68606.
                                                                                                                                                                                                                                       lymphocytopenia
                                                                                                                                                                                                                                                                                   WO200264612-A2
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                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                    12-JUN-2001;
                                                                                                                                                                                                                                                                                                            22-AUG-2002
                                                ABG92883;
RESULT 33
           ABG92883
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The invention describes an isolated polynucleotide encoding a first antibody at least 95-100% identical to a second antibody consisting of an amino acid sequence comprising at least one, three CDR regions of a variable heavy (VH) or variable light (VL) domain of the antibody expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8, XF27/28.1851, XF27/28.1851, XF27/28.1851, XF27/28.1852, XF27/28.1851, XF27/28.1852, XF27/28.1851, XF27/28.1852, XF27/28.
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against HDGNR10
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Disclosure; Fig 1A-B; 562pp; English.

The invention describes an isolated polynuclectide encoding a first antibody at least 95-100% identical to a second antibody consisting of an amino acid sequence comprising at least one, two or three CDR regions of a variable heavy (VH) or variable light (VL) domain of the antibody expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8, XF3.5A2, XF3.1088, XF3.2.9E6, XF27/28.1D5, XF27/28.1SF1, xF11.1F8 is useful treating, yreventing, ameliorating, prognosing or monitoring cancers or other diseases or disorders e.g. immunologic deficiency syndromes such as blood protein disorders and ataxia telanglectasia, inflammation associated disorders such as endotoxin lethality, nephritis and inflammatory bowel disease, conditions associated with an increase in

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                                                                                                                                                                                                                                                                   Immunoglobulin; variable heavy chain; variable light chain; human; G-protein chemokine receptor; CCR5, HDGNR10; cancer; inflammation; immunologic deficiency syndrome; blood protein disorder; nephritis; ataxia telanglectasia; endotoxin lethality; inflammatory bowel disease; histiocytosis; chemotaxis, infectious disease; autoimmune disease; Addison's disease; dermatitis; rheumatoid arthritis; allergy; meurodegenerative disorder; viral infection; poxvirus infection; HIV; human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma; pneumocystis carnii infection; cardiovascular disorder; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human G-protein Chemokine Receptor gene (HDGNRIO) useful for treating, preventing, ameliorating or monitoring diseases or disorders associated with aberrant expression of HDGNRIO e.g. cancer.
                                                Gaps
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0
                    100.0%; Score 95; DB 5; Length 352; 100.0%; Pred. No. 1.9e-07;
                                               0; Indels
                                                                                                                                                                                                                                              Human G-protein chemokine receptor (CCR5) HDGNR10 #1.
                                               Mismatches
                                                                                                                                                                     ABG92880 standard; protein; 352 AA.
                                                                                           297 YAFVGEKFRNYLLVFFQK 314
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                                                                          1 YAFVGEKFRNYLLVFFQK 18
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2001US-0297257P.
2001US-0310458P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-FEB-2002; 2002WO-US003634.
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                                                                                                                                                                                                                       19-NOV-2002 (first entry)
                                                   18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-643455/69.
N-PSDB; ABS68553.
                       Query Match
Best Local Similarity
Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                             lymphocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200264612-A2.
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12-JUN-2001;
08-AUG-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-DEC-2001;
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                                                                                                                                                                                              ABG92880;
                                                   Matches
                                                                                                                                            RESULT 34
                                                                                                                                                          ABG92880
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The invention relates to human G-protein chemokine receptor (CCR5), HDGMR10 proteins and nucleic acid molecules encoding such proteins. CCR5 antibodies are used for the treatment or prevention of inflammation, defective or aberrant chemotaxis of immune cells or T cell antigenpresenting cell interaction, viral infections (specifically human immune deficiency (including its early stages), cytomegalo or pox viruses), autoimmune disease, rheumatoid arthritis, neurodeganeration, Pneumocystis carlini infection, Kaposi's sarcoma or any condition associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
certain haematopoietic cells such as histiocytosis, defective or aberrant chemotaxis of immune cells or T-cell antigen presenting cell interaction, an infectious disease, an autoimmune disease such as Addison's disease, dermatitis and rheumatoid arthritis, allergies, a neurodegenerative poxyirus intection at the title for the form of the formative or poxyirus infection, a Pneumocystis carnii infection, Kaposi's sarcoma, cardiovascular disorder such as atherosclerosis, lymphocytopenias, or a disease or disorder associated with aberrant expression of novel human G-protein chemokine receptor (CCRS) HDGNR10. This is an amino acid sequence of Human G-protein chemokine receptor (CCRS) HDGNR10 #1
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                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 95; DB 5; Length 352; 100.0%; Pred. No. 1.9e-07;
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aberrant expression of CCR5 or their ligands. They are also used for the detection, diagnosis, prognosis and monitoring of cancers or other hyperproliferative diseases. The present sequence is human G-protein chemokine receptor (CCR5), HDGNR10 DNA
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22-SEP-2000; 2000US-0234336P.
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18; Conservative
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(ROSC/) ROSCHKE V.
(LIYY/) LI Y.
(RUBE/) RUBEN S M.
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          Similarity
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Ą. ABB81054 standard; protein; 352 05-NOV-2002 (first entry) ABB81054; RESULT 37

G-protein chemokine receptor, HDGNR10.

7-transmembrane receptor, G-protein coupled receptor; GPCR; HDGNR10; G-protein chemckine receptor; haemacopoletic; immunosuppressant; antiparasitic; antipsoriatic; antiallergic; antiinflammatory; cytostatic; antirheumatic; antiathritic; gene therapy; human; receptor.

Homo sapiens

US2002076745-A1.

20-JUN-2002

98US-00195662. 18-NOV-1998; 95US-00466343 06-JUN-1995;

RUBEN S M. LI Y. (LIYY/) | (RUBE/) |

Ruben SM; Li Y,

2002-598724/64. N-PSDB; ABN86542 New polynucleotide encoding a human G protein chemokine receptor HDGNR10, useful e.g. for treating tumors.

Claim 7; Fig 1; 22pp; English

The invention relates to a novel human 7-transmembrane receptor, HDGNR10, which has been identified as a G-protein chemokine receptor. The GPCR HDGNR10 polypeptide can be expressed by standard recombinant methodology. Compounds that activate or inhibit the receptor polypeptide, optionally expressed from DNA in gene therapy vectors, are used to treat diseases that require: (a) activation of the receptor (e.g. stimulation of haematopoissis, treatment of solid tumours, T-cell mediated autoimmune diseases, parasitic infections, psoriasis etc.); or (b) inhibition of the receptor (e.g. allergy, inflammation, rheumatoid arthritis, silicosis etc.) The present sequence represents the human HDGNR10 receptor ABB 1054
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XXX XXX ABB 1055
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ABB08343 standard; protein; 352 AA. 

ABB08343;

(first entry) 18-JUN-2002 Human chemokine (C-C motif) receptor 5 polypeptide.

Human chemokine C-C motif receptor 5; CCR5; haplotype pair; isogene; single nucleotide polymorphism; SNP; human immunodeficlency vitus 1; HIV-1 infection; acquired immunodeficiency syndrome; AIDS; antiviral; genotype; polymorphic variant; transgenic; drug screening; gene therapy; chromosome 3p21

Homo sapiens

Location/Qualifiers label= Leu, Misc-difference Misc-difference

'label= Phe, Misc-difference

/label= Arg,

WO200177125-A2

18-OCT-2001

04-APR-2001; 2001WO-US010708.

05-APR-2000; 2000US-0194361P.

(GENA-) GENAISSANCE PHARM INC.

ä Kliem SE, Choi JY,

WPI; 2002-041282/05. N-PSDB; ABA97318, ABA97319.

New haplotypes of the human chemokine (C-C motif) receptor 5 gene, useful to diagnose and treat diseases associated with its abnormal expression or function, including human immunodeficiency virus-1 infection.

Claim 29; Fig 3; 61pp; English

The present sequence is that of a polypeptide encoded by the human chemokine (C-C motif) receptor 5 (CRS) gene of the invention (see ABAA7318). The specification describes haplotyping the CCRS gene of an individual by determining if the individual has one of the CCRS paplotypes or haplotype pairs fully defined in the specification. The specification also describes an isolated polymulaciented comprising a mucleotide sequence which is a polymorphic variant of the reference CCRS gene sequence and comprises an isogene defined by a haplotype described in the specification and itse encoded polymorphide. The methods of the invention are useful to diagnose and develop treatment for diseases associated with abnormal expression or function of the gene. The CCRS isogenes and the screened compounds are useful for treating human immunodeficiency virus (HIV)-1 infection and the progression to acquired immunodeficiency syndrome (AIDS). The invention has antiviral applications. The specification describes genotyping the CCRS gene of an individual; predicting a haplotype pair for the CCRS gene of an individual; predicting a nasociation between a trait and a haplotype or haplotype pair for the CCRS gene. The specification describes composition comprising a genotyping oligonucleotide for detecting a CCRS polymorphism, a recombinant non-human organism transformed with CCRS polymucleotide syncessing a CCRS polymeled by the variant sequence; an isolated antibody specific for the CCRS polymeled by the variant sequence; an isolated antibody specific for the CCRS polymeled by the variant sequence.

Sequence 352 AA;

Score 95; DB 5; Length 352; Pred. No. 1.9e-07; 100.0%; Query Match Best Local Similarity

RESULT 38 ABB08343

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100.0%; Score 95; DB 6; Length 352; 100.0%; Pred. No. 1.9e-07;

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us-10-084-813-15.rag

Sequence 352 AA;

The invention discloses a G-protein chemokine receptor (sometimes referred to as a 7-transmembrane receptor) polypeptide, HDGNR10, and the polymucleotide encoding it. G-protein chemokine receptors are involved in signal transduction pathways. The polymucleotide and polypeptide can be useful to identify compounds which activate or inhibit activation of the protein and these compounds are useful for treating a patient having need to activate or inhibit a G-protein chemokine receptor. The compound is daministered by providing to the patient DNA encoding the agonist or antagonist and expressing them in vivo (gene therapy). The polymucleotides and polypeptide are also useful for for diagnosing a disease or susceptibility to a disease related to an under-expression of the protein for chromosome identification or as immunogens for producing articles are useful in stimulating haematopoiesis, wound healing, coagulation, angiogenesis, to treat solid tumours, chronic infections, psoriasis and to stimulate growth factor activity.

Antagonists are useful in the prevention and treatment of allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation, hattamine and igE-mediated allergic reactions, prosteals and to stimulate growth factor activity.

Antagonists are useful in the prevention and acute inflammation, hattamine and igE-mediated allergic reactions, prosteals and to stimulate growth factor activity.

Antagonists are useful in the prevention, where and acute inflammation, hattamine and igE-mediated allergic reactions, prosteals and the prevention and treatment of allergy, shock and hyper-eosinophilic syndrome. The sequence presented is the thuman HDGNR10 protein ö Novel human G-protein chemokine receptor polypeptide useful for diagnostic purposes and for identifying modulators of the polypeptide useful for treating leukemia, autoimmune diseases, psoriasis and allergic Human; receptor; G-protein chemokine receptor; 7-transmembrane receptor; HDGNR10; signal transduction; gene therapy; haematopoiesis; woud healing; coagulation; angiogenesis; tumour; chronic infection; leukaemia; T-cell mediated auto-immune disease; parasitic infection; psoriasis; growth factor; allergy; atherogenesis; anaphylaxis; malignamation; histamine; Ige-mediated; prostaglandin-independent fever; bone marrow failure; silicosis; sarcoidosis; rheumatoid arthritis; shock; hyper-eosinophilic syndrome. Gaps .. Indels Human G-protein chemokine receptor, HDGNR10, protein. .. 0 Mismatches Ä. ABG75540 standard; protein; 352 297 YAFVGEKFRNYLLVFFOK 314 ö 1 YAFVGEKFRNYLLVFFQK 18 Claim 7; Fig 1; 22pp; English 95US-00466343. 11-FEB-2000; 2000US-00502783 (HUMA-) HUMAN GENOME SCI INC (first entry) 18; Conservative WPI; 2003-208944/20. N-PSDB; ABX10635. Li Y, Ruben SM; US2002132269-A1. 06-JUN-1995; Homo sapiens. 16-APR-2003 19-SEP-2002. reactions. ABG75540; Matches g ઠે

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The present invention describes an isolated nucleic acid molecule, which comprises the sequence of any of the genes that are up-regulated or down-regulated in specific cancers (e.g. about 1031 genes up-regulated in regulated in specific cancers (e.g. about 1031 genes up-regulated in carter lymphocytic leukemia). ACC72641 to ACC72860 represent cancer related gene nucleotide sequences which encode the proteins given in ABR5851 to ABR58709. Also described: (1) determining the presence or absence of a pathological cell in a patient; (2) an expression vector comprising the vector; (4) an isolated polypeptide, which is encoded by comprising the vector; (4) an isolated polypeptide, which is encoded by comprising the vector; (5) an antibody that specifically binds the polypeptide of (4); (6) specifically targeting a compound to a pathological cell in a companient by administering to the patient the antibody above; and (7) a companient by administering to the patient the antibody above; and (7) a companient of the patient the antibody above; and (7) a companient of a pathological cell in a companient of a pathological cell in a companient of a pathological cell in a companient of the patient the nucleic acid is useful for therapeutic targets. In particular, the nucleic acid is useful for atheroselerosis and endometriosis. The nucleic acid is also useful in companient of any screening, particularly for identifying agents for treating these companients.
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heart disease; atherosclerosis; endometriosis.
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                                                                                                                                                                                                                                 Human cancer related protein SEQ ID NO:259.
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297 YAFVGEKFRNYLLVFFQK 314
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2002US-0355145P.
2002US-0355257P.
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2001US-0323887P.
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08-FEB-2002;
12-APR-2002;
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Zlotnik A;
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| Sequence 2. Application US/08466343D |
| Patent NO. 6025154 |
| TITLE OF INVENTION: |
| TITLE OF INVENTION: | CHEMOKINE RECEPTOR HOGNEID (AS AMENDED) |
| NUMBER OF SEQUENCES: |
| CORRESPONDENCE ADDRESS: |
| ADDRESSER: STERAF, KESSLER, GOLDSTEIN & FOX P.L.L.C. |
| STREET: 1100 NEW YORK AVE., NW, SUITE 600 |
| CONTRY: USA |
| COMPUTER READBLE FORM: |
| MEDIUM TYPE: | Flopy disk |
| COMPUTER: | IMP PC compatible |
| COMPUTER: | IMP PC compatible |
| OPERATING SYSTEM: | US/08/466,343D |
| TILNG DATE: 06-JUN-1995 |
| CLASSIFICATION NUMBER: US/08/466,343D |
| PILING DATE: 06-JUN-1995 |
| CLASSIFICATION NUMBER: 1488.1150000/EKS/KLM |
| REDISTATION NUMBER: 36.68 |
| REPRENCE/DOCKET NUMBER: 36.88 |
| REPRENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM |
| TELEPHONE: (202) 371-2500 |
| TELEPHONE: (202) 371-2500 |
| TELEPHONE: CHARACTERISTICS: |
| LENGTH: 352 amino acids |
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100.0%; Pred. No. 8.2e-09;
ive 0; Mismatches 0;
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US-08-661-244-2
US-08-461-244-2
US-09-045-583-56
US-09-53-152-8
US-09-503-1752-8
US-09-53-198-8
US-09-534-185-48
US-09-534-185-48
US-09-534-185-48
US-09-686-319A-1
US-09-866-319A-14
PCT-US95-00476-5
US-09-866-319A-14
US-09-868-319A-14
US-09-868-319A-14
US-09-868-319A-14
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US-08-86-319A-14
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Best Local Similarity 100...
Best Local 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-466-343D-2
          N
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          Sequence 2, Appli
Sequence 14, Appl
Sequence 24, Appli
Sequence 52, Appli
Sequence 52, Appli
Sequence 52, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 60, Appli
Sequence 50, Appli
Sequence 50, Appli
Sequence 50, Appli
Sequence 20, Appli
Sequence 17, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                             September 28, 2004, 09:00:23 ; Search time 16.2 Seconds (without alignments) 57.362 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Issued Patents AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-466-343D-2
US-09-087-232A-13
US-08-575-967A-2
US-08-575-967A-2
US-09-517-605-5
US-09-514-185-52
US-09-514-185-52
US-09-5134-187-52
US-09-5124-3
US-08-472-984A-2
US-08-472-984A-2
US-08-472-244-3
US-08-476-669-4
US-08-476-669-4
US-09-131-827A-20
US-09-045-583-51
US-08-875-967A-4
US-08-575-967A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-534-185-59
US-08-720-565-2
                                                                                                                                                                                                                                                                                                                                                             389414 segs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                          protein search, using sw model
                                                                                                                                                                                                                      US-10-084-813-15
95
1 YAFVGEKFRNYLLVFFQX 18
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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                                                                                                            OM protein
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Result No.

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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 625184and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/BOCKET NUMBER: 32918
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297 YAFVGEKFRNYLLVFFQK 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
ORGANISM: Hom
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Sequence 13, Application US/09087232A

Sequence 13, Application US/09087232A

Sequence 13, Application US/09087232A

Sequence 13, Application US/09087232A

GENERAL INFORMATION:
APPLICANT:
OUILIER OF UNIVENTION:
TITLE OF INVENTION: WARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
NUMBER OF SEQUENCES:
ADDRESSEE: BAKER & Botts, L.L.P. attn. Lisa Kole
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
CONTRY: New York
STATE: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G-COUPLED RECEPTORS ASSOCIATED WITH MACROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
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                                                                                                                                                                                                                                                                                                                COUNTRY: USA.

ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/087,232A
FILNG DATE: 28 MAY 1998
CLASSIFICATION 1435
PRICK APPLICATION NUMBER: 60/048,057
FILING DATE: 30 MAY 1997
ATTORNEY/AGENT INFORMATION:
NAME: KOLE, LISA B.
REGISTRATION NUMBER: 35,225
REGISTRATION NUMBER: 35,225
REFERENCE/DOCKET NUMBER: AP 31115
TELECOMMONICATION INFORMATION:
TELECOMMONICATION 1408-2628
TELEPHONE: (212) 408-2628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels
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; Sequence 14, Application US/08861105
; Patent No. 628627
; GENERAL INFORMATION:
; APPLICANT: LITTMAN, DAN R.
; APPLICANT: ELLMEIER, WILFRIED
; APPLICANT: ELLMEIER, WILFRIED
; APPLICANT: LANDAU, NATHANIEL R.
TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITE
; TITLE OF INVENTION: MACROFIAGE-TROPHIC HIV, AND DIAGNOS
; TITLE OF INVENTION: MACROFIAGE-TROPHIC HIV, AND DIAGNOS
; TITLE OF INVENTION: MACROFIAGE-TROPHIC HIV, AND DIAGNOS
; TITLE OF INVENTION: DASS THEREOF
; VORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Bsq.
STREET: #11 Hackensack Ave, Continental Plaza, 4th
STREET: PLOOT
CITY: Hackensack
STRIE: New Jersey
COUNTRY: USA
ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297 YAFVGEKFRNYLLVFFQK 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212) 765-2519
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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Gaps
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US-08-575-967A-2

US-08-575-967A-2

US-08-575-967A-2

Sequence 2, Application US/08575967A

Patent No. 6265184

GARNEAL INFORMATION:

APPLICANT: Gray et al.

ITILE OF INVENTION: Chemokine Receptor Materials and Methods NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago STATE: Illinois

COUNTY: USA

MEDIUM TYPE: Ploppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: IBM PC Compatible

CORRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/55,967A

FIRM DATA:

PATELICATION NUMBER: US/08/55,967A
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COMPUTER REALABLE FORM:
MEDIUM TYPE: FIDOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,105
FILING DATE: US/08/861,105
FILING DATE: 19-JUN-1996
CLASSIFICATION AND ATA:
APPLICATION NUMBER: US 08/666,020
FILING DATE: 19-JUN-1996
CLASSIFICATION ADATA:
APPLICATION NUMBER: US 08/227,319
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 1049-1-004 NI
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAN: 201-487-5800
TELEFRAN: 201-343-1684
INFORMATION FOR SEQ ID NO: 14:
SEQUINCE CHARACTERISTICS:
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100.0%; Score 95; DB 3; I
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0;
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RESULT 7
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US-09-045-583-52
Sequence 52, Application US/09045583
Sequence 52, Application US/09045583
Sequence 52, Application US/09045583
Sequence 52, Application US/09045583
Tarba 06, EARANTION:
TATULE OF INVENTION:
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSER! LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 352;
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AUGKESSE:
AUGKESSE:
CITY:
Boston
STREET:
ASAATE:
Boston
STREET:
ADSIGN
ADDION TYPE:
COMPUTER READABLE FORM:
MEDIUM TYPE:
FLOSDY disk
COMPUTER:
ATION NUMBER:
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                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature; OTHER INFORMATION: /= "88C amino acid sequence"
US-08-575-967A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 95; DB 3; 1 ilarity 100.0%; Pred. No. 8.2e-09; Conservative 0; Mismatches 0;
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       INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 352 amino acids TYPE: amino acids TYPE: amino acids TYPE: protein FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297 YAFVGEKFRNYLLVFFOK 314
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TYPE: amino acid
206-485-1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (617)227-740
TELEFAX: (617)742-4214
INFORWATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 18; Conserval
TELEPHONE:
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Gaps

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Sequence 2. Application US/08724984A

Sequence 2. Application US/08724984A

Patent No. 6388055

GENERAL INFORMATION:
APPLICANT: Derk Bergsma, Mary Brawner, and Usman Shabon
APPLICANT: Derk Bergsma, Mary Brawner, and Usman Shabon
TITLE OF INVENTION: OKRS Receptor
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road, P.O. Box 1539
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Patent No. 6548636

GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Dragic, William
ITILE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REPERRNCE: 2048/61010/JPW/SHS
CURRENT APPLICATION NUMBER: US/09/796,202
CURRENT FILING DATE: 201-02-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                  100.0%; Score 95; DB 4; Length 352; 100.0%; Pred. No. 8.2e-09; ive 0; Mismatches 0; Indels
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ZIF: 19406-0939
CONPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MD STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 95; DB 4; L
100.0%; Pred. No. 8.2e-09;
iive 0; Mismatches 0;
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OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: MICROSOFT WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,984A
FILING DATE: October 3, 1996
CURRENT APPLICATION NUMBER: US/09/502,783A
                    CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION UNBER: 08/466,343
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
LENGTH: 352
                                                                                                                                                                                                                                                                                                                                                                                                                           297 YAFVGEKFRNYLLVFFQK 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297 YAFVGEKFRNYLLVFFQK 314
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Best Local Similarity 100.
Matches 18; Conservative
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Best Local Similarity 100.0
Matches 18; Conservative
                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-09-502-783A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: human
US-09-796-202-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
US-08-724-984A-2
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LENGIH: 352
                                                                                                                                                                                            TYPE: PRT
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Sequence 2, Application US/09502783A
Parent No. 6511826
GENERAL INFORMATION:
APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: CONVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRS TITLE OF INVENTION: HDGNR10
FILE REFERENCE: 1488.1150006
                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08833752
Patent No. 6448375
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: SASSART, GILBERT
APPLICANT: PASSART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPATIBLE PATENTINE PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/833,752
FILING DATE: 9-APR-1997
CLASSIFICATION: 5.36
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHRARATERISTICS:

TOWNEY: ALTMAN TOWNER:
SEQUENCE CHRARATERISTICS:
                                                                                                                    Length 352;
                                                                                                                                                                  0; Indels
                                                                                                                  Ouery Match 100.0%; Score 95; DB 4; 1
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                      ; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
03-09-534-185-52
                                                                                                                                                                                                                                              297 YAFVGEKFRNYLLVFFQK 314
                                                                                                                                                                                                                1 YAFVGEKFRNYLLVFFOK 18
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LENGTH: 352 amino acids
; TYPE: amino acid
TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-833-752-5
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Gaps

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Sequence 4, Application US/08446669
; Patent No. 613287
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: RAMMALLAN MONOCYTE CHEMOATTRACTANT;
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83.2%; Score 79; DB 1; Length 360;
83.3%; Pred. No. 5.4e-06;
tive 1; Mismatches 2; Indels
   2; Indels
   1; Mismatches
                                                                        292 YAFVGEKFRYLSVFFRK 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 YAFVGEKFRRYLSVFFRK 322
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                                      1 YAFVGEKFRNYLLVFFQK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-802, TELERA: 380816CooleyPA
INFORMATION FOR SEQ ID NO: 4: SEQUEBNCE CHARACTERISTICS: LENGTH: 360 amino acids
TVPE: amino acids
TVPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 83.3
Matches 15; Conservative
   15; Conservative
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                                                                                                                              RESULT 13
US-08-450-393A-4
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US-08-446-669-4
     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 79; DB 1; Length 347; Pred. No. 5.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08461244

Patent No. 5776729

GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R.
APPLICANT: Ruben, Steven M.
APPLICANT: Roben, Craig A.
TITLE OF INVENTION: HIMAN G-PROTEIN RECEPTOR HGBER32
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BAIN, GILFILLAN, GECCHI,
ADDRESSEE: STUBRY & OLSTEIN
STREET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTERET: 6 Becker Farm Road
CITY: Roseland
STATE: Now Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,244
FILING DATE: 05-UN-1995
CLASSIFICATION NUMBER: US/08/461,244
FILING DATE: 05-UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: FERTARO, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 35,134
REFERENCE/DOCKET NUMBER: 35,134
REFERENCE/DOCKET NUMBER: 32,134
REFERENCE/DOCKET NUMBER: 32,134
CLASSIFICATION: 800

PRIOR APPLICATION DATA:
    APPLICATION NUMBER:
    TILING DATE:
    ATTORNEY/AGENT INFORMATION:
    NAME: William T. Han
    REGISTRATION NUMBER: 34,344
    REPERENCE/DOCKET NUMBER: ATG50023
    TELEFONE/DOCKET NUMBER: ATG50023
    TELEFONE/DOCKET NUMBER: ATG50023
    TELEFONE: 610 270 5024
    TELEFAN: 610 270 5090
    INPORMATION POR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
    LENGTH: 354
    TYPE: Amino Acid
    TOPOLOGY: Linear
US-08-724-984A-2
                                                                                                                                                                                                                                                                                                                                                                                                                              299 YAPVGEKFRSYLSVFFRK 316
                                                                                                                                                                                                                                                                                                                                                                                                       1 YAFVGEKFRNYLLVFFQK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ 10 NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 347 amino acids TYPE: amino acid STRANDEDIESS: TOPOLOGY: linear MOLECULE TYPE: protein
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Best Local Similarity
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RESULT to US-09-534-185-50

US-09-534-185-50

Sequence 50, Application US/09534185

Fatent No. 6403767

GENERAL INFORMATION:

APPLICANT: Graham, Gerard J. et al.

TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled

Heptahelical Receptor Superfamily and Uses
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MEDIUM TYPE: FLORM:

MEDIUM TYPE: FLORM:

COMPUTER: 1BM PC compatible

COMPUTER: 1BM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/534,185

FILING DATE: 24-Mar-2000

CLASSIFICATION **CURNOWN>

PRIOR APPLICATION **CURNOWN>

PRIOR APPLICATION NUMBER: 09/045,583

FILING DATA:

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: MNI-044

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEPHONE: (617) 227-7400

TELEPHONE: (617) 227-7400

TELEPHONE: (617) 227-7400

TELEPHONE: OF MAIN OF SO:

SEQUENCE CHARACTERISTICS:
                                                                                                                                       Length 360;
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                                                                                                                                  Query Match

83.2%; Score 79; DB 3; i
Best Local Similarity 83.3%; Pred. No. 5.4e-06;
Matches 15; Conservative 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS: COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-534-185-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 2, Application US/09131827A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 360 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                     305 YAFVGEKFRRYLSVFFRK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            305 YAFVGEKFRKLSVFFRK 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 83.3%;
Matches 15; Conservative
                                        ) MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-045-583-50
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 17
US-09-131-827A-2
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Patent No. 6287805

GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6287805e1 Molecules of the G Protein-Coupled NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STREET: USA MASSACHUSELES
COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM:
OPERATING SYSTEM:
OPERATING SYSTEM:
OPERATING SYSTEM:
OPERATING SYSTEM:
OFFICATION NUMBER:
FLING DATE:
OLASSIFICATION 435

PRIOR APPLICATION HATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME:
MANDERATION NUMBER:
SEGISTRATION NUMBER:
OFFICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME:
NAME:
NAME:
REGISTRATION NUMBER:
SIGNOR POCKET NUMBER:
TELEBHONE:
(617)227-7400

TELEBERA:
(617)227-7400

TELEBERA:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin NoTA:
APPLICATION NUMBER: US/08/446,669
FILING DATE: May 25, 1995
CILING DATE: May 25, 1995
ATTCRNEY/AGENT INFORMATION:
NAME: Neeley, Richard
RESISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAL-237/01US
TELEPOMUNICATION INFORMATION:
TELEPOMUNICATION INFORMATION:
TELEFAX: 415-843-5000
TELEX: 380816CooleyPA
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acids
TYPE: ATTORNEY: Linear
MINERAL WANDER: LINEAR
TYPE: ATTORNEY: Linear
TYPE: ATTORNEY: Linear
TYPE: ATTORNEY: Linear
TYPE: ATTORNEY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 79; DB 3; I
Pred. No. 5.4e-06;
1; Mismatches 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            305 YAFVGEKFRYLSVFFRK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83.2%;
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Best Local Similarity 83.3 Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein US-08-446-669-4
  COUNTRY:
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83.3%; Pred. No. 5.4e-06;
ive 1; Mismatches 2; Indels
                                                                                                       ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: FI-loppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00476
FILING DATE:
CLASSIFICATION:
201 N. Figueroa Street, 5th Floor
                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 555-291
TELECHONE: 310-977-1001
TELEPHONE: 310-977-1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305 YAFVGEKFRRYLSVFFRK 322
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REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 360 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                         Los Angeles
California
                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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US-09-131-827A-20
US-09-131-827A-20
Sequence 20, Application US/09131827A
Patent No. 6600030
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gaith, Michael
APPLICANT: 14014.033
CURRENT APPLICATION NUMBER: 08/095,659
PRIOR APPLICATION NUMBER: 60/055,659
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 20
SEQ ID NO 20
LENGTH: AND 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 19
PCT-US95-00476-4
; Sequence 4, Application PC/TUS9500476
; GENUERAL INFORMATION:
    APPLICANT: The Regents of the University of California; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT; TITLE OF INVENTION: 14
; CORRESPONDENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
                                               APPLICANT: O'Brien, Stephen J.
APPLICANT: O'Brien, Stephen J.
APPLICANT: Smith, Michael
APPLICANT: Smith Michael
APPLICANT: Smith Michael
APPLICANT: Spingle APPLICATION NUMBER: US/09/131,827A
CURRENT APPLICATION NUMBER: 1998-08-10
PRIOR APPLICATION NUMBER: 60/055,659
PRIOR APPLICATION NUMBER: 60/055,659
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FASELSQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match . 83.2%; Score 79; DB 4; Best Local Similarity 83.3%; Pred. No. 5.4e-06 Matches 15; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 15; Conserv
Patent No. 6600030
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-131-827A-20
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Query Match
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                                                                                                                                                                                                                                                                                                                              Sequence 51, Application US/09045583
Patent No. 6287805
GENERAL INFORMATION:
TITLE OF INVENTION: No. 6287805e1 Molecules of the G Protein-Coupled NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                     Gaps
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                                                                                                                               Length 360;
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                                                                                                                             Query Match

81.1%; Score 77; DB 4; Length 360
Best Local Similarity 77.8%; Pred. No. 1.2e-05;
Matches 14; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTE CATO

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM FC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/09/045,583

FILING DATE: 20-MAR-98

CLASSIPICATION: 435

PRIOR APPLICATION AND ATA:

APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 76; DB 3; I
Pred. No. 1.8e-05;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MANGENGAGOURAS, AMY E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECHMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 22
US-09-534-185-51
; Sequence 51, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
                                                                                                                                                                                                                                 305 YAFVGEKFRRYISVFFRK 322
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77.8%;
                                                    ; TOPOLOGY: linear
; MOLECULE TYPE: No. 6448375e
US-08-833-752-7
360 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 360 amino acids amino acid
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Best Local Similarity 77.81
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
PRAGMENT TYPE: internal
US-09-045-583-51
                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02109
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US-09-045-583-51
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APPLICANT: Graham, Gerard J. et al.

TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptahelical Receptor Superfamily and Uses
Therefor
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US-08-575-967A-4

Sequence 4, Application US/08575967A

Sequence 4, Application US/08575967A

Parent No. 6A561B-4

GENERAL INFORMATION:

APPLICANT: Gray et al.

TITLE OF INVENTION: Chemokine Receptor Materials and Methods

NUMBER OF REQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                      COMPUTER KEALDEL FORTH

MEDIUM TYPE: FORTH

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/534,185

FILING DATE: 24 Mar-2000

CLASSIFICATION: OUTA:

APPLICATION NUMBER: 09/045,583

APPLICATION NUMBER: 09/045,583

FILING DATE: CURKNOWN:

APPLICATION NUMBER: 09/045,583

ATTORNEY/AGENT INFORMATION:

NAME: MANDATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: 36,207

REFERENCE/DOCKET NUMBER: MMI-044

TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.0%; Score 76; DB 4; Length 360; 77.8%; Pred. No. 1.8e-05; cive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 6060 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/575,967A
FILING DATE:
                                                                                             NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: peptide
; FRACHENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-534-185-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 YAFVGEKFRRYLSMFFRK 322
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                                                                                                                                                                                               CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 77.8
Matches 14; Conservative
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
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; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
; Heptahelical Receptor Superfamily and Uses
                                                                                                                                                                                                                                                                                        VS-09-045-583-54

j Sequence 54, Application US/09045583

j Sequence 54, Application US/09045583

j Patent No. 6287084

j GENERAL INFORMATION:
    TITLE OF INVENTION: No. 6287805e1 Molecules of the G Protein-Coupled
    TITLE OF INVENTION: No. 6287805e1 Molecules of the G Protein-Coupled
    TOWNER OF SEQUENCES: 56
    CONRESPONDENCE ADDRESS:
    ADDRESSEE: LAHIVE & COCKFIELD, LLP
    STREET: 28 State Street
    COUNTY: Boston
    STATE: Massachusetts
    COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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68.4%; Score 65; DB 3; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0015;
Matches 12; Conservative 2; Mismatches 4; Indels
                                                                                     Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 68.4%; Score 65; DB 3; Best Local Similarity 66.7%; Pred. No. 0.0015; Matches 12; Conservative 2; Mismatches 4
                                                                                                                                                                                                    301 YAFVGERFRKYLRHFFHR 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 YAFVGERFRKYLRHFFHR 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-045-583-54
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-847-296B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 26
US-09-534-185-54
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                                                                                                                                                                                                                                                                                                                                                                                                             68.4%; Score 65; DB 3; Length 355; 66.7%; Pred. No. 0.0015; tive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08847296B

Sequence 1, Application US/08847296B

Patent No. 6271347

GENERAL INPORMATION:
APPLICANT: DEMCHERTY, BRUCE L.
APPLICANT: SICILIANO, SALVATORE J.
APPLICANT: SERNIGER, MARTIN J.
TITLE OF INVENTION: EOSINOPHIL EOTAXIN RECEPTOR NUMBER OF SEQUENCES:
ADDRESSES: Marc & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CUNTRY: Rahway
STATE: NUSA
ZITY: Rahway
STATE: NUSA
ZITY: RADABLE PREM:
MEDIUM TYPE: Diskette
COMPUTER READABLE PORM:
MEDIUM TYPE: Diskette
COMPUTER IN COMPATA:
COUNTRY: MET APPLICATION DATA:
APPLICATION NUMBER: US/08/447,296B
FILING DATE: 24-APR-1997
CLASSIFICATION NUMBER: 60/017,113
FILING DATE: 26-APR-1996
ATTORING APPLICATION NUMBER: 60/017,113
FILING DATE: 26-APR-1996
ATTORING APPLICATION NUMBER: 60/017,113
FILING DATE: 26-APR-1996
ATTORING APPLICATION NUMBER: 35,382
RESERVENCE/DOCKET NUMBER: 35,382
RESERVENCE/DOCKET NUMBER: 35,382
RESERVENCE/DOCKET NUMBER: 35,382
TELERAX: 908-594-4720
                                                                                                                                                                                                                                                                                                        FEATURE:
| NAME/KEY: misc feature
| OTHER INFORMATION: /= "88-2B amino acid sequence"
US-08-575-967A-4
  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 626184and, Greta E.
REGISTRATION NUMBER: 35,302
REPERENCE/FOOKET NUMBER: 32918
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-485-1960
TELEPHONE: 206-485-1662
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 YAFVGERFRKYLRHFFHR 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YAFVGEKFRNYLLVFFQK 18
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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Gaps
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APPLICANT: Gerard, No. 6537764ma P.
APPLICANT: Gerard, No. 6537764ma P.
APPLICANT: Gerard, No. 6537764ma P.
APPLICANT: Ponath, Paul D.
APPLICANT: Poet, Theodore W.
APPLICANT: Gin, Shixin C.
ALILE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND TITLE OF INVENTION: ANTAGONISTS THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STREET: WA
COURTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1EM PC compatible
COMPUTER: 1EM PC compatible
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,565
FILING DATE: 30-SEP-1996
CLASSIFICATION: 530
        CURKENT AFFLICATION DATA:

CLASSIFICATION NUMBER: US/08/720,565
FILING DATE: 30-SEP-1996
CLASSIFICATION SATA:
APPLICATION NUMBER: PCT/US96/00608
FILING DATE: 19-JAN-1996
FILING DATE: 19-JAN-1995
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BLOCK, DAVID E.
REGISTRATION NUMBER: 22,592
REGISTRATION UNDER: 22,592
REGISTRATION UNDER: 126,594
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
INFORMATION SECOND SATA:
TELEPHONE: 617-861-6240
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: PCT/US96/00608
FILING DATE: 19-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375,199
FILING DATE: 19-JAN-1995
ATTOMING DATE: N9-JAN-1995
ATTOMING DATE: NAM-1995
NAME: Brook, David E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 28
US-08-720-565-4
; Sequence 4, Application US/08720565
; Patent No. 6537764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 355 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-720-565-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
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APPLICANT: Gerard, No. 6537764ma P.
APPLICANT: Markay, Charles R.
APPLICANT: Markay, Charles R.
APPLICANT: Post, Theodore W.
APPLICANT: Oil, Shixin
TILLE OF INVENTION: GRACING PROTEIN-COUPLED RECEPTOR GENE CCR3 AND TITLE OF INVENTION: ANTAGONISTS THEREOF CORRESPONDENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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MEDIUM TYPE: Flopey disk

COMPUTER: IEM PC compatible

COMPUTER: IEM PC compatible

COMPUTER: IEM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/534,185

FILING DATE: 24 Mar-2000

CLASSIFICATION TOWN: CURNOWN:

PRIOR APPLICATION NUMBER: 09/045,583

FILING DATE: CURNOWN:

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REGISTRATION NUMBER: 36,207

REGISTRATION NUMBER: 36,207

REGISTRATION NUMBER: 36,207

REPERBNOK: (617)42-4214

INFORMATION FOR SEQ ID NO: 54:

SEQUENCE CHARACTERISTICS:

INFORMATION FOR SEQ ID NO: 54:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 68.4%; Score 65; DB 4; Length 355; Best Local Similarity 66.7%; Pred. No. 0.0015; Matches 12; Conservative 2; Mismatches 4; Indels
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COMPOTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGNENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 54:
US-09-534-185-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08720565
Patent No. 6537764
GENERAL INFORMATION:
Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 355 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 YAFVGERFRKYLRHFFHR 318
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Lexington STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 27
US-08-720-565-2
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Second 56, Application US/09045583

Patent No. 6287805

GENERAL INFORMATION:

APPLICANT: Graham, Gerard J. et al.

APPLICANT: Graham, Gerard J. et al.

TITLE OF INVENTION: No. 6287805e1 Molecules of the G Protein-Coupled NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

ADDRESSER: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street

COUNTRY: Massachusetts

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 66.3%; Score 63; DB 1; Length 355; Best Local Similarity 66.7%; Pred. No. 0.0034; Matches 12; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                  APPLICANT: Soppet, Daniel R.
APPLICANT: Soppet, Daniel R.
APPLICANT: Miben, Steven M.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBER32
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESSEE: GARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ALDRESSEE: Roseland
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPOTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBN PC comparatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,244
FILING DATE: 05-UWN-1995
CLASSIFICATION: 536
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                          Sequence 2, Application US/08461244 Patent No. 5776729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 YAFVGEKFKHLSEIFQK 317
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NAME: Ferraro, Gregory D.
REGIGSTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YAFVGEKFRNYLLVFFQK 18
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INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 355 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-461-244-2
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US-09-045-583-56
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US-08-461-244-2
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                                                                                                                                                                                                                                                                                                                                                                                                                  Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
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CUDNIKX: U.D.A.

CUDNIKX: U.D.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMFUTER: IBM FC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRING APPLICATION BATA:

APPLICATION NUMBER: US/08/567,882

FILING DATE: 08-DEC-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFRAMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: 34,090

REFERENCE/DOCKET NUMBER: DX0506

TELEPRONE: 415-852-9196

TELEPRONE: 415-486-1200

TELEPRAN: A-196-1200

TELEPRAN: A-196-1200

TELEPRAN: A-196-1200

TELEPRAN: A-196-1200

TELEPRAN: A-196-1200

TELEPRAN: A-196-1000

TELEPRAN: A-196-1000

TELEPRAN: A-196-1000

TELEPRAN: A-196-1000

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Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 68.4%; Score 65; DB Best Local Similarity 66.7%; Pred. No. 0.00 Matches 12; Conservative 2; Mismatches
22,592
RFR: LKS94-05A2
REGISTRATION NUMBER: 22,592
REFERNICE/DOCKET NUMBER: LKSS
TELECOMMUNICATION INPORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 YAFVGERFRKYLRHFFHR 318
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
IENGTH: 356 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-08-567-882-7
                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-720-565-4
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APPLICANT: SAMSON, MICHEL
APPLICANT: PARMENTIER, MARC
APPLICANT: PARMENTIER, MARC
APPLICANT: VASSART GLIBERT
APPLICANT: LIBERT, FEDERET
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

SOFTWARE: Petentin Release #1.0, Version #1.25 (EPO)

SOFTWARE: Petentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/833,752

FILING DATE: 9-APR-1997

CLASSIFICATION: 536

ATTORNEY, AGENT INFORMATION:

NAME: Altman, Daniel E

REGISTRATION NUMBER: 34,115

REFERENCE/DOCKET NUMBER:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.3%; Score 63; DB 4; Length 355; 61.1%; Pred. No. 0.0034; tive 3; Mismatches 4; Indels
                                                                                                                                         66.3%; Score 63; DB 4; Length 355; 66.7%; Pred. No. 0.0034; ive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: G20 Newport Center Drive 16th Floor CITY: Newport Beach STATE: CA
                      MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/09503219B
Patent No. 6645491
GENERAL INFORMATION:
APPLICANT: Oldham Elizabeth R.
APPLICANT: Homey, Bernhard
APPLICANT: Dieu-No. 6645491jean, Marie C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                              RESULT 33
US-08-833-752-8
F. Sequence 8, Application US/08833752
; Patent No. 6448375
                                                                                                                                                                                                                                                                         300 YAFVGEKFKKHLSEIFQK 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 355 amino acids
amino acid
                                                                                                                                               Query Match
Best Local Similarity 66.7°
Matches 12; Conservative
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 34
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Sequence 56, Application US/09534185
Batent No. 6403767
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled TITLE OF INVENTION: Heptahelical Receptor Superfamily and Uses
Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC compatible

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/534,185

FILING DATE: 24-MAR-2000

CLASSIFICATION DATA:

APPLICATION NUMBER: 09/045,583

FILING DATE: CURRIOWN:

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 63; DB 3; Length 355
Pred. No. 0.0034;
2; Mismatches 4; Indels
  SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESSES
ADDRESSES: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REPERBENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: S0. NO. 1 REFERENCE/DOCKET NUMBER: MNI-044 TELECOMMUNICATION INFORMATION: TELEFAM: (617) 742-4214
INFORMATION FOR SEQ ID NO. 56: SEQUENCE CHARACTERISTICS: LENGTH: 355 amino acids TYPE: amino acid TOPOLOGY: linear
                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 YAFVGEKFKKHLSEIFOK 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 YAFVGEKFRNYLLVFFOK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER: 36,20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-045-583-56
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US-09-534-185-56
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                                                                                                                                                                                                                                                                                                        Sequence 48, Application US/09534185
Sequence 18, Application US/09534185
Patent No. 6403767
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
TITLE OF HOPENHION: Heptahelical Receptor Superfamily and Uses
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Macrophage Inflammatory Protein-1 alpha (MIP-1
alpha)/RANTES Receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USER

COMPUTER REDABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
CORRENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/534,185
FILING DATE: 24-Mar-200
CLASSIFCATION NUMBER: 09/045,583
FILING DATE: CURROWN-
PRIOR APPLICATION NUMBER: 09/045,583
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
TELEPHONE: (617)227-7400
TELEPHONE: (617)27-7401

TELEPHONE: (617)27-4241

INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.2%; Score 61; DB 4; Length 374; 76.9%; Pred. No. 0.0081; tive 2; Mismatches 1; Indels
         76.9%; Pred. No. 0.0081;
tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESSES
ADDRESSES: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 374 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: poptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-06-012-988A-2; Application US/08012988A; Sequence 2, Application US/08012988A; Patent No. 5652133 GENERAL INFORMATION: APPLICANT: Murphy, Philip M. TITLE OF INVENTION: Macrophage Infl; TITLE OF INVENTION: Macrophage Infl; TITLE OF INVENTION: alpha)/RANTES F; NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    316 YAFIGQKFRNYFL 328
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316 YAFIGQKFRNYFL 328
                                                                                                  1 YAFVGEKFRNYLL 13
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Best Local Similarity 76.9
Matches 10; Conservative
         Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                           US-09-534-185-48
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Matches
                                       Matches
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Patent No. 6287805
Patent No. 6287805
GENERAL INTERMATION: No. 6287805el Molecules of the G Protein-Coupled
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
TITLE OF INVENTION: S6
CORRESPONDENCES: 56
CORRESPONDENCES: 6
COUNTRY: Boston
STREET: 48 State Street
CITY: Boston
STREET: 48 State Street
CITY: Boston
COUNTRY: Boston
COUNTR
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APPLICANT: Caux, Christophe
APPLICANT: Zlotnick, Albert
TITLE OF INVENTION: CHEMOKINE USES; COMPOSITIONS; METHODS;
FILE REPERENCE: DX0394K1
CURRENT PILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: US 60/118,335
PRIOR PELICATION NUMBER: US 60/118,335
PRIOR PELICATION NUMBER: 1999-02-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 64.2%; Score 61; DB 4; Length 365; Best Local Similarity 76.9%; Pred. No. 0.0079; Matches 10; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
; LOCATION: (579)
; OTHER INFORMATION: unknown nucleotide
US-09-503-219B-8
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INFORMATION FOR SEQ ID NO: 48.
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
TYPE: amino acid
TYPE: amino acid
MOLECULE TYPE: peptide
FRAGMENT TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               307 YAFIGOKFRNYFL 319
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US-09-045-583-48
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64.2%; Score 61; DB 3; Length 374;

Query Match

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Gaps
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Sequence 5, Application US/08446669

Patent No. 613287

GENERAL INCEMATION:

REPLICANT: Caughlin, Shaun

APPLICANT: Coughlin, Shaun

TITLE OF INVENTION: PROTEIN RECEPTORS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: California

COUNTRY: Palo Alto Square

COUNTRY: USA

STATE: California

COUNTRY: USA

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CLASSIFICATION NUMBER: 30,092

REGISTRATION NUMBER: 30,092

REERRONCENTONING NUMBER: 30,005

TELECOMMUNICATION NUMBER: 30,005

TELECOMMUNICATION NUMBER: 30,005
                                                                                                                                                                                                                                   Query Match 63.2%; Score 60; DB 1; Length 355; Best Local Similarity 61.1%; Pred. No. 0.011; Matches 11; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.2%; Score 60; DB 3; Length 355; 61.1%; Pred. No. 0.011; ive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                     301 YAFVGERFRKYLROLFHR 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 YAFVGERFRKYLRQLFHR 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YAFVGEKFRNYLLVFFQK 18
                                                                  : 355 amino acids
amino acid
3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 61.1<sup>§</sup>
Matches 11, Conservative
TELEX: 380816CooleyPA
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-857-0663
TELEX: 380816CooleyPA
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                 HYPOTHETICAL: N
HYPOTHETICAL: N
HANT-SENSE: NO
US-08-450-393A-5
                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 39
US-08-446-669-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-446-669-5
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; Sequence 5, Application US/08450393A
; Patent No. 570781S
; GENERAL INFORMATION:
    APPLICANT: Charo, Israel
    APPLICANT: Charo, Israel
    APPLICANT: Charo, Israel
    TILE OF INVENTION: MAWALLAN MONOCYTE CHEMOATTRACTANT
    TILE OF INVENTION: PROTEIN RECEPTORS
    NUMBER OF SEQUENCES: 1
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
    STREET: 5 Palo Alto Square
    CITY: Palo Alto
    CONTACTOR CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 63.2%; Score 60; DB 1; Length 355; Best Local Similarity 61.1%; Pred. No. 0.011; Matches 11; Conservative 2; Mismatches 5; Indels
                      ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco STATE: California
                                                                                                                                 ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Rclease #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: MAY 25, 1995
CLASSIFICATION: 424, 1295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: UCAL-237/02US
TELECOMONICATION INFORMATION:
TELEPHONE: 415-843-5165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 YAFVGERFRKYLRQLFHR 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 355 amino acids
AMINO ACID
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  415-8857-0663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-08-012-988A-2
      CORRESPONDENCE ADDRESS:
                                                                                                             COUNTRY: U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 38
US-08-450-393A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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RESCULT 40

UG-09-239-338-1

Sequence 1, 2010.

Patent No. 6329510

APPLICANT: Qin, Shixin

APPLICANT: Resear, Nasim

APPLICANT: Resear, Nasim

APPLICANT: Resear, Nasim

APPLICANT: Leukoŝite, Inc.

TITLE OF INVENTION: THEREFOR

FILE REFERENCE: LKS9-13

CURRENT APPLICATION NUMBER: US/09/239,938

CURRENT MATCH SAPENTALIAN OF US APPLICATION OF US APPL
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Search completed: September 28, 2004, 09:21:33 Job time : 16.2 secs

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13 ; Search time 59.625 Seconds (without alignments) 97.074 Million cell updates/sec
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| Cgn2 6/ptodata/1/pubpaa/RSO7 PUBCOMB.pep:*
| Cgn2 6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
| Cgn2 6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*
| Cgn2 6/ptodata/1/pubpaa/USO6 PUBCOMB.pep:*
| Cgn2 6/ptodata/1/pubpaa/USO6 PUBCOMB.pep:*
| Cgn2 6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*
| Cgn2 6/ptodata/1/pubpaa/USO9 NEW PUB.pep:*
| Cgn2 6/ptodata/1/pubpaa/USO9 PUBCOMB.pep:*
| Cgn2 6/ptodata/1/pubpaa/USO0 PUBCOMB.pep:*
| Cgn2 6/ptodata/1/pubpaa/USO0 NEW PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1349238 seqs, 321558718 residues
                                                                                                                                                                                                                                               September 28, 2004, 09:06:23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                          US-10-084-813-15
95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                           Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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RESULT 2 US-10-064-813-105 ; Sequence 105, Application US/10084813 ; Publication No. US20030068615A1

THAR WOU GUI GO WHIT WH	Sequence 2, Appli Sequence 62, Appli Sequence 2, Appli Sequence 4, Appli Sequence 1, Appli Sequence 5, Appli Sequence 5, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli
US-09-939-226 US-09-938-703 US-09-1734-223 US-09-1734-223 US-09-1734-223 US-10-106-62 US-10-106-62 US-10-106-62 US-10-086-81 US-10-086-81 US-10-086-81 US-10-086-81 US-10-086-81 US-10-086-81 US-10-086-81 US-10-086-81 US-10-086-81 US-10-086-81 US-10-086-81 US-10-28-56 US-10-28-56 US-10-28-56 US-10-28-67 US-10-28-67 US-10-28-67 US-10-28-67 US-10-28-67 US-10-28-67 US-10-28-67 US-10-28-67 US-10-28-67 US-10-28-67 US-10-28-67 US-10-28-67 US-10-28-67 US-10-28-67	US-10-135-839- US-10-135-839- US-10-439-845- US-10-439-845- US-10-439-845- US-10-439-845- US-10-661-798- US-10-6791-905- US-10-1791- US-09-104-792-3 US-10-176-078- US-10-176-078-
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## ALIGNMENTS

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US-10-084-813-15;

Sequence 15, Application US/10084813;
Sequence 15, Application WG. US20030068615A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC;
TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND METHODS OF USE;
TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE;
TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE;
CURRENT FILING DATE: 2000-08-25;
PRIOR APPLICATION NUMBER: PG7/US00/23505
PRIOR APPLICATION NUMBER: US 60/151,270
PRIOR APPLICATION NUMBER: US 60/151,270
PRIOR APPLICATION NUMBER: US 60/151,270
SOFTWARE: PARENTH VERSION 3.1
SOFTWARE: PREDIT ACIDING DATE: 1999-08-27
NUMBER OF SEQ ID NO 15
LENGTH: 18
TYPE: PAT
ORGANISM: Artificial Sequence
FEATURE:
CORGANISM: Artificial Sequence
FEATURE:
FEATURE:
FEATURE:
CORGANISM: Artificial Sequence
FEATURE:
FE
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CURRENT APPLICATION NUMBER: US/09/725,285
CURRENT FILING DATE: 200-11-29
PRIOR PEDLICATION NUMBER: 09/339,912
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 09/195,662
PRIOR PELLING DATE: 1998-11-18
PRIOR FILING DATE: 1998-11-18
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence: Genomic
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; ORGANISM: Homo sapiens
US-09-759-841-2
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LENGTH: 352
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US-09-759-841-2
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Sequence 2. Application US/09725285
Patent No. US2001000241A1
GENERAL INFORMATION:
APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: (CRE, Receptor)
FILE REFERENCE: 1488.1150003
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                       APPLICANT: SAXINGER, CARL
TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USS
FILE REPERENCE: 215875
CURRENT APPLICATION NUMBER: US/10/084,813
CURRENT APPLICATION NUMBER: US/10/080/23505
PRIOR APPLICATION NUMBER: PCT/US00/23505
PRIOR FILING DATE: 2000-08-25
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 1242
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
FEATURE:
CTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Au-Young, Janice; Bandman, Olga
APPLICANT: Au-Young, Janice; Bandman, Olga
APPLICANT: Coleman, Roger; Wilde, Craig G.
TITLE OF INVENTION: DNA ENCODING NOVEL CHEMOKINE RECEPTORS
FILE REFERENCE: PP-0060-1 CON
CURRENT APPLICATION NUMBER: US/10/095,876A
CURRENT APPLICATION NUMBER: US/10/095,876A
PRIOR APPLICATION NUMBER: US 08/638,081
PRIOR FILING DATE: 1996-04-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PERL Program
SOFTWARE: PERL Program
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"NAME/KEY: misc feature

OTHER KINCHATION: Incyte ID No. US20030148294A1 478861
US-10-055-876A-2
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Pred. No. 3.5e-08;
); Mismatches 0;
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Best Local Similarity 100.0%;
Matches 18; Conservative 0
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ORGANISM: Homo sapiens
       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   SEQ ID NO 105
LENGTH: 18
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APPLICANT: Rosen, Craig A.
APPLICANT: Rosenke, Viktor
APPLICANT: Li, Yi
APPLICANT: Li, Steven, M.
TILLE OF INVENION: Buman G-protein Chemokine Receptor (CCR5) HDGNR10
FILE REFERENCE: 1488.115000A
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                                                                                                                                          Query Match 100.0%; Score 95; DB 9; Length 352; Best Local Similarity 100.0%; Pred. No. 7.4e-07; Matches 18; Conservative 0; Mismatches 0; Indels
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FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence US-09-725-285-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INCORPATION US/09759841

PRICENT NO. US20010039026A1

GENERAL INCORMATION:

APPLICANT: Rickett, Graham A

APPLICANT: Berros, Manoussos

TILLE REFERENCE: PC10348APME

CURRENT FILING DATE: 2001-01-12

PRIOR APPLICATION NUMBER: GB 0000661.9

PRIOR FILING DATE: 2000-01-12

PRIOR APPLICATION NUMBER: GB 0000663.5

PRIOR FILING DATE: 2000-01-12

PRIOR FILING DATE: 2000-01-12
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Gaps

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Query Match 100.0%; Score 95; DB 9; Length 352; Best Local Similarity 100.0%; Pred. No. 7.4e-07; Matches 18; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0;
                 PRIOR APPLICATION NUMBER: US 60/181,258
PRIOR FILING DATE: 2000-02-09
PRIOR PAPLICATION NUMBER: US 60/187,999
PRIOR PILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/234,336
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin version 3.0
LENGTH: 352
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  2001-02-09
                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-880A-2
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ORGANISM: Homo sapiens
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US-09-813-653-15
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US-09-779-879A-22

US-09-779-879A-22

Sequence 22, Application US/09779879A

Patent No. US2002048786A1

GENERAL INFORMATION:

APPLICANT: Roschke, Viktor

APPLICANT: Li, Yi

APPLICANT: Li, Yi

APPLICANT: Ruben, Steven, M.

TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10

FILE REPRENCE: 1488.115000A

CURRENT FILING DATE: 2001-02-09

PRIOR PELING DATE: 2001-02-09

PRIOR PELING DATE: 2000-02-09

PRIOR FILING DATE: 2000-03-09

PRIOR FILING DATE: 2000-03-09

PRIOR FILING DATE: 2000-03-09

PRIOR FILING DATE: 2000-03-09

PRIOR FILING DATE: 2000-03-05

NUMBER OF SEQ ID NOS: 58

SOC ID NO 22

LENGTH: 352
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Patent No. US2020061834A1
GENERAL INFORMATION:
APPLICANT: Roschke, Viktor
APPLICANT: Roschke, Viktor
APPLICANT: Li, Yi,
APPLICANT: Ruben, Steven, M.
TITLE CP INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGNR10
FILE REFERENCE: 1488.115.000C
CURRENT APPLICATION NUMBER: US/09/779,880A
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100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
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100.0%; Score 95; DB 9; I
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/09/779,879A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,258
PRIOR FILING DATE: 2000-02-09
PRIOR PLING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/187,999
PRIOR PLING DATE: 2000-03-09
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 58
SEQ ID NOS: 58
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; ORGANISM: Homo sapiens
US-09-779-879A-22
                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
US-09-779-879A-2
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US-09-779-880A-2
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Sequence 15. Application US/09813653
; Sequence 15. Application US/09813653
; General Information:
; APPLICANT: Nestor, John
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehir, Christina
; APPLICANT: Tan Hehir, Christina
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
; FILE REFERENCE: CNS-005
; CURRENT APPLICATION NUMBER: US/09/813,653
; CURRENT FILING DATE: 2001-03-20
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US-9-//9-MDA-22

Sequence 22, Application US/09779880A

Patent No. US20020061834A1

GENERAL INFORMATION:

APPLICANT: Rosen, Carig A.

APPLICANT: Li, Yi steven, M.

APPLICANT: Li, Yi steven, M.

TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10

FILE REPERENCE: 1488.11500C

CURRENT APPLICATION NUMBER: US/09/779,880A

CURRENT PAPLICATION NUMBER: US 60/181,258

FRIOR FILING DATE: 2000-02-09

FRIOR FILING DATE: 2000-03-09

FRIOR FILING DATE: 2000-03-09

FRIOR FILING DATE: 2000-03-09

FRIOR PLICATION NUMBER: US 60/187,999

FRIOR FILING DATE: 2000-03-09

FRIOR PRICE FILING DATE: 2000-03-09

FRIOR PRICE FILING DATE: 2000-03-09

FRIOR PRICE FILING DATE: 2000-03-09

FRIOR FILING DATE: 2000-03-09
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Sequence 2, Application US/0933912A;

Sequence 2, Application US/0933912A;

Patent No. US2020099176A1

GENERAL INFORMATION:

APPLICANT: Li, Yi

TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10;

TITLE OF INVENTION: (CCES Receptor);

TITLE OF INVENTION: 0799399-06-25;

CURRENT PRIOR DATE: 1999-06-25;

PRIOR PELLOR DATE: 1999-06-25;

PRIOR PELLOR DATE: 1999-06-26;

PRIOR PELLOR DATE: 1999-06-06;

PRIOR PELLOR DATE: 1999-06-06;

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fatent No. US20020076745AI

Sequence 2. Application US/09195662A

Patent No. US20020076745AI

GENERAL INFORMATION:
APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Li, Yi
TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGNR10 (CCR5 Receptor)
FILE REFERENCE: 1488.1150002

CURRENT APPLICATION NUMBER: US/09/195,662A

CURRENT PILING DATE: 1998-11-18
PRIOR PILING DATE: 1998-11-18
PRIOR PRING PAIRE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
SEQ ID NO 2. Patentin version 3.0
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100.0%; Pred. No. 7.4e-07;
iive 0; Mismatches 0;
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100.0%; Score 95; DB 9; 1
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: Deduced Amino Acid Sequence US-09-195-662A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
CTHER INFORMATION: Deduced Amino Acid Sequence
US-09-339-912A-2
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ORGANISM: Artificial Sequence: Genomic
FEATURE:
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ORGANISM: Artificial Sequence: Genomic
                                                                                                                                                                                                                                                                                                                            297 YAFVGEKFRNYLLVFFQK 314
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                                                                                                                        Query Match
Best Local Similarity
                                     ; TYPE: PRT
; ORGANISM: human
US-09-796-202-1
                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
US-09-195-662A-2
            LENGTH: 352
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LENGIH: 352
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Patent No. US20020064770A1
| PAPLICANT: Nestor, John
| APPLICANT: Rese, Raymond
| APPLICANT: Tan Hehir, Christina
| TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
| TITLE OF INVENTION: Binding Compounds
| TITLE OF INVENTION: UNBER: US/09/813,653
| CURRENT FILING DATE: 2001-03-20
| PRIOR APPLICATION NUMBER: US 60/190,96
| PRIOR APPLICATION WUMBER: US 60/190,96
| PRIOR FILING DATE: 2000-03-21
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Patent No. US20020068813A1
GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William
TITLE OF INVENTION: SULFATED CCRS PEPTIDES FOR HIV-1 INFECTION
FILE REFERENT APPLICATION WINBER: US/09/796,202
CURRENT FILING DATE: 2001-02-28
NUMBER: OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 95; DB 9; Length 352; Best Local Similarity 100.0%; Pred. No. 7.4e-07; Matches 18; Conservative 0; Mismatches 0; Indels
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Pred. No. 7.4e-07;
; Mismatches 0;
PRIOR APPLICATION NUMBER: US 60/190,946
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PLILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/191,299
PRIOR FILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin version 3.0
SEQ ID NO 15
LENGTH: 352
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Best Local Similarity 100.0%;
Matches 18; Conservative 0
                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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SEQ ID NO 17
LENGTH: 352
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PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOXINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Pachable Form:
MEDIUM TYPE: Floppy disk
COMPUTER: In Per Compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION: <UNFADAMA
APPLICATION: <UNFADAMA
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
ANAWA: Altern Dariel F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: CASE OF THE CASE OF THE
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CORRESPONDENCE ADDRESS:
ADDRESSE: Martens, Olson & Bear
ADDRESSE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                     ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORWATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTER.STICS:
LENGTH: 352 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 24-Aug-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NDATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 5, Application US/09938703; Patent No. US20020110870A1; GENERAL INFORMATION:
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   CORRESPONDENCE ADDRESS:
                                                                                                                                                             U.S.A.
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US-09-938-703-5
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Patent No. US20020110805A1
GENERAL INPCRMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASCART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: TEM PC COMPATIBLE
COMPUTER: TEM PC COMPATIBLE
COMPUTER: DEACHING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: US/09/938,719
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
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                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
Best Local Similarity 100.0%; Pred. No. 7.4e-07; Matches 18; Conservative 0; Mismatches 0;
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REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION WUMBER: 09/626,939
FILING DATE: 27-UTLY-2000
ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: protein;

SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-719-5
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                                                                                                     1 YAFVGEKFRNYLLVFFOK 18
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Best Local Similarity 100.
Matches 18; Conservative
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US-09-939-226-5
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Sequence 477, Application US/09826509

Bublication No. US20030204073A1

GENERAL INFORMATION:

APPLICANT: Liaw, Chen W.

FILE REFERENCE: AREN-207

CURRENT FILING DATE: 2001-04-05

PRIOR APPLICATION NUMBER: 09/170, 496

PRIOR APPLICATION NUMBER: 09/170, 496

PRIOR APPLICATION NUMBER: 09/170, 496

PRIOR PILING DATE: 1998-10-13

NUMBER OF SEQ ID NOS: 589

SOFTWARE: PatentIn Version 2.1

LENGTH: 1352
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100.0%; Score 95; DB 11; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0
                                     COMPUTER EXABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/734,221A
FILING DATE: 11-Dec-2000
CLASSIFICATION AND COMPANIES OF THE CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION DATE: 19
APPLICATION NUMBER: US 08/666,020
FILING DATE: 19-JUN-1996
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRANTION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-004 NZ
TELEPHONE: 201-487-5800
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 95; DB 10; Best Local Similarity 100.0%; Pred. No. 7.4e-07; Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 352 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    297 YAFVGEKFRNYLLVFFQK 314
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-477
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US-09-826-509-477
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Patent No. US20020132269A1
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRS
TITLE OF INVENTION: POLYNUCLEOTION
FILE REFERENCE: 1488 115006
CURRENT APPLICATION NUMBER: 08/96502,783A
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: 08/466,343
PRIOR PLING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
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MACROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 95; DB 9; Length 352; Best Local Similarity 100.0%; Pred. No. 7.4e-07; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 95; DB 9; Length 352; Best Local Similarity 100.0%; Pred. No. 7.4e-07; Matches 18; Conservative 0; Mismatches 0; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                   TOPOLOGY: linear / MOLECTUE TYPE: protein / SEQUENCE DESCRIPTION: SEQ ID NO: 5: US-09-938-703-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DENG, HONGKUI
ELLMEIER, WILFRIED
LANDAU, NATHANIEL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/09734221A Publication No. US20030096221A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297 YAFVGEKFRNYLLVFFQK 314
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APPLICANT: LITTMAN, DAN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Hackensack
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ORGANISM: Homo sapiens
US-09-502-783A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 19
US-09-734-221A-14
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US-09-502-783A-2
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LENGTH: 352
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US-1100-623-20

Sequence 20, Application US/10106623

Publication No. US200201508881

Schweickart. Vicky L.

Raport. Carol J.

Raport. Carol J.

TITLE OF INVENTION: Chemokine Receptor Materials and Methods
NUMBER OF SEQUENCES 20

CORRESPONDENCE ADDERS: 20

CORRESPONDENCE ADDERS: 30

CONFESTS: An ADDERSSE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago

STATE: 1111nois

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: 09/10/106,623

FILING DATE: 26-Mar-2002

CLASSIFICATION NUMBER: 08/10/106,623

RELICATION NUMBER: 01/10/106,623

RELICATION NUMBER: 33,302

RELECOMMUNICATION NUMBER: 33,302

RELECOMMUNICATION NUMBER: 23,302

RELECOMMUNICATION NUMBER: 212-474-6300

TELECOMMUNICATION NO 20:

SEQUENCE CHARACTERISTICS:

INNFORMATION FOR SEQ IN NO: 20:

SEQUENCE CHARACTERISTICS:
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100.0%; Score 95; DB 13; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
OTHER INFORMATION: /= "88C amino acid sequence"
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 95; DB 13;
100.0%; Pred. No. 7.4e-07;
tive 0; Mismatches 0;
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
                                                                                                                                                                      LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 YAFVGEKFRNYLLVFFQK 314
                                      TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.0
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                                                                                                                                                                                                                                                                                             Sequence 5, Application US/10151274

Publication No. US20030064071A1

GENERAL INFORMATION:

APPLICANT: Littman, Dan R.

APPLICANT: Kwon, Douglas S.

APPLICANT: Gejitenbeck, Yvette

APPLICANT: Gejitenbeck, Theo

TITLE OF INVENTION: MATHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY

TITLE OF INVENTION: MATHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY

TITLE OF INVENTION: MATHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY

TITLE OF INVENTION: MATHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY

TITLE OF INVENTION: MATHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY

TITLE OF INVENTION: MATHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY

FILE REPERENCE: 1049-1-017

CURRENT APPLICATION NUMBER: US/09/517,605

PRIOR FILING DATE: 2000-03-02

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 5

MATHOD AND SECOND OF SE
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| Publication No. US20020150888A1
| CENERAL INFORMATION:
| APPLICANT Gray, Patrick W. Schweickart, Vicky L. Raport, Carol J. TITLE OF INVENTION: Chemokine Receptor Materials and Methods NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS: | CORRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BEATHILI Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/106,623
FILING DATE: 26-Mar-2002
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/771,276
FILING DATE: CUNKNOWN>
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: NO. US200201508884and, Greta E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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REFERENCE/DOCKET NUMBER: 27866/33670
TELECOMMUNICATION INFORMATION:
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                                                                            297 YAFVGEKFRNYLLVFFQK 314
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              1 YAFVGEKFRNYLLVFFQK 18
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STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT; ORGANISM: Homo sapiens
US-10-151-274-5
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US-10-106-623-2
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297 YAFVGEKFRNYLLVFFQK 314

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RESULT 24
US-10-232-686-2
'Sequence 2, Application US/10232686
'Publication No. US20030023044A1
'GENERAL INFORMATION:

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GENERAL INCRAMICANT:
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
APPLICANT: Rush, M.
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
FILE REFERENCE: 1488.1150001
CURRENT PAPLICATION NUMBER: US/10/067,800
CURRENT PELING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: PCT/US01/04153
PRIOR APPLICATION NUMBER: 06/297,257
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR PLICATION NUMBER: 60/297,257
PRIOR APPLICATION NUMBER: 60/297,257
PRIOR FILING DATE: 2001-06-12
PRIOR FILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-10-12
PRIOR PLING DATE: 2001-110-12
PRIOR FILING DATE: 2001-110-12
PRIOR PLOR FILING DATE: 2001-110-12
PRIOR FILING DATE: 2001-110-12
PRIOR FILING DATE: 2001-110-12
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                     Human G-protein Chemokine Receptor (CCR5) HDGNR10
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              TITLE OF INVENTION: Human G-protein Chemokine FILE REFERENCE: 1488.1150001
CURRENT APPLICATION NUMBER: US/10/67,800
CURRENT FILING DATE: 2002-02-08
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR PRILING DATE: 2001-03-08-08
PRIOR PILING DATE: 2001-03-08-08
PRIOR PILING DATE: 2001-01-2
PRIOR PILING DATE: 2001-01-2
PRIOR PILING DATE: 2001-01-2
PRIOR PILING DATE: 2001-10-12
PRIOR PILING DATE: 2001-10-12
PRIOR PILING DATE: 2001-10-12
PRIOR PILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PATENTIN VORTING 3.1
SEQ ID NO 2
LENGTH: 352
TYPE: PRI
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; Sequence 22, Application US/10067800
; Beduence 12, Application US/10058A1
; GENERAL INFORMATION:
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Best Local Similarity 100.0%; P:
Matches 18; Conservative 0;
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Ruben, Steven, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-10-067-800-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-800-22
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Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0;
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297 YAFVGEKFRNYLLVFFQK 314

à g US-10-086-814-1

/ TYPE: PRT / ORGANISM: Homo sapiens US-10-232-686-2

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Sequence 2, Application US/10067800 Publication No. US20030100058A1 GENERAL INFORMATION: APPLICANT: ROSCHKE, VIKTOR APPLICANT: ROSCHKE, Craig A.

RESULT 26 US-10-067-800-2

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; ORGANISM: Homo sapiens US-10-086-814-1

TYPE: PRT

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Sequence 1. Application US/10072301
| Sequence 1. Application No. US20030152913A1
| Publication No. US20030152913A1
| GENERAL INFORMATION:
| APPLICANT: Hua, Shao-bing
| APPLICANT: Pauling, Michelle H.
| APPLICANT: Dau, Li
| TITLE OF INVENTION: VIRUS
| TITLE OF INVENTION: UNMERR: US/10/072,301
| CURRENT APPLICATION NUMBER: US/10/072,301
| CURRENT APPLICATION NUMBER: US/10/072,301
| SOFTWARR: Patentin version 3.1
| SOFTWARR: Patentin version 3.1
| SOFTWARR: PATENTION NOTES
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Sequence 52, Application US/10164649

Sequence 52, Application WS/10164649

Publication No. US20030162943A1

GENERAL INFORMATION:

APPLICANT: Graham, Gerard J. et al.

TITLE OF INVENTION: No. US20030162943A1el Molecules of the G Protein-Coupled

TITLE OF INVENTION: No. US20030162943A1el Molecules of the G Protein-Coupled

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STABET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTWARRE: PATENTING SYSTEM: PC-DOS/MS-DOS

SOFTWARRE: PATENTING 
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100.0%; Pred. No. 7.4e-07;
tive 0; Mismatches 0;
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Pred. No. 7.4e-07;
; Mismatches 0;
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RAPLICATION NUMBER: US/10/164,649
FILING DATE: 07-Unu-2002
CLASSIFICATION: «Unknown»
CURRENT APPLICATION NUMBER: US/10/323,314
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 1
LENGTH: 352
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Best Local Similarity 100.0%;
Matches 18; Conservative 0
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Matches 18; Conservative
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US-10-072-301-1
                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: human US-10-323-314-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 31
US-10-072-301-1
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IS-201-225-567A-352

Sequence 352, Application US/10225567A

Publication No. US20030113798A1

GENERAL INFORMATION:

APPLICANT: LifeSpan Biosciences

APPLICANT: Brown, Joseph F.

APPLICANT: Brown, Joseph F.

APPLICANT: Brown, Christine L.

TITLE OF INVENTION ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

FILE REFERENCE: 1920-4-4

CURRENT APPLICATION NUMBER: US/10/225,567A

CURRENT APPLICATION NUMBER: 60/257,144

PRIOR APPLICATION NUMBER: 60/257,144

PRIOR APPLICATION NUMBER: 60/257,144

PRIOR APPLICATION NUMBER: 3000-12-19

NUMBER OF SEQ ID NOS: 2292

SSOT ID NO 352

LENGTH: 352
                                                                                                                                             Sequence 6, Application US/10290058A;
Sequence 6, Application US/2030104455A1;
GENERAL INFORMATION: US2030104455A1;
GENERAL INFORMATION: Silos-Santiago, Inmaculada
APPLICANT: Silos-Santiago, Inmaculada
TITLE OF INVENTION: Urological Disorders Using 313, 333, 5464, 18817 or 33524
TITLE OF INVENTION: Urological Disorders Using 313, 333, 5464, 18817 or 33524
FILE OF INVENTION: Urological Disorders Using 313, 333, 5464, 18817 or 33524
FILE OF INVENTION: UNDERS: US/10/290,058A
CURRENT APPLICATION NUMBER: 60/344,552
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
SEQ I
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US-10-323-314-1
Sequence 1, Application US/10323314
Publication No. US20030139571A1
GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Dragic, William
TITLE OF INVENTION: SULFATED CCRS PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/61010-1/JPW/MAP/DJK
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100.0%; Score 95; DB 14;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0;
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US-10-225-567A-352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo Sapien
US-10-290-058A-6
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Sequence 67, Application US/10239423
Publication No. US20303186889A1
Publication No. US203030186889A1
Publication No. US203030186889A1
GENERAL INFORMATION:
APPLICANT: FORSEMANN, Wolf-Georg; FORSEMANN, Ulf; ADERMANN, Knut;
APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikolaj
TITLE OF INVENTION: Disgnostic Agent and Medicament for Examining the
TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells and
TITLE OF INVENTION: For Treating Tumor Diseases and Inflammation Cells and
TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine
TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction
FILE REFERENCE: 022217us
CURRENT APPLICATION NUMBER: US/10/239,423
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Publication No. US20030166024A1

GENERAL INFORMATION:

APPLICANT: Rosen, Craig A.

APPLICANT: Rosenke, Viktor

APPLICANT: Liv, Yi

APPLICANT: Liv, Yi

APPLICANT: Ruben, Steven, M.

TITLE REFERENCE: 1488.11500A

CURRENT APPLICATION NUMBER: US/10/135,839

CURRENT PILING DATE: 2002-05-01

FRICA APPLICATION NUMBER: US/09/779,879A

FRICA PILING DATE: 2000-02-09

FRICA REPLICATION NUMBER: US 60/187,999

FRICA FILING DATE: 2000-03-09

FRICA REPLICATION NUMBER: US 60/187,999

FRICA RILING DATE: 2000-03-09

FRICA RILING DATE: 2000-03-09

FRICA RILING DATE: 2000-03-09

FRICA RILING DATE: 2000-03-09

FRICA FILING DATE: 2000-03-09

FRICA RILING DATE: 2000-03-09

FRICA FILING DATE: 2000-03-05

FRICA RILING DATE: 2000-03-05

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100.0%; Score 95; DB 14;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0;
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100.0%; Score 95; DB 14;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0;
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/187,999
PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 58
SSEYTARE: Patentin version 3.0
LENGTH: 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-135-839-2
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US-10-135-839-22
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US-10-135-839-22
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US-10-239-423-67
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Publication No. US2003016598A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hua, Shao-bing
APPLICANT: Pauling, Michelle H.
APPLICANT: And Li
TITLE OF INVENTION: HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST 1
TITLE OF INVENTION: FRAGMENTS DERIVED FROM MEMBRANE PROTEINS
FILE REPERENCE: 25636-117
CURRENT APPLICATION NUMBER: US/10/071,866
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 1.
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APPLICANT: Roschke, Viktor
APPLICANT: Esochke, Viktor
APPLICANT: Li, Yi
APPLICANT: Rosche, M.
TITLE OF INVENT: Reven, M.
TITLE OF INVENT: Reven, M.
TITLE OF INVENT: Li, Yi
TITLE
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Best Local Similarity 100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0: Indels Conservative 1
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100.0%; Score 95; DB 14;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0;
                                            APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-WAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MMI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)277-7400
TELEFRA: (617)742-4214
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear MOLECULE TYPE: peptide ; FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 52: US-10-164-649-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/10135839
Publication No. US20030166024A1
GENERAL INFORMATION:
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              PRIOR APPLICATION DATA:
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US-10-071-866-1
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RESULT 39
US-10-360-828-1
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; OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-67
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                                                                                                                                                                                                                                                            Length 352;
                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/439,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFFILCATION NUMBER: US/10/439,543
FILING DATE:
PRIOR APPLICATION
PRIOR APPLICATION
APPLICATION NUMBER: 08/664,458
FILING DATE: May 28, 1997
APPLICATION NUMBER: Provisional 60/018,508
FILING DATE: May 28, 1996
FILING DATE: ABOUT 10 NUMBER: 08930/030001
FELEPANT 619/678-5099
FILING MAY ATOM SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 352 and no acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: DE10016013.1
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 84
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 67
LENGTH: 352
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                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
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US-10-439-845-2
                                                                                                                                                                 FEATURE:
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1 YAFVGEKFRNYLLVFFQK 18

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US-JOL-641-798-5

Sequence 5, Application US/10661798

Publication No. US20040110127A1

GENERAL INFORMATION:
APPLICANT: Samoon, Michael
APPLICANT: Parmentier, Marc
APPLICANT: Vassart, Gilbert
APPLICANT: Vassart, Gilbert
APPLICANT: Variang Methods for Identifying Compounds which Decrease HIV ET
ITLE OF INVENTION: Screening Methods for Identifying Compounds which Decrease
TITLE OF INVENTION: Screening Methods for Identifying Compounds which Decrease
TITLE OF INVENTION: Screening Methods for Identifying DATE: 2003-09-12
PRIOR APPLICANTION NUMBER: 09/938,703
PRIOR FILING DATE: 1996-03-01
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100.0%; Score 95; DB 15; Length 352;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0
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PRIOR APPLICATION NUMBER: US 10/072,301
PRIOR FILING DATE: 2002-08
PRIOR FILING DATE: 2002-04-25
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin version 3.1
ENGITH: 352
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Best Local Similarity 100.(
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CRGANISM: Homo sapiens
US-10-360-828-1
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CRGANISM: Homo sapiens
US-10-661-798-5
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Search completed: September 28, 2004, 09:44:42 Job time : 59.625 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein September 28, 2004, 08:57:36; Search time 9.675 Seconds (without alignments) 178.961 Million cell updates/sec Run on:

1 YAFVGEKFRNYLLVFFQK 18 US-10-084-813-15 95 score: Perfect so Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 Total number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
2: pir1:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SIMMARIES

		дo			SUMMAKLES	
esult No.	Score	Query Match	Length	DB	ΩI	Description
-	95	100.0	I LO	2	A43113	chemokine (C-C) re
7	79	ന	360	(1	JC2443	chemokine (C-C) re
m	65	68.4	S	N	⋖	(G-G)
4,	64	7.	D	~	4934	MIP-1 alpha recept
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7	61	4.	9	~	350	G protein-coupled
œ	9	e.	LO.	~	517	m
σ,	58	ä	Ŋ	~	818	
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11	57	ö	9	~	716	chemokine (C-C) re
	53	S	L)	7	~	macrophage inflamm
13	53	TU.	S	N		ᅺ
14	52	4	φ	N	m	chemokine (C-C) re
15	52	54.7	7	~	B55735	lymphocyte-specifi
16	20	a	S	7	CT.	interleukin-8 rece
17	50	N	ß	N	$\alpha$	interleukin-8 rece
18	20	ä	ø	N	_	interleukin-8 rece
19	50	52.6	~	7	A45680	G protein-coupled
20	49	ä	76	~	E95247	hypothetical prote
21	49	ä	76	7	9811	
22	49	ä	_	~	3845	
23	48	ö	ø	7	JE0349	interferon-inducib
24	47	φ.	ഗ	7	5375	interleukin-8 rece
25	47	•	7	~	5573	G protein-coupled
56	46	48.4	S	N	99	interleukin-8 rece
27	46	48.4	S	~	012	interleukin-8 rece
28	45.5		377	N	18	glycosyltransferas
59	45	47.4	ហ	N	JN0621	G protein-coupled

angiotensin II rec	IL8-related recept	G protein-coupled	hypothetical prote	hypothetical prote	hypothetical prote	sugar transport pr	G protein-coupled								
JC1104	S44425	JC1194	A48857	A42656	JQ1516	S15403	JH0621	JC2134	G02670	JC5069	C81207	E64514	T03883	C90270	I65989
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Addition (C-C) receptor 5 - human Chemokine (C-C) receptor 5 - human Chemokine (C-C) receptor 5 - human Chemokine (C-C) receptor 6 - human Cybecies: Homo sapiens (man) Cybecies: Homo sapiens (man) Cybecies: Homo sapiens (man) Cybecies: Loui-1999 Heaquence revision 12-Jul-1996 Heaquence revision A3113; \$12808; \$28832; \$926533; \$A5833; \$A5833; \$A5833; \$A5833; \$A5833; \$A5833; \$A5832; \$A5833; \$A5833

R,Combadiere, C. submitted to the EMBL Data Library, May 1996

A.Reference number: H01541
A.Accession: G02653
A.Accession: BMB. U1-352
A.Accession: G02653
A.Accession: G

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(covalent) #status predicted
                                                                                                                                                                            1; Mismatches
F;14/Binding site: carbohydrate (Asn) (covald
F;113-190/Disulfide bonds: #status predicted
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A;Cross-references: GDB:579624; OMIM:601268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Status: nucleic acid sequence not shown A, Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                  305 YAFVGEKFRYLSVFFRK 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chemokine (C-C) receptor 3 - human
N;Alternate names: C-C CKR-3
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.4%;
                                                                                                       Query Match 83.2%;
Best Local Similarity 83.3%;
Matches 15; Conservative
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Best Local Similarity 66.7
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       Appearation: G protein-coupled receptor for chemokines MIP-lalpha, MIP-lbeta and RANTE Appearation: G protein-coupled receptor for chemokines MIP-lalpha, MIP-lbeta and RANTE Appearation to control granulocyte proliferation and differentiation (Superfamily: Vertebrate rhodopsin (Superfamily: Vertebrate rhodopsin (Steywords: AIDS); G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane #status predicted <TMI> F;32-56/Domain: transmembrane #status predicted <TMI> F;67-87/Domain: transmembrane #status predicted <TMI> F;103-124/Domain: transmembrane #status predicted <TMI> F;103-124/Domain: transmembrane #status predicted <TMI> F;23-257/Domain: transmembrane #status predicted <TMI> F;20-269,101-178/Disulfide bonds: #status predicted <TMI> F;20-269,101-178/Disulfide bonds: #status predicted <TMI> F;26/Binding site: carbohydrate (Asn) (covalent) #status predicted F;336,337,342/Binding site: phosphate (Thr) (covalent) #status predicted
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R; Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A; Title: Molecular cloning and functional expression of two monocyte chemoattractant pro
A; Reference number: A53477; MUID:94195821; PMID:8146186
A; Accession: I38463
A; Accession: I38463
A; Residues: Preliminary
A; Molecule type: mRNA
A; Residues: 1-360 «RES>
A; Cross-references: EMBL:U03905; NID:g472557; PIDN:AAA19120.1; PID:g472558
C; Genetics: A; Genetics: A; Genetics: A; Cross-references: CBB:337364; OMIM:601267
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Subperfamily: vertebrate rhodopsin

C;Superfamily: vertebrate rhodopsin

C;Superfamily: vertebrate rhodopsin

C;Superfamily: vertebrate splicing, G protein-coupled receptor; glycoprotein; transmembrane #status predicted <TM1>
F;43-70/Domain: transmembrane #status predicted <TM2>
F;115-136/Domain: transmembrane #status predicted <TM3>
F;154-178/Domain: transmembrane #status predicted <TM4>
F;267-226/Domain: transmembrane #status predicted <TM4>
F;244-268/Domain: transmembrane #status predicted <TM6>
F;242-268/Domain: transmembrane #status predicted <TM6>
F;247-309/Domain: transmembrane #status predicted <TM7>
                                                                                                           A;Cross-references: GB:U54994; NID:g1457945; PIDN:AAC50598.1; PID:g1457946
C;Comment: This is a receptor for chemokines MIP-lalpha (see FIR:A30574), MIP-lbeta (see
C;Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chemokine (C-C) receptor 2, splice form B - human
NiAlternate names: C-C CRR-2; monocyte chemoattractant protein 1 receptor; monocyte chem
C;Species Bome sapiens (man)
C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
C;Accession: JC2443; I38463
E;Amergami, S.; Tokuda, Y.; Ishli, K.; Tanaka, H.; Endo, N.
Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
A;Title: cDNA cloning and functional expression of a human monocyte chemoattractant prot
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                                                                                                                                                                                                                                                    Gene: GDB:CMKBR5; CCR5; CKR-5; CC-CKR-5; CKR5; ChemR13; Cross-references: GDB:1230510; CMIM:601373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                297 YAFVGEKFRNYLLVFFQK 314
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C; Function:
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Best Local Similarity
Matches 18; Conserv
                                      A; Molecule type: mRNA
A; Residues: 1-352 < RAP>
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A; Residues: 1-360 < YAM>
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       A;Accession: A58833
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149341

MIP-1 alpha receptor like-2 - mouse

MIP-1 alpha receptor like-2 - mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1998

C;Accession: 149341

R;Gao, J.L.; Murphy, P.M.

J. Biol. Chem. 270, 17494-17501, 1995

A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokin.

A;Reference number: 149339; MUID:95340546; PMID:7542241
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C; Superfamily: vertebrate rhodopsin
F; 36-60/Domain: transmembrane #status predicted <TM2>
F; 71-91/Domain: transmembrane #status predicted <TM2>
F; 108-129/Domain: transmembrane #status predicted <TM3>
F; 205-223/Domain: transmembrane #status predicted <TM5>
F; 240-261/Domain: transmembrane #status predicted <TM5>
F; 240-261/Domain: transmembrane #status predicted <TM5>
F; 288-305/Domain: transmembrane #status predicted <TM6>
F; 288-305/Domain: transmembrane #status predicted <TM7>
F; 244-273, 106-183/Disulfide bonds: #status predicted <TM7>
F; 245-281/Domain: transmembrane #status predicted <TM5-
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A;Cross-references: GB:U28694; NID:g1199579; PIDN:AACS0469.1; PID:g1199580
A;Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AACS0469.1
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-355 <-PON>
A;Residues: 1-355 <-PON>
A;Cross-references: EMBL:U49727; NID:G1477560; PIDN:AAB09726.1; PID:g1477561
A;Crombadiere, C.; Ahuja, S.K.; Murphy, P.M.
J. Biol. Chem. 270, 16491-16494, 1995
A;Title: Cloning and functional expression of a human eosinophil CC chemokine receptor.
A;Reference number: A57237; MUID:95348056; PMID:7622448
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                                                                                                                                          Gaps
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Pred. No. 0.0035;
Score 79; DB 2; Ler
Pred, No. 1.6e-05;
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Chemokine (C-C) receptor 1 - human
NyAlternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A45177; I55671
R;Neore, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
Cell 72, 415-425, 1993
A;Fitle: Molecular cloning, functional expression, and signaling characteristics of a C-C A;Reference number: A45177; MUID:93161416; PMID:7679328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G protein-coupled receptor CKR-L3 - human
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cistes: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
Cistession: JC5068
R;Zaballos, A; Varona, R; Gutierrez, J; Lind, P; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A;Title: Molecular cloning and RNA expression of two new human chemokine receptor-like gf
A;Reference number: JC5067; MUID:97040707; PMID:8886020
A;Accession: JC5068
A;Molecule type: DNA
A;Residues: 1-369 <ZAB>
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C;Species: equine herpesvirus 2
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
C;Accession: S55594
S;Telford, B.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A;Title: The DNA sequence of equine herpesvirus 2.
A;Reference number: S55594; MUID:95302501; PMID:7783207
A;Reference number: S55594
A;Status: Proliminary; nucleic acid sequence not shown
A;Residues: 1-383 <-TEL>
A;Residues: 1-383 <-TEL>
C;Cross-references: GB:U20824; NID:g695172; PIDN:AAC13788.1; PID:g695173
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor
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A;Cross-references: GDB:5370639; OMIM:601835
A;Map position: 6427-6427
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
C;Keywords: G protein-coupled receptor; transmembrane protein
C;Keywords: G protein-coupled receptor; transmembrane protein
C;Keywords: G protein-coupled receptor; transmembrane predicted <TM1>
F;79-99/Domain: transmembrane #status predicted <TM2>
F;115-136/Domain: transmembrane #status predicted <TM3>
F;120-131/Domain: transmembrane #status predicted <TM5>
F;220-271/Domain: transmembrane #status predicted <TM5>
F;220-271/Domain: transmembrane #status predicted <TM6>
F;292-315/Domain: transmembrane #status predicted <TM7>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    311 YAFIGOKFRNYFL 323
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JUGGOF
G protein-coupled receptor CKR-L1 - human
G protein TER1; GPR-CY6
G protein-coupled receptor CKR-L1 - human
N.Alternate names: chemokine receptor-like protein TER1; GPR-CY6
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Accession: JUGGOFF, Requence revision 31-Jan-1997 #text_change 21-Jul-2000
C; Accession: JUGGOFF, Requence revision 31-Jan-1997 #text_change 21-Jul-2000
C; Accession: JUGGOFF, Rediemrez, J.; Lind, P.; Marquez, G.
Blocham. Blophys. Res. Commun. 227, 846-853, 1996
A; Title: Molecular cloning and RNA expression of two new human chemokine receptor-like g
A; Reference number: JUGGOFF, MUID:97040707; PMID:8886020
A; Molecula type: DNA
A; Residues: 1-355 cZAB>
A; Molecule type: DNA
A; Residues: 1-355 cZAB>
A; Molecule type: DNA
A; Residues: Homber: JUDGOFF, MUD:G1668735; PIDN:CAB02142.1; PID:G1668736
A; Molecule type: DNA
A; Residues: Homber: JUDGOFF, MUD:G1668735; PIDN:CAB02142.1; PID:G1668736
A; Molecule to the EMBL Data Library, June 1996
A; Receince number: Hol714
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A; Status: translated from GB/EMBL/DDBJ
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-355 < NAP>
A; Cross-references: EMBL: U62556; NID: 91468979
A; Cross-reference EMBL: Data Library, January 1996
A; Reference number: H01154
A; Accession: G02387
A; Reference promper: H01154
A; Molecule type: DNA
A; Residues: 1-355 < BON>
A; Residues: 1-355 < BON>
A; Residues: 1-355 < BON>
A; Cross-references: EMBL: U45983; NID: 91245056; PID: 91245057
C; Comment: This protein belongs to the family of beta chemokine receptors.
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llarity 66.7%; Pred. No. 0.0076;
Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                    Length 359
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A,Gene: GDB: CMKBRL2, TER1, CKR-L1
A,Cross-references: GDB: 6053733; OMIM:601834
A,Map position: 3p21-3p21
C,Superfamily: vertebrate rhodopsin
C,Swperfamily: vertebrate shodopsin
C,Keywords: G protein-coupled receptor; transmembrane protein
C,Keywords: Transmembrane #status predicted <TM1>
F;36-63/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                          Query Match 67.4%; Score 64; DB 2; Length 355
Best Local Similarity 61.1%; Pred. No. 0.0052;
Matches 11; Conservative 4; Mismatches 3; Indels
                                                                                   A,Molecule type: DNA
A,Residudes 1.359 «RES.
A;Crosa-references: EMB:U28406; NID:9881551; PID:9881552
C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;108-129/Domain: transmembrane #status predicted <TM3>F;147-171/Domain: transmembrane #status predicted <TM4>F;202-222/Domain: transmembrane #status predicted <TM5-F;239-260/Domain: transmembrane #status predicted <TM5-F;281-304/Domain: transmembrane #status predicted <TM7>F;281-304/Domain: transmembrane #status predicted <TM7>F;281-304/D
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G protein-coupled receptor El - equine herpesvirus 2
                                    preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 YAFVGERFRKHLRLFFHR 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 YAFVGEKFRNYLLVFFQK 18
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Matches 12; Conserv
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RESULT 6

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A;Accession: UC4304
A;Aolecule type: mRNA
A;Residues: 1-355 - MRAP
A;Cross-references: GB:U20350; NID:g665580; PIDN:AAA91783.1; PID:g665581
A;Cross-references: GB:U20350; NID:g665580; PIDN:AAA91783.1; PID:g665581
C;Comment: This protein is a cell-surface receptor which recognizes extracellular signals:
C;Comment: This protein is a key regulator of many immune and homeostatic responses, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.T.O.P.T.ELECTELLES (1971)

A.Map Dostrion: 3921-3921

C.Superfamily: vertebrate rhodopsin

F.76-97/Domain: transmembrane #status predicted <TM2>
F.76-97/Domain: transmembrane #status predicted <TM3>
F.712-137/Domain: transmembrane #status predicted <TM5>
F.72-175/Domain: transmembrane #status predicted <TM5>
F.72-175/Domain: transmembrane #status predicted <TM5>
F.72-276/ID-197/Domain: transmembrane #status predicted <TM5>
F.72-276/ID-197/Diminifide bonds: #status predicted <TM5>
F.72-350/Rinding site: phosphate (Ser) (covalent) (by protein kinase II) #status predicted F.185/Rinding site: carbohydrate (Asn) (covalent) #status predicted F.185/Rinding site: carbohydrate (Asn) (covalent) #status predicted F.185/Rinding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted F.321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted F.321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
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R;Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; We Biol. Chem. 270, 19495-19500, 1995
A;Title: Molecular cloning and functional expression of a novel CC chemokine receptor cDl A;Reference number: A57160; MUID:95370289; PMID:7642634
A;Accession: A57160
C;Species: Homo sapiens (man)
C;Daces 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 19-May-2000
C;Dacession: JG4304
R;Raport, C:J: Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Gene 163, 295-299, 1995
A;Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related A;Reference number: JC4304; MUID:96011651; PMID:7590284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chemokine (C-C) receptor 4 - human
N;Alternate names: C-C KRR-4
C;Species: Homo sapiens (man)
C;Species: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C,Superfamily: vertebrate rhodopsin
C,Superfamily: vertebrate rhodopsin
C,Keywords: G protein-coupled receptor; lymphokine; transmembrane protein
E,35-57/Domain: transmembrane #status predicted <TM1>
F;66-88/Domain: transmembrane #status predicted <TM3>
F;104-125/Domain: transmembrane #status predicted <TM4>
F;146-165/Domain: transmembrane #status predicted <TM4>
F;197-217/Domain: transmembrane #status predicted <TM6>
F;230-254/Domain: transmembrane #status predicted <TM6>
F;235-254/Domain: transmembrane #status predicted <TM7>
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Pred. No. 0.078;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293 YAFAGEKFRRYLYHLYGK 310
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Best Local Similarity 61.1%;
Matches 11; Conservative :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: GDB:CMKBR4
A;Cross-references: GDB:677463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 3pter-p21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: v28
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A,Reference number: 155671; MUID:93240122; PMID:7683036
A,Accession: 155671
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A;Cross-references: GDB:138446; OMIN:601159
A;Cross-references: GDB:138446; OMIN:601159
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; t: Superfamily: transmembrane #status predicted <TML>
F)36-60 Domain: transmembrane #status predicted <TML>
F)1-31 Domain: transmembrane #status predicted <TML>
F)40-24 Domain: transmembrane #status predicted <TML>
F)40-223 Domain: transmembrane #status predicted <TML>
F)505-223 Domain: transmembrane #status predicted <TMS>
F)268-305 Domain: transmembrane #status predicted <TMS>
F)268-305 Domain: transmembrane #status predicted <TMS>
F)288-305 Domain: transmembrane #status predicted <TMS>
F)340-264 Domain: transmembrane #status predicted <TMS>
F)345 Binding site: carbohydrate (Ser) (covalent) #status predicted
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
C;Accession: I58186
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A,COSS-references: EMBL:U04808; NID:g2558635; PIDN:AAB87093.1; PID:g439861
C,Superfamily: vertebrate rhodopsin
C,Superfamily: ortebrate receptor
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                                                                                                                                                                 A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
A;Experimental source: HL60 cells
A;Note: sequence extracted from NCBI backbone (NCBIP:124876)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
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Neurosci. Lett. 169, 85-89, 1994
A; Title: cDNA cloning of a G-protein-coupled receptor expressed
A; Reference number: IS8186; MUID:94323113; PMID:8047298
A; Accession: IS8186
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
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61.1%; Pred. No. 0.053;
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                                   A,Status: nucleic acid sequence not shown A,Molecule type: mRNA
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                                                                                                                                  -355 . <NEO>
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Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-355 <RES>
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ð d 60.0%; Score 57; DB 2; Length 360;

Query Match

orphan G protein-coupled receptor - human N;Alternate names: V28 protein

RESULT 10 JC4304

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hab/cyle-specific G protein-coupled receptor EBI1 - human
NyAlternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1
C;Species: Homo sapiens (man)
C;Date: 107-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000
C;Accession: B55735; B52443
R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B., Genomics 23; 643-650, 1994
A;Title: Cloning of human and mouse EBI1, a lymphoid-specific G-protein-coupled receptor A;Reference number: A55735; MUID:95154835; PMID:7851893
A;Accession: B55735
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1.378 GSCH3
A;Accession: 1.378 GSCH3
A;Residues: 1.378 GSL31581; NID:9468319; PIDN:AAA74231.1; PID:9468320
R;Burgstahler, R.; Kempkes, B.; Staeube, K.; Lipp, M.
Submitted to the EMBL Data Library, February 1995
A;Description: The expression of the chemokine receptor BLR2/EBI1 is specifically transact A;Reference number: S52443
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g1167852
A;Experimental source: thymus
C;Genetics:
A;Gene: cc ckr-4
A;Gene: cc ckr-4
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Reywords: glycoprotein; phosphoprotein; receptor; thymus
F;2,183,194/Binding site: phosphate (Ser) (covalent) #status predicted
F;72,203,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F;72,181,181nding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
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Cispecies: Rattus norvegicus (Norway rat)
Cibate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999
Cjaccession: 842096
Rigobl, A.E., Nang, S.; Zhou, Y.; Oeberg, K.
Rigobl, A.E., Nang, S.; Zhou, Y.; Oeberg, K.
A;Description: Molecular cloning of the rat IL8 receptor.
A;Reference number: 842096
A;Accession: 842096
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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58.8%; Pred. No. 0.57;
ive 2; Mismatches
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A,Cross-references: GDB:342065; OMIM:600242
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C,Superfamily: vertebrate rhodopsin
C,Keywords: G protein-coupled receptor
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Best Local Similarity 58.8%;
Matches 10; Conservative
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Best Local S
Matches 9
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Cypecies Mus musculus (house mouse)
Cyaccession: JC4587
Extra Proudécar, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996
A;Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to A;Reference number: JC4587; MUD:96136324; PMID:8573157
A;Accession: JC4587
A;Accession: JC4587
A;Residues: 1-360 < HOO>
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C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Date: 02-Jul-1994
D: Biol. Chem. 270, 17494-17501, 1995
J; Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemoki
A;Reference number: 149339; MUID:95340546; PMID:7542241
                                                                                                                                                                                                                                                                                                                                 macrophage inflammatory protein-1 alpha receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: O2-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: 149339
R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemoki A;Reference number: 149339; MUID:95340546; PMID:7542241
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A;Nolecule type: DNA
A;Mosicus: 1-35 cRES.
A;Cross-references: EMBL:UZ8404; NID:G881547; PIDN:AAA89153.1; PID:G881548
C;Superfamily: vertebrate rhodopsin
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A;Nolecule type: DNA
A;Nosidues: 1-36 cRES.
A;Residues: 1-36 cRES.
A;Cross-references: EMBL:U28405; NID:g881549; PIDN:AAA89154.1; PID:g881550
C;Superfamily: vertebrate rhodopsin
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                              Pred. No. 0.079;
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Pred. No. 0.37;
2; Mismatches
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Pred. No. 0.37
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Best Local Similarity 55.6%;
Matches 10; Conservative
                              58.8%;
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nes 9; Conservative
                          Best Local Similarity 58.8
Matches 10; Conservative
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52.6%; Score 50;
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313 YAFIGOKFRHGLL 325
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Best Local Similarity 69.2
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A;Molecule type: DNA
A;Residues: 6-360 <SPR>
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A;Title: Identification, chromosomal location, and genome organization of mammalian G-pr A;Reference number: A48909; MUID:94116980; PMID:8288218
A;Accession: H48909
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A,Residues: 1-559 KRES>
A;Cross-references: EMBL:U31207; NID:q950174; PIDN:AAC52239.1; PID:g950175
A;Cross-references: EMBL:U31207; NUD:q950174; PIDN:AAC52239.1; PID:g950175
D: Biol. Chem. 269, 29355-29358, 1994
A;Title: The murine interleukin 8 type B receptor homologue and its ligands. Expression A;Reference number: 155421; MUID:95050766; PMID:7961909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NiAlternate names: G-profein coupled receptor Gpcr16
C;Species: Mus musculus (house mouse)
C;Species: Was musculus (house mouse)
C;Date: 20-Feb-1995 #text change 05-Nov-1999
C;Accession: A48921; A53677; I49348; D. 20-Feb-1995 #text change 05-Nov-1999
C;Accession: A48921; A53677; I49348; D. 20-Feb-1995 #text change 05-Nov-1999
C;Accession: A48921; A53677; I49348; D. 20-Feb-1995 #text change 05-Nov-1999
C;Accession: A48921; MulD: 94117014; PMID: 8288247
A;Accession: A48921; MulD: 94117014; PMID: 8288247
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A; Readules: 1-359 c(ERs)
A; Residules: 1-359 c(ERs)
A; Cross-references: GB:L23637; NID:g435093; PIDN:AAA39305.1; PID:g435094
A; Suzuki, H.; Prado, G.N.; Wilkinson, N.; Navarro, J.
J. Biol. Chem. 269, 18263-18266, 1994
A; Title: The N terminus of interleukin-8 (IL-8) receptor confers high affinity binding A; Reference number: A53677; MUID:94308043; PMID:7518426
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A;Residues: 145-258 <WIL>
A;Cross-references: GB:L20337; NID:g438800; PIDN:AAA16853.1; PID:g438801
A;Across-references: GB:L20337; NID:g438800; PIDN:AAA16853.1; PID:g438801
B;Harada, A.; Kuno, K.; Nomura, H.; Mukaida, N.; Murakami, S.; Matsushima, K.
Gene 142, 297-300, 1994
A;Harada, Carama, Carama,
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A;Cross-references: GB:L26549
A;Oross-references: GB:L26549
A;Note: sequence extracted from NCBI backbone (NCBIP:149812)
B;Note: J; Cacalano, G.; Camerato, T.; Toy, K.; Moore, M.W.; Wood, W.I.
J. Immunol. 155, 2158-2164, 1995
A;Title: Chemokine binding and activities mediated by the mouse IL-8 receptor.
A;Reference number: 149348; MUID:95363183; PMID:7636264
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A,Residues: 1-359 <RE2>
A,Cross-references: GB:L13239; NID:g293665; PIDN:AAA62109.1; PID:g293666
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                                                                                                                                                                                                                                                                                              Length 356;
                                         A,Residues: 1-356 <GOB>
A,COSs-references: BMBL:X77797
C,Superfamily: vertebrate rhodopsin
C,Superfamily: vertebrate rhodopsin
C,Keywords: G protein-coupled receptor; transmembrane protein
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Pred. No. 1.2;
3; Mismatches
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Molecule type: DNA
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YAFIGQKFRHGLL 322
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Matches 9; Conservative
A, Molecule type: mRNA
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interleukin-8 receptor type B - human (5/8) for the control of the
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A;Rolecule type: mRNA
A;Cross.references: 1.5 RED.
A;Cross.references: EMBL:U11872; NID:9511808; PIDN:AAA64380.1; PID:9511809; EMBL:U11873;
11876; NID:9511816; PID:9511817; EMBL:U11877; NID:9511818; PID:9511819; EMBL:U11878; NID:
A;Sprenger, H.; Lloyd, A.R.; Lautens, L.L.; Bonner, T.I.; Kelvin, D.J.
A;Title: Structure, genomic organization, and expression of the human interleukin-8 receg
A;Reference number: A53611; MUID:94209273; PMID:7512557
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A,Residues: 6-360 <MUR>
A,Cross-references: GB:M73969
C,Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8, inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Cross-references: GB:M99412; GB:L19593
R;Murphy, P.M.; Tiffany, H.L.
Science 233, 1280-1283, 1991
A;Title: Cloning of complementary DNA encoding a functional human interleukin-8 receptor.
A;Reference number: A39446; MUID:91368200; PMID:1891716
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A;Residues: 1.360 «RES>
A;Cross-references: EMBL:U11869; NID:g511801; PIDN:AAB60656.1; PID:g511803
A;Accession: 138712
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A;Molecule type: mRNA
A;Residues: 1-359 <RE3>
A;Cross-references: GB:D17630; NID:g493671; PIDN:BAA04536.1; PID:g493672
C;Genetics:
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GiSuperfamily: vertebrate rhodopsin
GiSuperfamily: vertebrate rhodopsin
GiSuperfamily: vertebrate rhodopsin
GiSuperfamily: rensmembrane #status predicted <TMI>F;84-106/Domain: transmembrane #status predicted <TMI>F;120-141/Domain: transmembrane #status predicted <TMI>F;163-182/Domain: transmembrane #status predicted <TMI>F;213-234/Domain: transmembrane #status predicted <TMI>F;213-234/Domain: transmembrane #status gredicted <TMI>F;213-234/Domain: transmembrane #status gredicted <TMI>F;210-271/Domain: transmembrane #status gredicted <TMI>F;308-328/Domain: transmembrane #status gredicted <TMI)
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Pred. No. 1.2;
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C, Superfamily: vertebrate rhodopsin
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Length 360;

DB 2;

Tue Sep

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chemokrane (C-C) receptor 2, splice form A - human chemotrate names: C-C CKR-2; monocyte chemotractant protein 1 receptor; monocyte chemotractant brotein 1 receptor; monocyte chemotractas: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 13-Aug-1999
C;Accession: I38450
R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R. Procon, Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A;Title: Molecular cloning and functional expression of two monocyte chemoattractant prot A;Reference number: A53477; MuID:94195821; PMID:8146186
A;Accession: I38450
A;Status: preliminary
A;Residues: L-374 <RES>
A;Cross-references: EMBL:U03882; NID:q472555; PIDN:AAA19119.1; PID:g472556
C;Genetics:
A;Genetics:
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A/crose: GDB:337364, OMIM:601267
A/Map position: 3p21-3p21
C|Superfamily: vertebrate rhodopsin
C|Superfamily: vertebrate rhodopsin
C|Superfamily: vertebrate rhodopsin
F|44-68|Domain: transmembrane #status predicted <TML>
F|79-99|Domain: transmembrane #status predicted <TMI>
F|79-99|Domain: transmembrane #status predicted <TMS>
F|115-136|Domain: transmembrane #status predicted <TMS>
F|144-465|Domain: transmembrane #status predicted <TMS>
F|24-478|Domain: transmembrane #status predicted <TMS>
F|24-465|Domain: transmembrane #status predicted <TMS>
F|24-465|Domain: transmembrane #status predicted <TMS>
F|24-148|Domain: transmembrane #status predicted <TMS>
F|24-465|Domain: transmembrane #status predicted <TMS>
F|24-465|Domain: transmembrane #status predicted <TMS>
F|24-188|Domain: transmembrane #status predicted <TMS>
F|34-188|Domain: transmembrane #status predicted <TMS>
F|32-277,113-190|Disulfide bonds: #status predicted
C.Accession: B98112
R.Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Es, F.; Hoskins, J.A.; Alborn Jr., W.; Larkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; McY, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Accession: B98112
A;Cocss-references: GB:AE007317; FIDN:AAL00727.1; FID:G15459622; GSPDB:GN00174
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C;Species: Mus musculus (house mouse)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
C;Accession: JE0349
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Pred. No. 1.8;
1; Mismatches
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Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
Matches 9; Conserv
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C; Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C; Accession: B95247
R; Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.B.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: E95247
A;Acc
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C;Genetics:
A;Gene: SP2115
                                                                                                                                                                                                                                                                                                                                                                                                                         A45680
G protein-coupled peptide receptor EBI 1 - human
G)species: Homo sapiens (man)
G)species: Homo sapiens (man)
G)species: Homo sapiens (man)
G)species: Homo sapiens (man)
G)species: Homo sapiens
G)species: Homo sapien
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E95247
hypothetical protein SP2115 [imported] - Streptococcus pneumoniae (strain TIGR4)
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C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:L08176; NID:g183484; PID:g183485
A;Experimental source: B-lymphocytes
A;Note: sequence;extracted from NCBL backbone (NCBIN:127094, NCBIP:127095)
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                 Gaps
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                            Pred. No. 1.2;
3; Mismatches
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                            69.2%;
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Best Local Similarity 62.5
Matches 10; Conservative
                            Similarity 69.3
9; Conservative
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                            Best Local
Matches
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V.; Lyman, S.; Gerard
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A; Residues: 1-355 <BEC>
A; Residues: 1-355 <BEC>
A; Createrences: GE:M74240; NID:g165438; PIDN:AAA31375.1; PID:g165439
A; Libe, J: Xuang, WJ.; Rice, G.C.; Wood, W.I.
J. Immunol. 148, 1261-1264, 1992
A; Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor.
A; Reference number: A46483; MUID:92148149; PMID:1737938
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C.Species: Clostridium acetobutylicum
C.Species: Clostridium acetobutylicum
C.Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C.Accession: B97185
R.Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
T. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
                                                       Interleukin-8 receptor, high affinity - rabbit
Nylternate names: fMLP receptor
Cjopecies: Oryctolagus cuniculus (domestic rabbit)
Cjopecies: Oryctolagus cuniculus (domestic rabbit)
Cjopecies: Oryctolagus cuniculus (domestic rabbit)
Cjope: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 05-Nov-1999
Cjocession: A23669
RThomas, K.M.; Pyun, H.Y.; Navarro, J.
J. Biol. Chem. 265, 20061-20064, 1990
A;Title: Molecular cloning of the fMet-Leu-Phe receptor from neutrophils.
A;Reference number: A23669; MUID:91056034; PMID:1700779
A;Accession: A23669
A;Accession: A2368
A;Accession: A2368
A;Accession: A2368
A;Cossion: A2368
A;Cossion: A2368
A;Cossion: A2368
A;Cossion: Cospertant chodopsin
C;Superfamily: Vertebrate rhodopsin
C;Superfamily: Vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; membrane protein; neutrophil
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus
C;Accession: Jo1-1992 #sequence_revision 31-Mar-1992 #text_change 05-Nov-1999
C;Accession: JQ1231; A46483
R;Beckmann, M.P.; Munger, W.E.; Kozlosky, C.; VandenBos, T.; Price, V.; Lyma
Biochem. Biophys. Res. Commun. 179, 784-789, 1991
A;Title: Molecular characterization of the interleukin-8 receptor.
A;Reference number: JQ1231; MUID:91376994; PMID:1898400
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A;Experimental source: neutrophils
A;Note: sequence extracted from NCBI backbone (NCBIN:81526, NCBIP:81530)
C;Superfamily: vertebrate riodogosin
C;Keywords: G protein-coupled receptor; transmembrane protein
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Pred. No. 5.5;
2; Mismatches
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Pred. No. 5.5;
2; Mismatches
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Best Local Similarity 61.5
Matches 8; Conservative
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Best Local Similarity 61.5
Matches 8; Conservative
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A; Molecule type: mRNA
A; Residues: 1-355 < LEE>
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AS5735
G protein-coupled receptor EBI1 - mouse
C, Species: Mus musculus (house mouse)
C, Species: Mus musculus (house mouse)
C, Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999
C, Accession: AS5735
A, Schweckart, V. U.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
Genomics 23, 643-650, 1994
A, Title: Cloning of human and mouse EBI1, a lymphoid-specific G-protein-coupled receptor A, Accession: AS5735, MUID:95154835; PMID:7851893
A, Accession: AS5735
A, Status: preliminary
Biochem. Biophys. Res. Commun. 251, 41-48, 1998

A;Title: Cloning of the murine interferon-inducible protein 10 (IP-10) receptor and its A;Reference number: JE0349; MUID:99009219; PMID:9790904

A;Acession: JE0349

A;Molecule type: mRNA

A;Residues: 1-367 <TAM>
A;Residues: 1-367 <TAM>
C;Cross-references: DDBJ:AB003174; NID:93798731; PIDN:BAA34045.1; PID:93798732

C;Comment: This protein is important for lymphocyte trafficking to lymphoid organs.
C;Superfamily: vertebrate rhodopsin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interleukin-8 receptor (clone 591a) - rabbit interleukin-8 receptor (clone 591a) - rabbit c'Species: Oryctolagus cuniculus (domestic rabbit) (c)stee of 6-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999 (c)stee of 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999 (c)steesion: A53752 R:Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Navai, J. Bibl. Chem. 269, 12331-1234, 1394 (c)steering contact characterization of a novel rabbit interleukin-8 receptor isotype. A; Reference number: A53752; MulD:94230294; PMID:8175642 A; Status: preliminary A; Status: preliminary A; Residues: 1-358 < PRA> A; Catus: preliminary A; C; Superiamily: vertebrate rhodopsin C; Keywords: G protein-coupled receptor; transmembrane protein
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A, Molecule type: mRNA
A, Molecule type: mRNA
A, Residues: 1-378 < SCH>
A, Residues: 1-378 < SCH>
C, Superfamily: vertebrate rhodopsin
C, Keywords: G protein-coupled receptor
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Pred. No. 3.8;
2; Mismatches
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326 YAFIGVKFRSDLFKLFK 342
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YAFIGQKFRYGLL 324
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Best Local Similarity 50...
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Best Local Similarity 69.2
Matches 9; Conservative
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A; Ascession: Udled to the total course: Lord to the total course type: DNA A; Residues: 1-359 - FTEXA A; Residues: 1-359 - FTEXA A; Residues: 1-359 - FTEXA A; Cross-references: EMBL, Z11162; NID:9287109; PID:928710
A; Experimental source: Lymphocyte
R; Bicerseme. D. J.; Bills, C.; Kumar, C.; Nuthulaganti, P.; Kersten, H.; Elshourbagy, N.; G; Biochem. Biophys. Res. Commun. 183, 989-959, 1992
A; Title: Cloning and characterization of a human angiotensin II type I receptor.
A; Reference number: J80574; MUID:92231907; PMID:1567413
A; Reference number: J80574; MUID:92231907; PMID:1567413
A; Reference number: J80574; MUID:92231907; PMID:1567413
A; Residues: 1-359 - EEEE
A; Takayanaqi, R.; Ohnaka, K.; Sakai, Y.; Nakao, R.; Yanase, T.; Haji, M.; Inagami, T.; F. Biochem. Biophys. Res. Commun. 183, 910-916, 1992
A; Takayanaqi, R.; Ohnaka, K.; Sakai, Y.; Nakao, R.; Yanase, T.; Haji, M.; Inagami, T.; F. Biochem. Biophys. Res. Commun. 183, 910-916, 1992
A; Takayanaqi, R.; Ohnaka, K.; Sakai, Y.; Nakao, R.; Yanase, T.; Haji, M.; Inagami, T.; F. R; Rakayanaqi, R.; Ohnaka, K.; Sakai, Y.; Nakao, R.; Yanase, T.; Haji, M.; Inagami, T.; F. R; Rakacesion: J10267; MUID:92198490; PMID:155056
A; Molecule type: mRNA
A; Residues: 1-359 - TAK>
A; Residues: 1-359 - TAK>
A; Reference number: A44014; MUID:92375105; PMID:1508224
A; Title: Genetic analysis of the human type-1 angiotensin II receptor.
A; Residues: 1-359 - TAK>
A; R
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A/Gene: A/Ge
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C;Species: Canis lupus familiaris (dog)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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R;Burns, L; Clark, K.L.; Bradley, J.; Robertson, M.J.; Clark, A.J.L.
FEBS Lett. 343, 146-150, 1994
A;Title: Molecular cloning of the canine angiotensin II receptor. An
A;Reference number: $44425, MUID:94222188; PMID:8168620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Pred. No. 8.2;
3; Mismatches 3; Indels
A; Reference number: JQ1402; MUID:92181475; PMID:1543512
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: S44425
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A,Residues: 1-359 <MAU>
R,Furuta: H.; Guo, D.F.; Inagami, T.
Biochem. Biophys. Res. Commun. 183, 8-13, 1992
A,Title: Molecular cloning and sequencing of the gene encoding human angiotensin II type
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JOING4
angiotensin II receptor type 1 - human
NyAlternate names: angiotensin II receptor 1A
CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
CiSpecies: O-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jul-2000
CiAccession: JC1104, JQ1402; JH0574; JH0267; A44014; S18983
RiMauzy, C.A.; Hwang, O.; Egloff, A.M.; Wu, L.H.; Chung, F.Z.
Biochem. Biophys: Res. Commun. 186, 277-284, 1992
A;Title: Cloning, expression, and characterization of a gene encoding the human angioten
A,Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld A,Reference number: A96900; MUID:21359325; PMID:21359325
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A;Accession: JN0621
A;Rolecule type: mRNA
A;Residues: 1-350 cMRNA
A;Residues: 1-350 cMRNA
A;Residues: 1-350 cMRNA
A;Cross-references: GB.563848; NID:g399710; PIDN:AAB27547.1; PID:g399711
A;Experimental source: tongue taste papillae
C;Comment: This protein is involved in modulating taste sensitivity or regeneration of C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane #status predicted <TML>
F;242-67,Domain: transmembrane #status predicted <TML>
F;114-135/Domain: transmembrane #status predicted <TMA>
F;114-135/Domain: transmembrane #status predicted <TMA>
F;242-265/Domain: transmembrane #status predicted <TMA>
F;2
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                                                                                          A;Accession: B97185
A;Status: preliminary
A;Nocestion: B97185
A;Status: preliminary
A;Status: preliminary
A;Status: 1-377
A;Cross-references: GB:AE001437; PIDN:AAK80269.1; PID:g15025320; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics: A;Gene: CAC2313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 29
JORG21
G protein-coupled receptor type B - bovine
G protein-coupled receptor type B - bovine
C;Species: Bos primigenius taurus (cattle)
C;Bate: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 19-May-2000
C;Accession: JN0621
R;Matsucka, I.; Mori, T.; Acki, J.; Sato, T.; Kurihara, K.
Bicchen. Biophys. Res. Commun. 194, 504-511, 1993
A;Title: Identification of novel members of G-protein coupled receptor super
A;Title: Identification of novel members of G-protein coupled receptor super
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Pred. No. 8;
5; Mismatches
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Best Local Similarity 38.9
Matches 7; Conservative
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Best Local Similarity 47.4
Matches 9; Conservative
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Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative 3
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53.8%;
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Best Local Similarity 53.8
Matches 7; Conservative
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A; Residues: 1-6, 1', 8-165, H', 167-172, E', 174-204, V', 206-231, T', 233-238, F', 240-359 <8
A; Residues: 1-6, 1', 8-165, H', 167-172, E', 174-204, V', 206-231, T', 233-238, F', 240-359 <8
A; Cross-references: GB: S37491; NID: 9249947; PIDN: AAB22270.1; PID: 9249948
A; Experimental source: Balb/C
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
F; 30-53/Domain: transmembrane #status predicted <TM1>
F; 65-90/Domain: transmembrane #status predicted <TM2>
F; 103-123/Domain: transmembrane #status predicted <TM3>
F; 147-166/Domain: transmembrane #status predicted <TM5>
F; 141-166/Boinding site: carbohydrate (Asn) (covalent) #status predicted
F; 141/Binding site: phosphate (Thr) (covalent) #status predicted
F; 331, 338, 348/Binding site: phosphate (Ser) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                    angiotensin II receptor 1B - mouse
C;Species: Mus musculus (house mouse)
C;Species: To-Apr-1993 #text_change 05-Nov-1999
C;Accession: JO-Apr-1994 #Sequence_revision 17-Apr-1993 #text_change 05-Nov-1999
C;Accession: JO-1994 #H6622
R;Yoshida, H.; Kakuchi, J.; Guo, D.F.; Furuta, H.; Iwai, N.; van der Meer-de Jong, R.;
Biochem. Biophys. Res. Commun. 186, 1042-1049, 1992
A;Title: Analysis of the evolution of angiotensin II type 1 receptor gene in mammals (m. A;Reference number: JC1193; MUID:92359981; PMID:1497638
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Daces: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C;Accession: A48857
R;Burns, K.D.; Inagami, T.; Harris, R.C.
Am. J. Physiol. 264, F645-F654, 1993
A;Title: Cloning of a rabbit kidney cortex AT1 angiotensin II receptor that is present A;Reference number: A48857; MUID:93236091; PMID:7916579
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Sasamura, H.; Hein, L.; Krieger, J.E.; Pratt, R.E.; Kobilka, B.K.; Dzau, V.J.
Sasamura, H.; Hein, L.; Krieger, J.E.; Pratt, R.E.; Kobilka, B.K.; Dzau, V.J.
tochem. Biophys. Res. Commun. 185, 253-259, 1992
Title: Cloning, characterization, and expression of two angiotensin receptor (AT-1)
*Reference number: JH0621; MUID:92287102; PMID:1599461
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A;Molecule type: nucleic acid
A;Rosidues: 1-359 <BURN>
A;Residues: 1-359 <BURN>
A;Cresidues: 1-359 <BURN>
A;Cresidues: 1-558 <BURN>
A;Cresidues: 1-558 <BURN>
A;Cresidues: proximal tubule cells
A;Experimental source: proximal tubule cells
A;Note: sequence extracted from NCBI backbone (NCBIN:129600)
                                                                                                                                  Gaps
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                                                                 Length 359;
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Pred. No. 8.2;
3; Mismatches 3; Indels
                                                                                                                                  3; Indels
                                                                 DB 2;
                                                                 Score 45; DB;
Pred. No. 8.2;
                                                                                                                              3; Mismatches
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C;Superfamily: vertebrate rhodopsin
                                                                 47.4%;
53.8%;
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                                                                                            Local Similarity 53.8
nes 7; Conservative
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A, Molecule type: DNA
A, Residues: 1-359 < ELT>
A, Residues: 1-359 < ELT>
A, Residues: 1-359 < ELT>
A, Rote: the authors translated the codon AGC for residue 120 as Thr, GTC for residue 225
B, Rakar, S.S.; Sellers, J.C.; Devor, D.C.; Musgrove, L.C.; Neill, J.D.
Biochem. Biophys. Res. Commun. 183, 1090-1096, 1992
A; Title: Angiotensin II type-1 receptor subtype cDNAs: differential tissue expression and A, Reference number: JH0578
A, Reference number: JH0578
A, Molecule type: mRNA
A, Residues: 1-74, L., 76-119, 'T', 121-224, 'A', 226-359 < KAK>
A, Cross-references: GB:M87003; NID:g202920; PIDN:AA440739.1; PID:g202921
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Oct-1999
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Oct-1999
C;Accession: QQL516; JH0578; PH0850
R;Elton, T.S.; Stephan, C.C.; Taylor, G.R.; Kimball, M.G.; Martin, M.M.; Durand, J.N.;
Biochem: Biochypy Res. Commun. 184, 1067-1073, 1992
A;Title: Isolation of two distinct type 1 angiotensin II receptor genes.
A;Reference number: JQ1516; MUID:92246922; PMID:1575725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Note: sequence extracted from NCBI backbone (NCBIN:100262, NCBIP:100268)
R;Iwai, N.; Inagami, T.
FBSE Lett. 298, 257-260, 257-260, RFBS Lett. 298, 257-260, RFBS Lett. 298, 257-260, RFBS Lett. A;Reference number: S20423; MUID:92183879; PMID:1544458
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NyAlternate names: angiotensin II receptor chain B
Cypecies: Ratus norvegiuus (Norway rat)
Cypecies: Atatus norvegiuus (Norway rat)
Cybacession: A42656; S20423
RySandberg, K.; Ji, H.; Clark, A.J.; Shapira, H.; Catt, K.J.
J. Biol. Chem. 267, 9455-9458, 1992
A;Title: Cloning and expression of a novel angiotensin II receptor subtype.
A;Reference number: A42656; MUID:92250585; PMID:1374402
A;Accession: A42656
A;Status: preliminary
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A;Cross-references: GB:M90065; NID:g202801; PIDN:AAA40704.1; PID:g202802
A;Experimental source: adrenal cortex
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C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
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C,Superfamily: vertebrate rhodopsin
C,Keywords: G protein-coupled receptor; transmembrane protein
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Pred. No. 8.2;
3; Mismatches
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Pred. No. 8.2;
3; Mismatches
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A;Experimental source: strain Balb/c
A;Experimental source: strain Balb/c
B;Sybaida, H; Rakuchi, J; Guo, DF;; Furuta, H;; Iwai, N; van der Meer-de Jong, R; Ir
B;Sybaida, H; Rakuchi, J; Guo, DF;; Furuta, H;; Iwai, N; van der Meer-de Jong, R; Ir
B;Sybaida, H; Rakuchi, J; Guo, DF;; Furuta, H;; Iwai, N; van der Meer-de Jong, R; Ir
B;Sybaida, H; Res, Commun. 186, 1042-1049, 1992
A;Title: Analysis of the evolution of angiotensin II type 1 receptor gene in mammals (mo. A;Reference number: Joil93, MUID:9235981; PMID:1497638
A;Accession: JC1193
A;Status: nucleic acid sequence not shown
A;Residues: 10, 17, 18, 187, 22-37, W', 39-133, K', 135-359 < YOS>
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Seperfamily: vertebrate shodopsin
C;Seperfamily: vertebrate status predicted < TM2>
F;G5-65/Domain: transmembrane #status predicted < TM3>
F;G5-65/Domain: transmembrane #status predicted < TM4>
F;G1-220/Domain: transmembrane #status predicted < TM4>
F;G1-220/Domain: transmembrane #status predicted < TM3>
F;G1-230/Domain: transmembrane 
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Allernder names: Alia receptor; Alia receptor

NiAlternder names: Alia receptor; Alia receptor

Cispecies: Rattus norvegicus (Norway rat)

Cispecies: Rattus norvegicus (Norway rat)

Cispecies: Ang-1985 #sequence revision 07-Oct-1994 #text_change 24-Nov-1999

Cispecies: Assection of Cistieis, M.E.; Bibreau, C.; Corvol, P.; Clauser, E.

Biochem. Biophys. Res. Commun. 199, 1347-1354, 1994

A; Title: Synthetic cDNA encoding the rat Alia receptor: a useful tool for structure-funct

A; Accession: JC2134; MJDD: 94197726; PMID: 8147879
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A;Residues: 1-80,'C',82-108,'T',110-359 <1W2>
A;Cross-references: GB:My4054; NID:g202918; PIDN:AAA40738.1; PID:g202919
A;Experimental source: Kidney
C;Comment: A11 receptor consists of two closely related A71 isoforms of angiotensin II re
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EBS Lett. 298, 257-260, 1992
Title: Identification of two subtypes in the rat type I angiotensin II receptor.
Reference number: S20423; MVID:92183879; PMID:1544458
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A,Residues: 1-359 <CON-
A,Residues: 1-359 <CON-
A,Note: the amino acid sequence of this protein is not given
R,Murphy, T.J.; Alexander, R.W.; Griendling, K.K.; Runge, M.S.; Bernstein, K.E.
R,Mutre 351, 233-236, 1991
A,Title: Isolation of a cDNA encoding the vascular type-1 angiotensin II receptor.
A,Reference number: S15404; MUID:91251901; PMID:2041570
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A;Molecule type: mRNA
A;Residues: 1-559 kWNR>
A;Cross-references: GB:X62295; NID:g57773; PIDN:CAA44183.1; PID:g57774
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A;Residues: 1-359 <IMA>
R;Iwal, N; Yamano, Y.; Chaki, S.; Konishi, F.; Bardhan, S.; Tibbetts,
Biochem. Biophys. Res. Commun. 177, 299-304, 1991
A;Title: Rat angiotensin II receptor: CDNA sequence and regulation of A;Reference number: JQ1055; MUID:91254291; PMID:2043116
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Pred. No. 8.2;
3; Mismatches 3; Indels
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C; Species: Bos primigenius taurus (cattle)
C; Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
C; Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
C; Date: 19-Mar-1997
Rscession: S15403

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53.8%; Pred. No. 8.2;
tive 3; Mismatches 3; Indels
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53.8%; Pred. No. 8.2;
tive 3; Mismatches 3; Indels
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Matches 7; Conservative
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nes 7; Conserv
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K.; He

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A,Molecule type: DNA
A,Residues: 1-311,'T',313-375 <FEN>
A,Cross-references: GB:U77827; NID:g1906591; PIDN:AAC51173.1; PID:g1906592
C,Comment: This protein plays a role in B-cell functions and is involved in endothelial c
        A,Title: Cloning of a novel member of the G protein-coupled receptor family related to pe A,Reference number: JCS294; MUID:97224403; PMID:9070864
                                                                                                                                                                                                                                                                                                                                                                                                               C'Superfamily: vertebrate rhodopsin
C'Swperfamily: vertebrate rhodopsin
C'Skeyords: G protein-coupled receptor; glycoprotein; transmembrane protein
F;64-83/Domain: transmembrane #status predicted <TM1>
F;65-114/Domain: transmembrane #status predicted <TM3>
F;126-148/Domain: transmembrane #status predicted <TM3>
F;180-198/Domain: transmembrane #status predicted <TM4>
F;20-238/Domain: transmembrane #status predicted <TM5>
F;20-237/Domain: transmembrane #status predicted <TM5>
F;308-327/Domain: transmembrane #status predicted <TM5>
F;308-327/Domain: transmembrane #status predicted <TM7>
F;25,32,44/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 2; Length 375; Pred. No. 13; 7; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: September 28, 2004, 09:07:11
Job time : 10.925 secs
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324 YSFLGETFRDKLRLYIEQ 341
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ilarity 38.9%;
Conservative 7
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GDB:3929190
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Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                          A; Gene: GDB: CMKRL2;
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C, Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; glycoprotein; GTP binding; receptor; transmembra
C; Keywords: G protein-coupled receptor; glycoprotein; GTP binding; receptor; transmembrane
F; 27-06, Domain: transmembrane #status predicted <TM1>
F; 103-123/Domain: transmembrane #status predicted <TM5>
F; 147-167/Domain: transmembrane #status predicted <TM6>
F; 140-263/Domain: transmembrane #status predicted <TM6>
F; 270-299/Domain: transmembrane #status predicted <TM7>
F; 278-299/Domain: transmembrane #status predicted <TM7>
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NAlternate names: constitutively expressed peptide-like receptor; flow-induced endothel

C,Species: Homo sapiens (man)

C,Date: 31-Jan-1997 #sequence_revision 28-Aug-1998 #text_change 21-Jul-2000

C,Date: 31-Jan-1997 #sequence_revision 28-Aug-1998 #text_change 21-Jul-2000

C,Date: 31-Jan-1997 #sequence_revision 28-Aug-1998 #text_change 21-Jul-2000

R,Corcession: C, Blay, P, Nilsson, C, Lolait, S.J.

Biochem. Biophys. Res. Commun. 228, 285-292, 1996

A,Title: Cloning of human cDNA encoding a novel heptahelix receptor expressed in Burkith

A,Reference number: JC5069, MUID:97079175, PMID:8920907
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A; Residues: 1-375 < 00W3
A; Cross-references: GB: Y08162; NID: g1707499; PIDN: CAA69354.1; PID: g1707500
A; Cross-references: GB: Y08162; NID: g1707499; PIDN: CAA69354.1; PID: g1707500
A; Cross-references: GB: Y08162; NID: g170741, Ng Ando, J.
B; Chiem: Biophys: Res Commun. 240, 737-741, 1997
B; Cross-reference number: GDNAs encoding G protein-coupled receptor expressed in human endothe A; Reference number: JC5786; MUID: 98063308; PMID: 9398636
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C;Genetics:
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C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 24-Nov-1999
C;Accession: G02670;
R;McCoy, R.L.; Perlmutter, D.H.
submitted to the EMBL Data Library, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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A;Molecule type: mRNA
A;Residues: 1-358 <MCC>
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 45; DB 2
Pred. No. 8.2;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.3%; Score 44; DB
llarity 38.9%; Pred. No. 12;
Conservative 7; Mismatches
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C,Superfamily: vertebrate rhodopsin
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YGFLGKKFKKYFL 314
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Best Local Similarity 53.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: H01575
A;Accession: G02670
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Best Local Similarity
Matches 7; Conserv
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A, Residues: 1-375 <TAK>
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P51679 P564821 Q92213 ( P51675 1 P51676 1 P51248 0 P32248 0 Q28807 1

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
-I- SUBCELIULAR LOCATION: Integral membrane protein.
-I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                     15-UTL-1998 (Rel. 36, Created)
15-UTL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C.C. chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB015944; BAA31328.1; -.
EMBL; AB015944; BAA31328.1; -.
PLICATYO: TRR000276; GPCR. Rhodpsn.
PRINTS; PR00237; GFCRHODOPSN.
PROSTIE; PS00237; G-PROTEIN RECEP_F1_1; 1.
PROSITE; PS50252; G-PROTEIN RECEP_F1_2; 1.
G-protein, coupled receptor; Transmembrane; Glycoprotein; Sulfation;
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TSSUBE.Aidney,
MEDIINE=88001187; PubMed=9343222;
Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.;
Kuhmann F.E., Platt E.J., Kozak S.L., Kabat D.;
In Polymorphisms in the CCRS genes of African green monkeys and mice implicate specific amino acids in infections by simian and human immunodeficiency viruses.";
                                                                                                                                                                                                                                                                                                                                                 Cercopithecus aethiops (Green monkey) (Grivet).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murayama Y., Matsunaga S., Inoue-Murayama M.; "cDNA sequence of African green monkey CCR-5 chemokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                               352 AA
                                                                                                                                                                                           ALIGNMENTS
                        CKR4 HUMAN
CKR1 MACMU
CKR3 CAVPO
CKR1 MOUSE
CKR4 MOUSE
CKR4 MOUSE
CKR4 MOUSE
CKR7 HUMAN
ILBB MACMU
                                                                                                                                     IL8B_PANTR
IL8B_CANFA
                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virol. 71:8642-8656(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U83324; AAC51795.1; -. EMBL; U83325; AAC51796.1; -.
                                                                                                                                                                                                                                                               STANDARD;
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Polymorphism.
DOMAIN
                                                                                                                                                                                                                                                               CERAE
P56493;
                                                                                                                                                                                                                                    CERAE
                                                                                                                                                                                                                                   RESULT
CKR5_CE
459789004894
                                                                                                                                                                                                                                                                  P56493 cercopithec 091442 cercopithec 062743 cercocluss P56439 gorilla gor P51681 home sapien 097881 hylobates m 095nc6 hylobates m 1095nc6 hylobates m 1097810 pongo pygma p56440 pan. troglod P5682 mus musculu P51682 mus musculu P51683 mus musculu P51683 mus musculu P51684 mus musculu P51684 mus musculu P51684 mus musculu P56484 mus musculu P56484 mus musculu P56484 mus musculu P51684 home sapien P5684 home sapien P5684 home sapien P51684 mus musculu P51684 mus musculu P51684 home sapien P5484 mus musculu P51684 home sapien P5489 mus musculu P5489 mus musculu P5489 mus musculu P5489 mus musculu P5489 mus musculu
                                                                                            September 28, 2004, 08:55:11; Search time 5.625 Seconds (without alignments) 166.624 Million cell updates/sec
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              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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CKR5_MOUSE
CKR2_MOUSE
CKR2_RAT
CKR2_MACMU
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CKR2_MACMU
CKR3_HUMAN
CKR3_HUMAN
CKR3_MOUSE
CKR3_MOUSE
CKR3_RAT
CKR3_RAT
CKR8_HUMAN
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CKR6 HUMAN
CKR1 HUMAN
CKR6 MOUSE
C3X1 RAT
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CKRS_CERPY
CKRS_GORGO
CKRS_HUNAN
CKRS_HYLLE
CKRS_HYLLE
CKRS_HYLLE
CKRS_HYLLE
CKRS_PANTR
CKRS_PANTR
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Maximum Match 100%
Listing first 45 summaries
                                                                   protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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DB seg length: 200000000
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Match Length
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Score

Result No.

Post-processing:

Minimum I Maximum I

Database :

score:

Sequence:

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Run on:

Scoring table:

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PROSITÉ; PS00237; G_PROTEIN_RECEP_F1_1; 1.
ROSSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297 YAFVGEKFRNYLLVFFOK 314
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                                                                                                                                                                                                                                                                                                                                                                                         40558 MW;
 GPCRRHODOPSN
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nes 18; Conservative
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 PRINTS; PR00237;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Muller-Truckin M.C., Corbet S., Hansen J., Georges-Courbot M.-C., Diop O., Rigoulet J., Barre-Sincussi F., Fomegaard A.;

"Mutations in CCR5-coding sequences are not associated with SIV carrier status in African nonhuman primates.";

AIDS Res. Hum. Retroviruses 15:31-391(1999).

-!- FUNCTION: Receptor for a C-C type chemobine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.
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ID CKR5_CERPY

CR79_T42_0,

AC 091742_1,

DT 15-WAR-2004 (Rel. 43, Last sequence update)

DT 15-WAR-2004 (Rel. 43, Last sequence update)

DT 15-WAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLUTAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cercopithecus pygerythrus (Vervet monkey).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 95; DB 1; Length 352; 100.0%; Pred. No. 6.9e-09;
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                                                                                             EXTRACELLULAR (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

S (POTENTIAL).

6 (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

SULFATION (BY SIMILARITY).

SULFATION (BY SIMILARITY).
                                 2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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                CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                         40561 MW;
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1es 18; Conservative
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Mismatches

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Score 95; DB 1; Length 352; Pred. No. 6.9e-09;

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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).

1 (POTENTIAL). CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL). EXTRACELLULAR (POTENTIAL). 7 (POTENTARY).

CYTOPLASMIC (POTENTIAL).

(POTENTIAL)

(POTENTIAL)

BY SIMILARITY.
SULFATION (BY SIMILARITY)
SULFATION (BY SIMILARITY)
SULFATION (BY SIMILARITY) EF17D67CBCCC3DB0 CRC64;

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                                                                                                                                                                                                                                                                                                                                                             STRAIN=ISOLATE 079, 085, 087, and 089;

XX MEDLINE=S821155; PubMed=966599;
Chen Z., Gettie A., Ho D.D., Marx P.A.;
Thinary SIVEM isolates use the CCR5 coreceptor from sooty mangabeys
T naturally infected in west Africa: a comparison of coreceptor usage
of primary SIVEM, HIV-2, and SIVMAC.";
Virology 246:113-124(1998).
C. I PUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
C. I SUBCELLULAR LOCATION: Integral membrane protein.
C. I SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CKR5_CERTO STANDARD;

062743, 062744; 062746;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5)
CCR5 OR CMKBR5.
                                                                                                                                                                                 Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                               Cercopithecinae, Cercocebus.
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EMBL; AF03522; AAD44015.1; -. InterPro; IPR000276; GPCR\_Rhodpsn. Pfam; PF00001; 7tm\_1; 1.

us-10-084-813-15.rsp

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increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.
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      EMBL; AF051902; AAC39830.1; -.

REMBL; AF051903; AAC39831.1; -.

REMBL; AF051905; AAC39831.1; -.

REMBL; AF051905; AAC39831.1; -.

REMBL; AF051905; AAC39831.1; -.

REMBL; AF051095; AAC3983.1; -.

REMBL; AF051095; AAC3983.1; -.

REMBL; AF051005; AAC3983.1; -.

REMBL; AF051005; AAC3983.1; -.

REMBL; AF051005; AAC3983.1; -.

REMBL; AF051005; AAC3983.1; -.

REMBL; AAC3983.1; -.

REMBC; AAC3983.1; 
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Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,

Edinger A.L., Amedee A., Miller K., Clements J.E., Murphey-Corb M.,

Edinger A.L., Amedee A., Miller K., Doranz B.J., Murphey-Corb M.,

Edinger S.C., Parmentier M., Erder C.C., Dome R.W.;

"Differential utilization of CCR5 by macrophage and T cell tropic

simian immunodeficiency virus strains.";

Proc. Natl. Acad. Sci. U.S.A. 944005-4010(1997).

-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

MIP-1-beta and RANTES and subsequently transduces a signal by
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15-JTL-1998 (Rel. 36, Last sequence update)
15-JTL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2011 (Rel. 40, Last annotation update)
16-OCT-2011 gorilla (Lowland gorilla).
16-OCT-2011 gorilla (Lowland gorilla).
17-OCT-2011 gorilla (Lowland gorilla).
18-Dkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
18-Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
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Y -> D (IN ISOLATE 087).
Y -> D (IN ISOLATE 087).
M -> K (IN ISOLATE 087).
L -> V (IN ISOLATE 089).
V -> G (IN ISOLATE 079).
T -> I (IN ISOLATE 089).
T -> I (IN ISOLATE 085).
T -> I (IN ISOLATE 079).
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Pred. No. 6.9e-09;
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BROSITE; PS00237; GPROTEIN RECEP F1 2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein, Sulfation. FT DOMAIN 31 58 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 31 58 CYTOPLASMIC (POTENTIAL).

SO GREATERLULAR (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

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01-0CT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 34, Last innotation update)
15-Mar-2004 (Rel. 37, Last innotation update)
16-C chemokine receptor type 5 (C-C CRR-5) (CC-CR-5) (CC-C HUV-1 fusion co-receptor) (CHEMR13) (CD195 antigen).
SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Samson M., Labbe O., Mollereau C., Vassart G., Parmentier M.;
"Molecular cloning and functional expression of a new human
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Pred. No. 6.9e-09;
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EXTRACELULAR (POTENTIAL)
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Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,
Nagashima K.A., Cayanan C., Maddon P.J., Koup R.A., Moore J.P.,
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APO11501; AAB65700.1;
APO11503; AAB65702.1;
APO11505; AAB65702.1;
APO11505; AAB65702.1;
APO11505; AAB65706.1;
APO11509; AAB65706.1;
APO11510; AAB65709.1;
APO11511; AAB65712.1;
APO11513; AAB65712.1;
APO11513; AAB65712.1;
APO11514; AAB65712.1;
APO11515; AAB65712.1;
APO11516; AAB65712.1;
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                                                                           Nature 381:667-673(1996).
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EMBL; AF011500; A
EMBL; AF011501; A
EMBL; AF011502; A
EMBL; AF011503; A
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    Raport C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F., "Molecular cloning and functional characterization of a novel human CC chemokine receptor (CCR5) for RANTES, MIP-lbeta, and MIP-lalpha.", J. Biol. Chem. 271:17161-17166(1996).
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Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;
Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;
"The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts with 5'-end heterogeneity, dual promoter usage, and evidence for polymorphisms within the regulatory regions and noncoding exons.";
J. Biol. Chem. 272:30662-30671(1997).
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MEDIINE=98001387; PubMed=9343222;
Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.;
Kuhmann S.E., in the CGR5 genes of African green monkeys and mice implicate specific amino acids in infections by simian and human immunodeficiency viruses.";
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MEDLINE=98022612; PubMed=2359654;
Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn
Ho D.D.;
                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-96295970; PubMed-8699119;
Combadiere C., Ahuja S.K., Tiffany H.L., Murphy P.M.;
Coning and functional expression of CC CKRS, a human monocyte chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and RANTES.";
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McCombie W.R., Milson R., Chen E., Gibbs R., Zuo L., Johnson D.,

Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,

Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J.,

Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,

Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,

Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,

Watanabe M., Doggett N., Garcia D., Sagripanti J.L.,

Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=96260017, PubMed=8649511;
Deng H., Liu R., Ellmeier W., Choe S., Unutmaz D., Burkhart M.,
di Marzio P., Marmon S., Sutton R.E., Hill C.M., Davis C.B.,
Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;
"Identification of a major co-receptor for primary isolates of
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Maglerowska M., Barre-Sinoussi F., Issafras H., Theodorou I.,
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MEDLINE=96260018; PubMed=8649512;
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Biochemistry 35:3362-3367(1996)
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                                                                                                                                                                                                                                                                   Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M., Gerard N.P., Gerard C., Sodroski J., Choe H.; "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1
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-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
Paxcon W.A.;
"HIV-1 entry into CD4+ cells is mediated by the chemokine receptor
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differentiation.
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EWBL; AF011533; AAB65733.1; -.

EWBL; AF011534; AAB65733.1; -.

EWBL; AF011535; AAB65735.1; -.

EWBL; AF011535; AAB65735.1; -.

EWBL; AF011537; AAB65737.1; -.

EWBL; AF011537; AAB65737; AAB65737; AAB67737.1; AAB67.1; AAB67737.1; AAB67
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MEDLINES=9941643; PubMed=10486970;

MEDLINES=9941643; PubMed=10486970;

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Sequence evolution of the CCR5 chemokine receptor gene in primates.";

Mol. Biol. Evol. 16:1145-1154 (1999).

-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or

differentiation.
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PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation; Polymorphism.
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30-MAY-2000 (Rel. 39, Last sequence update)
28-RES-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hylobatidae, Hylobates.
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
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Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
"Sequence evolution of the CCRS chemokine receptor gene in primates.";
"Sequence evolution of the CCRS chemokine Biol. Brol. 16:1145-1154(1999).

-I. Brol. 16:1145-1154(1999).

-I. PUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
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-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                               EMBL; AF075451; AAD19863.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Print, PF00001; 7tm 1; 1.
PRINTS; PR00237; GFCRHODODSN.
PROSITE; PS00262; GFROTEIN RECEP_F1_1; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
TRANSMEM 31 58 1 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCRS OR CMKBRS.

Hydobates moloch (Silvery gibbon).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
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BY SIMILARITY.
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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100.0%; Pred. No. 6.9e-09;
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RESULT 9
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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WEDLINE-99416438; PubMed=10486970;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
"Sequence evolution of the CGR5 chemokine receptor gene in primates.";
"Sequence evolution of the CGR5 chemokine. Binds to MIP-1-alpha,
Mol. Biol. Evol. 16:1145-1154(1999).

-I-FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.

-I-SUBCELLULAR LOCATION: Integral membrane protein.
-I-SUBCELLULAR LOCATION: Integral membrane protein.
-I-SUBCELLULAR LOCATION: Integral membrane protein.
-I-SUMILARITY: Belongs to family 1 of G-protein coupled receptors:
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15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCRS).
                                                                                                                        EMBL, AF177899; AAK43382.1; -.
InterPro; PR000276; GPCR_Rhodpsn.
Pfam. PF00001; 7Tm.1; 1.
PRINTS; PR00137; GFCRHODPSN.
PROSITE; PS00237; GFROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
DOMAIN
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hylobatidae, Hylobates.
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Pred. No. 6.9e-09;
); Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                    GYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

S (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

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BY SIMILARITY.
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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9623CA98340CF274 CRC64;
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Best Local Similarity
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Q95NCS;
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CKR5_HYLSY
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EMBL, AF177884; AAK43367.1; -..

EMBL, AF177884; AAK43367.1; -..

EMBL, AF177884; AAK43367.1; -..

EMBL, AF177884; AAK43367.1; -..

Pfam, PR00127; GPR0017, Tam 1; 1..

PR05ITE; PS00237; GPROTEIN RECEP F1 1; 1.

PR05ITE; PS0262; GPROTEIN RECEP F1 2; 1.

PR05ITE; PS0262; GPROTEIN RECEP F1 2; 1.

PR05ITE; PS0262; GPROTEIN RECEP F1 2; 1.

GPROTEIN COUPLE RECEPTION.

1 (POTENTIAL).

1 (POTENTIAL).
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P79436; 002746;
01-NOV-1997 (Rel. 35, Careated)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKS)
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Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
Macaca nemestrina (Pig-tailed macaque).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marcon L., Choe H., Martin K.A., Farsan M., Ponath P.D., Wu L., Newman W., Gerard N., Gerard C., Sodroski J.; "Utilization of C-C chemokine receptor 5 by the envelope glycoproteins of a pathogenic simian immunodeficiency virus, SIVmac239.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 95; DB 1; Length 352; 100.0%; Pred. No. 6.9e-09;
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                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
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EXTRACELLULAR (POTENTIAL)
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SPECIES=M.mulates, STRAIN=Indian macaque,
MPDI-INE=97213934; PubMed=9060623;
Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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MEDLINE=97184592; PubMed=9032394;
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ses 18; Conservative
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14
352 AA;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                   NCBI_TaxID=9598;
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CKR5 PANTR
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                                                                                                                                                          SPECISS=M.mulatta, M.fascicularis, and M.nemestrina;
SPECISS=M.mulatta, M.fascicularis, and M.nemestrina;
MEDLINE=97268687; PubMed=9108095;
Beinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
Sharron M., in Z.H., Clements J.E., Murphey-Corb M.,
Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
"Differential utilization of CCR5 by macrophage and T cell tropic
simian immunodefliciency virus strains.";
Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
-: FUNCTION: Receptor for a C-C type chemckine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
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INTERPRO, IPR000276; GPCR_Rhodpsn.
Prant, Pr00001; 7rm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; GPROTEIN RECEP_F1_1; 1.
PROSITE; PS002637; GPROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
suecically divergent strains of simian immunodeficiency virus use RS as a coreceptor for entry."; Virol. 71:2705-2714(1997):
                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
M -> I (IN REF. 3).
I -> M (IN REF. 3).
M, SBB96C859097ACB2 CRC64;
                                                                   SPECIES=M.mulatta;
MEDLINE=21354176; PubMed=11461684;
Margulies B.J., Hauer D.A., Clements J.E.;
"Identification and comparison of eleven rhesus macaque chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRACELL. (POTENTIAL).
                                                                                                                   receptors.";
AIDS Res. Hum. Retroviruses 17:981-986(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY
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CYTOPLASMIC (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, U96762; AAC34132.1; -.
EMBL, AR000560; AAR62554.1; -.
EMBL, AF0005661; AAB62555.1; -.
EMBL, AF005662; AAB62556.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40507 MW;
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     "Genetically divergent st
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352
178
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268
241
292
352 AA;
                                                                                                                                                                                                                                                                                                           differentiation.
                                                                                                                                                      SEQUENCE FROM N.A.
                                                           SEQUENCE FROM N.A.
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CONFLICT
SEQUENCE
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-I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

-I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

MIP-1-beta and RANTES and subsequently transdeduces a signal by

increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or

differentiation.
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                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5)
CCR5 OR CWKBR5.
Pan troglodytes (Chimpanee).
Pan troglodytes (Chimpanee).
Pan aryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIJNE-97426118; PubMed-9282822;
Zacharova V., Zachar V., Goustin A.S.;
"Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M., Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M., Peiper S.C., Parmentier M., Broder C.C., Doms R.W.; "Differential utilization of CCR5 by macrophage and T cell tropic simian immunodeficiency virus strains."; Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
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                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zimmerman P.A., Buckler-White A., Alkhatib G.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases
100.0%; Score 95; DB 1; 1
100.0%; Pred. No. 6.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AIDS Res. Hum. Retroviruses 13:1159-1161(1997).
                                                                            Mismatches
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                                                                                                                                                                                                                         297 YAFVGEKFRNYLLVFFOK 314
                                                                                                                                                 1 YAFVGEKFRNYLLVFFOK 18
    Query Match 100.
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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SEQUENCE FROM N.A.
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1 YAFVGEKFRNYLLVFFOK 18
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352 AA;
                                                                                                                                  SEQUENCE FROM N.A.
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Best Local Similarity
Matches 18; Conserv
                                                                                                                                              SPECIES=P.anubis;
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TRANSMEM
DOMAIN
TRANSMEM
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MOD_RES
CARBOHYD
SEQUENCE
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                   PRINTS; PRO0237; GPCRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).

TRANSMEM 31 F8 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CRR-5) (CCRR-5) (CCR5).
                                                                                                                                                                                                                                                                    4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASHIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASHIC (POTENTIAL).

7 (POTENTIAL).

SYMPATION (BY SIMILARITY).

SULFATION (BY SIMILARITY).

T -> S (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Papio hamadryas (Hamadryas baboon), and
Papio anubis (Olive baboon).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=P.hamadryas;
MEDLINE=97286887; Pubhed=9108095;
Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
Sharron M., Samson M., Lu Z.H., Clements J.B., Murphey-Corb M.,
Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 95; DB 1; Length 352,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                         1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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4A33E698B80FE34C CRC64;
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Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                352 AA.
                                                                       EMBL, AF011542; AAB65742.1;
EMBL, U97666; AAC51670.1;
EMBL, PG011540; AAB65740.1;
EMBL; AF177894; AAR63377.1;
InterPro; IPR000276; GPCR_Rhodpsn.
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0
                                                    EMBL; AF00563; AAB62557.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      40539 MW;
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Matches 18; Conservative (
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NCBL TaxID=9557, 9555;
                                                                                                                                         Pfam; PF00001; 7tm
                                                                                                                                                                                                                                                                                                                                                                                                                                     352 AA;
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CARBOHYD
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CKR5_PAPHA
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                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
SPECIES-P.handryas,
MEDLINE-99210133; PubMed=10195758;
MEDLINE-99210133; PubMed=10195758;
MEDLINE-99210135 PubMed=10195758;
MEDLINE-99210135 PubMed=10195758;
Maksena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.;
"Species-specific changes in the CCR5 gene from African and Asian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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EMBL, AF105289, AAD20557.1; -...
EMBL, AF105299, AAD20558.1; -...
EMBL, AF105290, AAD20558.1; -...
EMBL, AF0023452; AAG63830.1; -...
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPROTEIN RECEP_F1_1; 1.
PROSITE; PS502627; GPROTEIN RECEP_F1_2; 1.
PROSITE; PS502627; GPROTEIN RECEP_F1_2; 1.
DOMALN 30 EXTRACELLULAR (POTENTIAL).
TRANSMEM 31 (POTENTIAL).
"Differential utilization of CCR5 by macrophage and T cell tropic simian immunodeficiency virus strains.";
Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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7 (POTENTIAL).
CYTOPLASHIC (POTENTIAL).
BY SIMILARITY.
SULFATION (BY SIMILARITY).
N-LINKED (GLCNAC...) (POT)
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EXTRACELLULAR (POTENTIAL)
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SE1504A9BA1FE8B2 CRC64;
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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Pred. No. 6.9e-09;
; Mismatches 0;
                                                                                                                                                                                                                                         nonhuman primates.";
AIDS Res. Hum. Retroviruses 15:479-483(1999).
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ilarity 100.0%; Pr
Conservative 0;
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CCRS OR CMKBRS.
Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
Bukaryota; hatazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; butheria; Prinates; Catarrhini; Cercopithecidae; Colobinae;

SEQUENCE FROM N.A. MEDLINE=99416438; PubMed=10486970;

NCBI\_TaxID=61621;

Pygathrix

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352

STANDARD;

CKRS PYGBI 097880;

297 YAFVGEKFRNYLLVFFQK 314

297 YAFVGEKFRNYLLVFFQK 314

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                                                                                                                                                                                                                Zhang Y.-W., Ryder O.A., Zhang Y.-P., "Sequence evolution of the CCR5 chemokine receptor gene in primates."; Mol. Biol. Evol. 16:1145-1154(1999).
                                                                                                                                                                                                                                                       FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBSTRUCTAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
48-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5)
CCR5 OR CMKBR5.
                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pongo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 95; DB 1; Length 35
100.0%; Pred. No. 6.9e-09; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
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F4E2F47135AF658A CRC64;
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL)
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=99416438; PubMed=10486970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40527 MW;
                                                                                                                      pygmaeus (Orangutan).
                          STANDARD;
                                                                                                                                                                                                                                                                                                                  differentiation.
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352 AA;
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Best Local Similarity
Matches 18; Conserv
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                        CKRS PONPY
097881;
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RESULT 12
CKR5_PONPY
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                                                                                                                                                                                                                                                                                                                                                                                             Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
M.Sequence evolution of the CCRS chemokine receptor gene in primates.";
M.S. Biol. Evol. 16:1145-1154 (1999).
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RAWTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
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InterPro; IRR000276; GPCR_Rhodpsn.
Pfan, PF00011; 7tm 1; 1.
PRINTS; PR00237; GPRRHOOPSN.
PROSITE; PS00237; G PROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; G PROTEIN RECEP_F1_2; 1.
PROSITE; PS50262; G PROTEIN RECEP_F1_2; 1.
GPROSITE; PS50262; G PROTEIN RECEP_F1_1; 1.
GPROSITE; PS50262; G PROTEIN RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  differentiation.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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4366F142730F938F CRC64;
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EXTRACELLULAR (POTENTIAL)
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6.9e-09;
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Best Local Similarity 100.
Matches 18; Conservative
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Conservative

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                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINES=99416438; PubMed=10486970;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;

"Sequence evolution of the CCR5 chemokine receptor gene in primates.";
Mol. Biol. Evol. 16:1145-1134 (1999).

-I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
Increasing the intracellular calcium ions level. May play a role
in the control of gramulocytic lineage proliferation or
                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-F8B-2003 (Rel. 41, Last annotation update)
CC chemokine receptor type 5 (C-C CKR-5) (CC-CKF).
                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AF075448; AAD19860.1; -.
EMBL, AF075448; AAD19860.1; -.
InterPro; IPR00027; GPCR_RhodopsN.
PROSITE; PS00237; GPCRHODOPSN.
PROSITE; PS00262; GPROTEIN RECEP_F1_2; 1.
PROSITE; PS50262; GPROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLUTAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLUTAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
SULFATION (BY SIMILARITY)
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297 YAFVGEKFRNYLLVFFQK 314
                                                                                                                                              Pygathrix nemaeus (Dove langur)
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14 SI
15 SI
40532 MW;
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MEDLINE-99416438; PubWed=10486970;

Zhang Y.-W., Ryder O.A., Zhang Y.-P.;

Zhang Y.-W., Ryder O.A., Zhang Y.-P.;

Sequence evolution of the CCR5 chemokine receptor gene in primates.";

Mol. Biol. Evol. 16:1145-1154(1999).

-I. FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

MIP-1-beta and RANTES and subsequently transduces a signal by

increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or

differentiation.

-I. SUBCELLULAR LOCATION: Integral membrane protein.

-I. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                            Trachypithecus francoisi (Francois' langur) (Indochinese langur).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
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28-FBB-2003 (Rel. 41, Last anotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5).
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InterPro; IPR000276; GPCR_Rhodpsn.
PRAMTS; PR0001; 7fm_1; 1.
PRINTS; PR00237; GPCREHOOPSN.
PROSITE; PS00237; GPROTEIN RECEP_F1_1; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
DOMAIN

EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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297 YAFVGEKFRNYLLVFFQK 314
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                                                                                                                                                            STANDARD;
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Local Similarity 100. ses 18; Conservative

Best Loca Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang Y.-W., Ryder O.A., Zhang Y.-P., "Sequence evolution of the CCRS chemokine receptor gene in primates."; Mol. Biol. Evol. 16:1145-1154 (1999).
-I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RAWIES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or
                                                                                                                                                                                                                                                                                                                                                                  Trachypithecus phayrei (Phayre's leaf monkey),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
Trachypithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Or Sello ...

EMBL, AF075443; AAD19855.1; -.

EMBL, AF075443; AAD19855.1; -.

EMBL, PRO00201; GPCR_Hhodpsn.

PERNTS; PR00221; GPCRHDODPSN.

PROSITE; PS02237; G PROTEIN RECEP_F1_2; 1.

PROSITE; PS02262; G_PROTEIN RECEP_F1_2; 1.

PROSITE; PS02262; G_PROTEIN RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

I (POTENTIAL).
                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR-5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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MEDLINE=99416438; PubMed=10486970;
                                                     297 YAFVGEKFRNYLLVFFQK 314
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Score 95; DB 1; ] Pred. No. 6.9e-09;

100.0%;

Best Local Similarity

Query Match

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Sprague-Dawley;
MEDLINE=9818173; PubMed=9655467;
Jiang Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
Deficibre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
"Chemokine receptor expression in cultured glia and rat experimental
allergic encephalomyeritis.";
J. Neuroimmunol. 86:1-12(198).
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SUBCELLULAR Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
Gaps
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, Last sequence update)
, Last annotation update)
--- +vve 5 (C-C CKR-5) (MIP-1
                                                                                                                                                                                                                                                                                                                                                   STRAIN=Wister, TISSUE=Brain;
MEDIINE=98134064; Pubmed=9670989;
Spleiss O., Gourmala N., Boddeke H.W.G.M., Sauter A., Flebich B.L.,
Berger M., Gebicke-Haerter P.J.;
Cloning of rat HIV-1-chemokine coreceptor CKRS from microglia and
upregulation of its mRMA in ischemic and endotoxinemic rat brain.";
J. Neurosci. Res. 53:16-28(1998).
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EMBL; Y12009, CAA72737.1; -.
EMBL; Y12009, CAA72737.1; -.
InterPro; IPR00276, GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHODOPSN.
PROSITE; PS0237; G PROTEIN RECEP_R1 1; 1.
PROSITE; PS0262; G_PROTEIN_RECEP_R1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                297 YAFVGEKFRNYLLVFFQK 314
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   18; Conservative
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"Molecular cloning and functional expression of murine JE (monocyte molecular cloning protein 1) and murine macrophage inflammatory protein chemoattractant protein 1 alpha receptors: evidence for two closely linked C-C chemokine receptors on chromosome 9.";
J. Biol. Chem. 271:7551-7558 (1996).
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MEDLINE=9740635; PubMed=9261347;
MEDLINE=9740635; PubMed=9261347;
DOCHAIX B.J., LU Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H.,
Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.,
"Two distinct CCRS domains can mediate coreceptor usage by human
immunodeficiency virus type 1.";
J. Virol. 71:6305-6314(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                          CKRS MOUSE STANDARD; PRT; 354 AA.
P51682; 035313; 035891; P97308; P97405; Q61867;
10-COT-1996 (Rel. 34, Created)
15-UL-1998 (Rel. 36, Last annotation update)
10-CCT-2003 (Rel. 42, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (MIP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CS7BL/6, and NIH Swiss; TISSUE=Kidney, Liver, and Spleen; MEDLINE=98001387; PubMed=9343222, Kabat D.; Kabat D.; Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.; Potlymorphisms in the CCRS genes of African green monkeys and mice implicate specific amino acids in infections by simian and human immunodeficiency viruses "; virol. 71:8642-865 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDIINE=86278910; PubMed=8662890;

Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;

Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;

Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;

Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;

Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;

Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;

Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;

Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;

Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;

Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;

Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;

Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;

Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=129/SvJ; TISSUE=Spleen;
MEDLINE=96205938; PubMed=8631787;
Boring L., Gosling J., Monteclaro F.S., Lusis A.J., Tsou C.-L.,
                                                                                    LINKED (GLCNAC. . .) (POTENTIAL)
77EDB368AA4C868D CRC64;
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Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
    EXTRACELLULAR (POTENTIAL)
                     7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
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Pred. No. 3.7e-07;
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nes 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alpha receptor).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCR5 OR CMKBR5
DOMAIN
TRANSMEM
                                                                   DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                            Query Match
                                                DOMAIN
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; V9451; CAA63867.1; -.

REMBL; V84551; CAA63867.1; -.

REMBL; V85565; AAB7272.1; -.

REMBL; V80556; AAB7183.1; -.

REMBL; AF022990; AAC53389.1; -.

ROGO; GO:0006952; Pidefense response; IMP.

InterPro; IPR000276; GPCR_Rhodopsn.

ROGO; GO:0006957; GPCRHCHODOPSN.

REMBL; AF0237; GPROTEIN_RECEP_F1_1; 1.

REMBL; AF0237; GPROTEIN_RECEP_F1_2; 1.

REMBL; AF0237; GPROTEIN_REMB, AF0237; GPROTEIN_REMB, AF0237; AF023
Guo B., Kuno K., Harada A., Matsushima K.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level.
-!- SUBCELULIAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
-!- but nonhematopolatic cell lines.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
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No. 2.7e-06;
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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BY SIMILARITY.
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83.3%; Pred. No.
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2; Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMEDINE=97026720; PubMed=8872898;
A MEDINE=97026720; PubMed=8872898;
A Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,
A Post T.W., Gerard C., Dorff M.E.;
Theogener of the chemokines MCP-1 and KC, but reverse transcriptase-polymerase chain reaction does not detect mRNA for the KC or new MCP-1 receptor.";
T. Anscriptase-polymerase chain reaction does not detect mRNA for the KC or new MCP-1 receptor.";
J. Neurosci. Res. 45:382-391(1996).
J. Neurosci. Res. 45:382-391(1996).
J. PUNCTION: Receptor for the MCP-1 (UE), MCP-3 (FIC) and MCP-5 chemokines. Transduces a signal by increasing the intracellular calcium ions level.

J. SUBCELLULAR LOCATION: Integral membrane protein.
J. TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines, but not in nonhematopoletic cell lines.

L. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular cloning and functional expression of murine JE (monocyte chemoattractant protein 1) and murine macrophage inflammatory protein lalpha receptors: evidence for two closely linked C-C chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U47035; AAC52453.1; -.
EMBL; U47035; AAC52557.1; -.
EMBL; U51717; AAC52557.1; -.
EMBL; U56319; AAC52784.1; -.
MGD; MGI:106185; Ccr2.
GO; GO:0016483; FC-C chemokine receptor activity; IDA.
GO; GO:0019955; F:Cytokine binding; IPT.
GO; GO:0016066; P:cellular defense response (sensu Vertebrata); IMP.
GO; GO:0016595; P:hemopoleais; IMP.
GO; GO:0016599; P:humoral immune response; IMP.
GO; GO:0016594; P:inflammatory response; IMP.
                                                                                                                                                                                                                          PSI6E3; O61172;
1-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2 OR CWKBR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kurihara T., Bravo R.;
Cloning and functional expression of mCCR2, a murine receptor for
the C-C chemokines JE and FIC. ";
J. Biol. Chem. 271:11603-11606(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=96205938; PubMed=8631787;
Boring L., Gosling J., Monteclaro F.S., Lusis A.J., Tsou C.-L.,
                                                                                                                                                                                                          373 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptors on chromosome 9.";
J. Biol. Chem. 271:7551-7558(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BALB/c;
MEDLINE=96216064; PubMed=8662823;
                                                           299 YAFVGEKFRSYLSVFFRK 316
                             1 YAFVGEKFRNYLLVFFOK 18
                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              macrophages.
--- INDOCTION: In animals in which experimental allergic encephalomyelitis (EAB) has been induced.
--- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
LeCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 78; DB 1; Length 373
Pred. No. 6.4e-06;
?; Mismatches 2; Indels
                                                                                                                                                                      2 (POTENTIAL).

EXTRACELLUTAR (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).

EXTRACELLUTAR.
5 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                  6 (POTENTIAL).
EXTRACELLUAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
                                                                                                                     EXTRACELLUIAR (POTENTIAL)

1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                          Y -> H (IN REF. 1).
A -> G (IN REF. 1).
V -> G (IN REF. 1).
FA012C10F4C9325A CRC64;
                                                                                                                                                                                                                                                                                 5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
GO, GO:0030334; P:regulation of cell migration; IMP.
InterPro; IPR00227; GPCR_Rhodpsn.
PR00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; GPCRRHODOPSN.
PROSITE; PS50262; G-PROTEIN RECEP FI 1; 1.
G-protein coupled receptor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318 YAFVGEKFRYLSIFFRK 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42782 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.1%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 77.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                              264
373 AA;
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055193;
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CKR2_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AIDS Res. Hum. Retroviruses 17:981-986(2001).
-!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
Transduces a signal by increasing the intracellular calcium ions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Last sequence update)

SeyEBB-2003 (Rel. 41, Last annotation update)

C-C chemokine receptor type 2 (C-C CR-2) (CCR-2) (CCR2)

(Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=018793-2; Sequence=Not described; -i- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCR2 OR CMKBR2.

Macaca mulatta (Rhesus macaque).

Macaca mulatta (Rhesus macaque).

Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21354176; PubMed=11461684;
Margulies B.J., Hauer D.A., Clements J.E.;
"Identification and comparison of eleven rhesus macaque chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                              Score 78; DB 1; Leus-
Pred. No. 6.4e-06;
2; Indels
                                                                                                                                                          EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                         2E7BB012F5D6FD09 CRC64;
                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
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SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                360 AA.
                                                   EMBL; U77349; AAC03242.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 1; 1.
G-protein coupled receptor; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318 YAFVGEKFRYLSIFFRK 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 YAFVGEKFRNYLLVFFQK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                          42763 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                       82.1%;
77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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SEQUENCE FROM N.A.
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018793;
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CKR2 MACMU
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InterPro; IPR000276; GPCR_Rhodpsn.
PROMO PRONO PROMO PROMO PROMO PROMO PROSTES; PRO0237; GPCRHOODPSN.
PROSITE; PS0237; GPROTEIN RECEP F1 1; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
30-MX-2006 (Rel. 36, Last sequence update)
30-MX-2000 (Rel. 39, Last annotation update)
C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3) (CCR-3) (CCR)
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                   7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
SULPATION (BY SIMILARITY).
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EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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Pred. No. 1.4e-05;
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77.8%;
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statement is not removed. Usage by and for commercial a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                  Gaps
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P51677; Q15748; Q86WD2; Q9ULX8;
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
C-C chemokine receptor type 3 (C-C CR-3) (CC-CR-3) (CCR-3) (CCR3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Daugherty B.L., Siciliano S.J., Demartino J.A., Malkowitz L., Sirotina A., Springer M.S.; Cloning, expression, and characterization of the human eosinophil eotaxin receptor.", J. Exp. Med. 183:2349-2354(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                               Score 65, DB 1; Length 355;
Pred. No. 0.0011;
2; Mismatches 4; Indels
                                                                                          EXTRACELLULAR (POTENTIAL).

1 (POTENTIAL).

2 (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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(POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                  PROSITE; PS00237; G PROTEIN RECEP F1 1; 1. PROSITE; PS50262; G PROTEIN RECEP F1 2; 1. G-protein coupled receptor; Transmembrane.
                                                                                                                                                                              CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Combadiere C., Ahuja S.K., Murphy P.M.; J. Biol. Chem. 270:30235-30235(1995).
         entities requires a license agreement (
or send an email to license@isb-sib.ch)
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                              EMBL, Y13775; CAA74106.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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MEDLINE=95348056; PubMed=7622448;
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PRINTS; PR00237; GPCRRHODOPSN
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66.7%;
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POINTLY BE STATEMENT OF THE WARD J., WU L., Gerard N.P.,

Noman W., Gerard C., Macky C.R.,

Noman W., Gerard C., Macky C.R.,

Nomen W., Gerard C., Macky C.R.,

Nolecular Cloning and Characterization of a human ectaxin receptor

RE STATEMENT CLONING and Characterization of a human ectaxin receptor

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                                                                                                                                  SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SOL N., Treboute C., Gomas E., Ferchal F., Shacklett B., Alizon M.;

SOL N., Treboute C.CR3 chemokine receptor is a cell entry cofactor for HVV-2, but not for HV-1.";

FOR HVV-2, but not for HV-1.";

NICHOSY 240:213-220(1998)

-I FUNCTION: Receptor for a C-C type chemokine. Binds to ectaxin,

NCP-3, MCP-4 and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level.

-I SUBCELLULAR LOCATION: Integral membrane protein.

-I SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                               Margulies B.J., Hauer D.A., Clements J.E.; "Identification and comparison of eleven rhesus macaque chemokine
 Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 65; DB 1; Length 355;
Pred. No. 0.0011;
2; Mismatches 4; Indels
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CYTOPLASMIC (POTENTIAL).

EXTRACELLUAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

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K -> R (IN REF. 2).
E271F1E694970D9F CRC64;
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EMBL; Y13776, CAA74107.1; --
Interpro; IPR00276, GPCR Rhodpsn.
Pfam; PR00101; 7rm 1; 1.
RINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; GPCRRHODOFSN.
PROSITE; PS502262; G PROTEIN RECEP F1 1; 1.
G-protein coupled receptor; Transmembrane.
                                                                                                                       AIDS Res. Hum. Retroviruses 17:981-986(2001)
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                                                                   MEDLINE=21354176; PubMed=11461684;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CKR8 MOUSE STANDARD; ID CKR8_MOUSE STANDARD; I ACR = MOUSE STANDARD; I DT 15-JUL-1998 (Rel. 36, Created)
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Guery Local Similarity 60....
Best Local Similarity 60....
             Cercopithecinae, Macaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                355 AA;
                                                     SEQUENCE FROM N.A.
                            NCBI_TaxID=9544;
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                  TAS.
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                                                                                                                                                                                MIM: 601268; -.

GO; GO:0005887; C:integral to plasma membrane; TAS.

GO; GO:0004950; F:chemokine receptor activity; TAS.

GO; GO:0007155; P:cell adhesion; TAS.

GO; GO:000588; P:cellular defense response; TAS.

GO; GO:0005915; P:chemotaxis; TAS.

GO; GO:0007189; P:chemotaxis; TAS.

GO; GO:0007189; P:chemotaxis; TAS.

GO; GO:0007189; P:chemotaxis; TAS.

GO; GO:0007189; P:inflammatory response; TAS.

GO; GO:0007125; P:inflammatory response; TAS.

GO; GO:0007125; P:inflammatory response; TAS.
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-UU-1998 (Rel. 41, Last annotation update)
C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)
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Macaca mulatta (Rhesus macaque).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the population; may show reduced
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CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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S -> T (IN REF. 4 AND 5).
E95DCD7A6C643874 CRC64;
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                                    EMBL, U28694, AAC50469.1, EMBL, U51241, AAB16831.1; EMBL, U49727, AAB18331.1; EMBL, AF026635, AAB82869.1, EMBL, AF028635, AAB82869.1, EMBL, AF02887, BAA8664.1, EMBL, AY221092, AAB5154.1, EMBL, AY221092, AAB3514.1, EMBL, BC033514, AAB33514.1, EMBL, BC03486, G02486, G02486, MMM, 601269.
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355 AA; 41043 MW;
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CKR3_MACMU
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                                                                                                                                                                                                                                                                       Zingoni A., Soto H., Hedrick J.A., Stoppacciaro A., Storlazzi C.T., Sinigaglia F., D'Ambrosio D., O'Garra A., Robinson D., Rocchi M., Satoria A., Ziotnik A., Napolitano M.; "The chemokine receptor CCR8 is preferentially expressed in Th2 but not Th1 cells.";

    J. Immunol. 161:547-551(1998).
    -!- FUNCTION: Receptor for the TCA-3 chemokine.
    -!- SUBCELLULAR LOCATION: Integral membrane protein.
    -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

                                                              Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .) (POTENTIAL)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
CCC chemokine receptor type 8 (C-C CKR-8) (CC-CKR-8)
CCR8 OR CMKER8 OR TERL.
                                                                                                                                                                         Zaballos A., Goya I.I., Gutierrez J., Varona R., Marquez G., Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; 298205; CAB10895.1; -.

R EMBL; Z98205; CAB10895.1; -.

R EMBL; Z98205; CAB10895.1; -.

R GO; MG:1201402; CCT6.

MGO; MG:1201402; CCT6.

R GO; GO:0016493; F:C-C chemokine receptor activity; IDA.

GO; GO:0005315; F:protein binding; IPI.

GO; GO:0005315; F:protein binding; IPI.

R InterPro; IPR000276; GPGR_Rhodpsn.

R RINTS: PR01530; GFRRHODDPSN.

R PRINTS; PR01530; GFRCHINER8.

R PROSITE; PS00237; GPRCTEIN RECEP FI 1; 1.

M G-protein coupled receptor; Transmembrane; Glycoprotein.

J G-protein coupled receptor; Transmembrane; Glycoprotein.

TRANSMEM 34 61 1 (CYTOPLASMIC (POTENTIAL).

TRANSMEM 72 91 2 (POTENTIAL).

T TRANSMEM 128 127 3 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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N-LINKED (GLCN
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MEDLINE=98334001; PubMed=9670926;
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Best Local Similarity 61.1
Matches 11; Conservative
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91
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231
3302
1353
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                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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298 YAFIGEKFKKHLMDVFQK 315
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359 AA

STANDARD;

MOUSE

CKR3\_r

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                          01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Probable C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3) (CCR) (CRR) (Macrophage inflammatory protein-1 alpha receptor-like 2) (MIP-1 alpha RL2).
CCR3 OR CMKBR3 OR CWKBR1L2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gao J. L., Murphy P.M.;
"Cloning and differential tissue-specific expression of three mouse "Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.";
J. Bloi. Chem. 270:17494-17501(1995).
-I- FUNCTION: Receptor for a C-C type chemokine. Binds to ectaxin, MCP-3, MCP-4 and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level.
-I- SUBCELLULAR LOCATION: Integral membrane protein.
-I- TISSUE SPECIFICITY: Detected in skeletal muscle and in trace
                                                                                                                                                                                                                                                                                                                                 "Molecular characterization of two murine eosinophil beta chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amounts in Leukocytes.
                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                               MEDLINE=96072806; PubMed=7594543;
Post T.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U29677; AAA86118.1; -...

EMBL; U28406; AAA89155.1; -...

MOJ; MOI: 104616; Corr3.

GO; GO: 10016493; F: Corr3.

GO; GO: 10016493; F: Corr3.

GO; GO: 10016493; F: Corrania binding; IPI.

GO; GO: 10016935; F: Chemotaxis; IDA.

R FRINTS; PRO02707; GPCR.Rhodpsn.

R FRINTS; PRO037; GPCRRHODPSN.

R PROSITE; PSO0237; GPCRRHODPSN.

R PROSITE; PSO0237; GPROTEIN RECEP F1 1; 1.

GPICOLETIN COUPLED RECEP F1 2; 1.

GPICOLETIN COUPLED RECEP F1 2; 1.

GPICOLETIN COUPLED RECEP F1 2; 1.
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1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                   J. Immunol. 155:5299-5305(1995).
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64
68
95
1111
133
                                                                                                                                                     Mus musculus (Mouse).
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                               FROM N.A.
                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                        receptors
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CKR3 MOU
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Gaps

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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                       41643 MW;
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                                                                                                                                                                                                                                                                                                                                                                11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
  receptor-like genes.";
                                                                                                                                                                                                             265
289
310
164
359 AA;
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                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CKR8_HUMAN
TRANSMEM
DOMAIN
TRANSMEM
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DOMAIN
TRANSMEM
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CONFLICT
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TRANSMEM
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CKR8_HUMAN
                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
STRAIN=Wistar; TISSUE=Spleen;
MEDLINE=9318173; Pubmed=9659467;
Jiang Y., Salafranca M.N., Abhikari S., Xia Y., Feng L., Sonntag M.K.,
Defiebre C.M., Pennell N., Atheit W.J., Harrison J.K.;
"Chemokine receptor expression in cultured glia and rat experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRAINSUBLET, TISSUB-Spleen,
Harrington P.M., Newton D.J., Coleman J.W., Flanagan B.F.,
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,
MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUB_SPECIFICITY: Expressed in spleen but not in astrocytes or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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10-CT-2003 (Rel. 42, Last sequence update)
10-CT-2003 (Rel. 42, Last annotation update)
C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)
                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                             Length 359;
                                                                                                                                                                                                             Score 64; DB 1; Length 359
Pred. No. 0.0016;
1; Mismatches 3; Indels
                  5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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InterPro; IPR002276; GPCR_Rhodpsn.
Pfam; PF00001, 7tm 1; 1.1
PRINTS; PR000237; GPCRHODOPSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; GPROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane.
DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
    EXTRACELLULAR (POTENTIAL)
                                                                                                                                  BY SIMILARITY.
R -> S (IN REF. 2).
AC11ED66E283CEAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          359 AA.
                                                                                                                                                                                                                                                                                                              305 YAFVGERFRKHLRLFFHR 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         allergic encephalomyelitis.";
J. Neuroimmunol. 86:1-12(1998).
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                                                                                                                                                                                                                                                                                         1 YAFVGEKFRNYLLVFFOK 18
                                                                                                                                                                           41825 MW;
                                                                                                                                                                                                               67.4%;
                                                                                                                                                                                                                                                   11; Conservative
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    201
2227
2243
2268
3309
1359
270
                                                                                                                                                                         359 AA;
                                                                                                                                                                                                                               Local Similarity
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O54814; O55169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCR3 OR CMKBR3.
  DOMAIN
TRANSMEM
DOMAIN
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DOMAIN
TRANSMEM
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CONFLICT
SEQUENCE
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Matches
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01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 8 (C-C CKR-8) (CC-CKR-8) (GPR-CY6)
(GPRCY6) (Chemokine receptor-like 1) (CKR-L1) (TER1) (CMKBRL2) (CC-CHEMOKINE receptor CHEKR1).
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MEDLINE-97351133; PubMed-9207005;
Tiffany H.L., Lautens L.L., Gao J.-L., Pease J., Locati M.,
Combadiere C., Modi W., Bonner T.I., Murphy P.M.;
Identification of CCR8: a human monocyte and thymus receptor for the
CC chemokine 1-309.",
J. Exp. Med. 186:165-170 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDINIS=99129363; PubMed=9469461;
MEDINIS=99129363; PubMed=9469461;
MEDINIS=99129363; PubMed=9469461;
I Gutierrez J., Varona R., Kremer L., Zaballos A., Marquez G.;
"Identification of CCR8 as the specific receptor for the human beta-
chemokine I-309: cloning and molecular characterization of murine
CR8 as the receptor for TCA-3.";
CR8 as the 160:1975-1981 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata, Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97040707; PubMed-8886020;
Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;
"Molecular cloning and RNA expression of two new human chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
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MEDLINES-97131825; PubMed=8977299;
Sanson M., Stordeur P., Labbe O., Soularue P., Vassart G.,
Parmentler M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 64; DB 1; Length 359;
Pred. No. 0.0016;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                   POTENTIAL.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  -> L (IN REF. 2).
880F682984F501DA CRC64;
                                                                                          EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL) POTENTIAL.
                                                                                                                                                         CYTOPLASMIC (POTENTIAL). POTENTIAL.
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F -> L (IN REF. 2).
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POTENTIAL. CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YAFVGEKFRNYLLVFFOK 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptors.";
AIDS Res. Hum. Retroviruses 17:981-986(2001).
-!- FUNCTION: Receptor for the chemckines SCYA1/I-309, SCYA4/MIP-1-
beta and SCYA1/TARC. My regulate monocyte chemctaxis and thymic
cell line apoptosis (By similarity).
-!- SUBCELUULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
  Gaps
                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Spleen;
Marghine=21354176; PubMed=11461684;
Marguline=2154176; Hauer D.A., Clements J.E.;
"Identification and comparison of eleven rhesus macaque chemokine
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                                                                                                                                                                                     CKR8 MACMU STANDARD; PRT; 356 AA.
097655;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 8 (C-C CKR-8) (CCR-8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF100205; AAC72403.1; -.
InterPro; IPR004068; CC 8 receptor.
InterPro; IPR004068; CC 8 receptor.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR001530; CHEMOXINER8.
PRINTS; PR00237; GPCRRHODDESN.
PROSITE; PS00237; GPCRRHODDESN.
PROSITE; PS00227; GPCRTEND RECEP F1 1; 1.
PROSITE; PS00202; GPROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
DOMAIN 1 35 EXTRACELLULAR (POTENTIAL).
TRANSEM 36 63 I (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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Pred. No. 0.0024;
2; Mismatches 4; Indels
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
    4.
  Mismatches
                                                                   300 YAFVGEKFKKHLSEIFQK 317
                                                                                                                                                                                                                                                                                                                                         Macaca mulatta (Rhesus macaque)
5
                                        1 YAFVGEKFRNYLLVFFQK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41210 MW;
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12; Conservative
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Best Local Similarity
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356 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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Matches
                                                                                                                                                 RESULT 29
                                                                                                                                                                                                              ACOUNTS, CINTEGRAL to plasma membrane, TAS.

ROJ GO:0005887; C:integral to plasma membrane, TAS.

ROJ GO:00015026; F:concecptor activity; TAS.

ROJ GO:00015026; F:concecptor activity; TAS.

ROJ GO:00015026; F:cell adhesion; TAS.

ROJ GO:00015026; F:cell adhesion; TAS.

ROJ GO:000126; P:cell adhesion; TAS.

ROJ GO:000186; P:G-protein calcium ion concentration elevation; TAS.

ROJ GO:000186; P:G-protein capled receptor protein signalin. .; TAS.

ROJ GO:000186; P:G-protein coupled receptor.

InterPro; IRR004066; CC & receptor.

InterPro; IRR004066; CC & receptor.

InterPro; RR004066; CC & receptor.

R THANTS; PR01237; GPRRHODOFSN.

R RINTS; PR01237; GPRRHODOFSN.

R ROSITE; PS00237; GPROTEIN RECEP FI 1; 1.

R ROSITE; PS00237; GPROTEIN RECEP FI 2; 1.

R PROSITE; PS00237; GPROTEIN RECEP FI 2; 1.

R PROSITE; PS00237; GPROTEIN RECEP FI 2; 1.

R PROSITE; PS00237; GPROTEIN RECEP FI 2; 1.

R PROMAIN 1 35 GROTEIN RECEP FI 2; 1.

R PRANKENEN SAGRACELULAR (POTENTIAL).

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R PROMAIN 1 1 35 RITERITALD.
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                                                                                              DIGAND BINDING.

MEDIINE=98180363; PubMed=9521068;

MEDIINE=98180363; PubMed=9521068;

Bernardini G., Hedrick J., Sozzani S., Luini W., Spinetti G.,

Bernardini G., Hedrick A., Mantovani A., Santoni A.,

Napolitano M.;

"Identification of the CC chemokines TARC and macrophage inflammatory
protein-1 beta as novel functional ligands for the CCR8 receptor.";

Eur. J. Immunol. 28:582-588(1998).

-!- FUNCTION: Receptor for the chemokines SCYA1/I-309, SCYA4/MIP-1-

beta and SCYA1/TARC. May regulate monocyte.chemotaxis and thymic
                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                 SEQUENCE FROM N.A.
Nakajima T., Yoshida R., Harada S.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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EMBL; U62556; AAB05542.1; --
EMBL; Z79782; CAB02142.1; --
EMBL; X08456; CAA69712.1; --
EMBL; AF005210; AA865971.1; --
EMBL; AF005210; AA862547.1; --
PIR; JC5067; JC5067.
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106
355 AA;
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Gaps

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66.78;

Matches 12; Conservative

Score 63; DB 1; Length 355; Pred. No. 0.0024;

66.3%;

Best Local Similarity

Query Match

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SEQUENCE FROM N.A.

MIDLINE=22935763; PubMed=14574404;

MIDGAIL A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L.,

MINDGAIL A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L.,

MILLING L., Jones M.C., Horton R., Hunt S.E., Scott C.E.,

Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainscough R.,

Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,

Babbage A.K., Bagguldy C.L., Bailey J., Banerjee R., Barker D.J.,

Babbage A.K., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,

Barlow K.F., Burtill W., Burton J., Brown J.Y.,

Burford D.C., Burrill W., Burton J., Brown J.Y.,

Burford D.C., Clark S.Y., Clark G., Clee C.M., Cleeg S., Cobley V.,

Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J.,

Culley K.M., Dhami P., Davies J., Dunn M., Barthrowl M.E.,

Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIZINE 97313465; PubMed=9169459;
MEDIZINE=97313465; PubMed=9169459;
Babba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K., Nomiyama H., Yoshie O.;
"Identification of Cork, the specific receptor for a novel "Imphocyte-directed CC Chemokine LARC.";
"Ilymphocyte-directed CC Chemokine LARC.";
J. Biol. Chem. 272:14893-14898(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                C-C chemokine receptor type 6 (C-C CKR-6) (CC-CKR-6) (CCR-6) (LARC receptor) (GPR-CY4) (GPRCY4) (Chemokine receptor-like 3) (CKR-L3)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIANE=97040707; PubMed=8886020;
Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;
"Molecular cloning and RNA expression of two new human chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

Warren C.N., Aronstam R.S., Sharma S.V.;

"cDNA clones of human proteins involved in signal transduction
sequenced by the Guthrie cDNA resource center (www.cdna.org).";

Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lautens L.L., Modi W., Bonner T.I.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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McCoy R., Perlmutter D.H.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor-like genes.";
Biochem. Biophys. Res. Commun. 227:846-853(1996).
                                                                                                                                                                                                                          HUMAN
CKR6 HUMAN
STANCE

PEL684; P78553; Q92846;

01-0CT-1996 (Rel. 34, Created)
15-JUL-1998 (Rel. 34, Last sequence update)
... -2004 (Rel. 43, Last annotation update)
... -2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCR6 OR CMKBR6 OR STRL22 OR GPR29 OR CKRL3.
                                                                    301 YAFVGEKFKKHLSEIFQK 318
                                  YAFVGEKFRNYLLVFFOK 18
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MEDLINE=97040707: 1
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Chickle G. Gillend J. Genrol L. Gillendor R.J. Gerland D.V. Grant N. S. Ratchian G. C. Gillendor R.J. Gerland D.V. Grant N. S. Ratchian G. S. Harley J.L., Hart E.A., Heach D.D., Heachcott R., Shandon P.J., Hondon P.J., Heach D.D., Heachcott R., Shandon P.J., Hondon P.J., Hart E.A., Heach D.D., Heachcott R., Shandon P.J., Hondon P.J., Hondon D.J., Hart E.A., Heach D.D., Heachcott R., Shandon P.J., Hondon P
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE FROM N.A.
                    NCBI_TaxID=9606;
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                                                              GO: GO:0005887; C:integral to plasma membrane; TAS.
GO: GO:0004950; F:chemokine receptor activity; TAS.
GO: GO:0004972; F:receptor activity; TAS.
GO: GO:00069872; F:receptor activity; TAS.
GO: GO:0006928; P:call motility; TAS.
GO: GO:0006928; P:call motility; TAS.
GO: GO:0006928; P:callular defense response; TAS.
GO: GO:0006935; P:chemotaxis; TAS.
GO: GO:0006935; P:chemotaxis; TAS.
GO: GO:0006935; P:thmoral immune response; TAS.
GO: GO:0006939; P:signal transduction; TAS.
InterPro; IPR004067; CC_ G. Receptor.
InterPro; IPR004067; CC_ G. Receptor.
InterPro; IPR00276; GPGR_Rhodpsn.
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01-0CT-1993 (Rel. 27, Last sequence update)
01-0CT-1993 (Rel. 27, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
C-C chemokine receptor type 1 (C-C CKR-1) (CC-CKR-1) (CCR-CKR-1)
(Macrophage inflammatory protein-1 alpha receptor) (MIP-lalpha-R)
(RANTES-R) (HM145) (LD78 receptor).
CCR1 OR CKKRR1 OR CKKR1.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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N-LINKED (GLCNAC. .) (POTENTIAL)

N-LINKED (GLCNAC. .) (POTENTIAL)

N-LINKED (GLCNAC. .) (POTENTIAL)

Y -> M (IN REF. 4).

Y -> N (IN REF. 4).
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S -> T (IN REF. 5).
C -> T (IN REF. 5).
C -> L (IN REF. 4).
E -> V (IN REF. 4).
SSFTM -> VULHYVIES (IN REF. 4).
W, D7F963534E990EC4 (RC64).
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                                                                                                                                                                                                                                                                 HIGHLE, L., L., L., L., ERAM, PROBLES, PROBLES, PROBLES, PROCESS, CHEMOKINERG.
PRINTS; PROCESS; GPROTEIN_RECEP_F1_1; 1.
PROSITE; PSOCO62; GPROTEIN_RECEP_F1_2; 1.
PROSITE; PSSOC62; GPROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
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EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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EMBL; BC037960; AAH37960.1;
HSSP; P34996; 1DDD.
Genew; HGNC:1607; CCR6.
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603,
744
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344 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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TAS.
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MEDLINE-94092629; PubMed=7505609;
Nomura H., Mielsen B.W., Matsushima K.;
Nomura H., Dielsen B.W., Matsushima K.;
Int. Immunol. 5:1239-1249 (1993).
Int. Immunol. 5:1239-1249 (1993).
Int. Immunol. 5:1239-1249 (1993).
Int. Immunol. 5:1239-1249 (1993).
Int. Int. ANVIES, and MCP-3 and, less efficiently, to MIP-1-beta or MCP-1 and subsequently transduces a signal by increasing the intracellular calcium ions level. Responsible for affecting stem cell proliferation.
ISUBCELLULAR LOCATION: Integral membrane protein.
ITSUES SPECIFICITY: Widely expressed in different hematopoietic
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MIM; 601159; -.

GO; GO:0005807; C:integral to plasma membrane; TAS.

GO; GO:0005155; P:cell adhesion; TAS.

GO; GO:0007155; P:cell adhesion; TAS.

GO; GO:0007155; P:cell adhesion; TAS.

R O; GO:0007267; P:cell-cell signaling; TAS.

R O; GO:0006935; P:cell-cell signaling; TAS.

R O; GO:0007367; P:cell-cell signaling; Coupled to cyclic nucl. .; TF.

R O; GO:0007187; P:celprotein signaling, coupled to cyclic nucl. .; T;

R O; GO:0006955; P:imwane response; TAS.

R O; GO:0006955; P:inwasive growth; TAS.

R O; GO:000125; P:invasive growth; TAS.

R O; GO:0000125; P:invasive growth; TAS.

R D; GO:000125; P:invasive growth; TAS.

R D; GO:000100125; P:invasive growth; TAS.

R D; GO:0001001000000000000000000000000000
                                                                                                                                                                                                                                                                                                                      [2]
SOUDNCE FROM N.A.
MEDLINE=93240122; PubMed=7683036;
Gao J.-L., Kuhns D., Tiffany H.L., McDermott D., Li X., Francke U.,
Murphy P.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structure," and functional expression of the human macrophage inflammatory protein 1 alpha/RANTES receptor."; J. Exp. Med. 177:1421-1427(1993).
SEQUENCE FROM N.A. MEDLINE=93161416; PubMed=7679328; MEDLINE=93161416; PubMed=7679328; Mebcle K., Digregorio D., Mak J.Y., Horuk R., Schall T.J.; Molecular cloning, functional expression, and signaling characteristics of a C-C chemokine receptor.";
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CYTOPLASMIC (POTENTIAL).
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EMBL; L10918; AAA3643.1; -.
EMBL; D10925; BAA01723.1; -.
PIR; A45.177; A45177.
Genew; HGNC:1602; CCR1.
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DOMAIN
TRANSMEM
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                                                                FRANSMEM
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C3X1_RAT
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SPETTLESSEET SETTLESSON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99077268; PubMed=9862452; Varona R., Zaballos A., Gutierrez J., Martin P., Roncal F., Albar J.P., Ardavin C., Marquez G.; Molecular cloning, functional characterization and mRNA expression analysis of the murine chemokine receptor CCR6 and its specific ligand mnp-setha.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEES Lett. 440:188-194(1998).
-!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-3-alpha/LARC and subsequently transduces a signal by increasing the intracellular calcium ions level.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
38-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 6 (C-C CKR-6) (CC-CKR-6) (KY411).
                                                                                                                                                                                                                                                                                                                                                     Gaps
            EXTRACELLULAR (POTENTIAL).

S (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLONAC. . .) (POTENTIAL).

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                    63.2%; Score 60; DB 1; Length 355; ilarity 61.1%; Pred. No. 0.0079; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yanagihara S., Komura E., Yamaguchi Y.; "Yanagihara S., Komura E., Yanagihara S., Komura G., Youngihar receptor KY411."; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                 337 E -> D (IN REF. 3).
41172 MW; B2C100FFED275985 CRC64;
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PRINTS; PRO1237; GPCRAHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB009369; BAA23776.1; -.
EMBL; AJ722714; CAA10956.1; -.
MGD; MGI:1333797; Cer6.
GO; GO:0005515; Frortein binding; IPI.
IncerPro; IPR004067; CC 6_receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                               301 YAFVGERFRKYLRQLFHR 318
                                                                                                                                                                                                                                                                                                                                                                                                  1 YAFVGEKFRNYLLVFFQK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                          355 AA;
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tes 11; Conserv
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  CCR6 OR CMKBR6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 32
CKR6 MOUSE
AC 054689;
DT 30-MAY-2000
DT 30-MAY-2000
DT 28-FEB-2003
DE C-C Chemokin
GN CCR6 OR CMKHE
OS Mus musculus
OS Mus musculus
OC Bukaryota; MOC MAMMalla; ENO
RA Yanagihara S
RA Mususe G pro
RA Yanagihara S
RY SEQUENCE FRO
RA Yanagihara S
RY MONGRE G PRO
RY MADLINES907
RY MODICULAT OF
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    TRANSMEM
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-94323113; PubMed-8047298;

MEDLINE-94323113; PubMed-8047298;

MEDLINE-94323113; PubMed-8047298;

MEDLINE-94323113; PubMed-8047298;

"CDMA cloning of a G-protein-coupled receptor expressed in rat spinal cord and brain related to chemokine receptors.";

Neurosci. Lett. 169:85-89(1994).

-I FUNCTION: Receptor for the CX3C chemokine fractalkine and mediates both its adhesive and migratory functions.

-I SUBCELULAR LOCATION: Integral membrane protein.

-I SUBCELULAR LOCATION: Integral membrane protein.

-I ISSUE SPECIFICITY: Most abundant in adult spinal cord, brain, kidney, gut, uterus and testes.

-I PTM: This protein is not N-glycosylated which is unusual for G-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
30-MY-2000 (Rel. 39, Last annotation update)
CX3C chemotine receptor 1 (G-X3-C CRR-1) (CX3CR1) (Fractalkine receptor) (GPR13) (RBS11).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
nomain 139 EXTRACELLULAR (POTENTIAL).
                                                                                                                                            3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                  1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 59; DB 1;
Pred. No. 0.012;
; Mismatches
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PIR; I58186; I58186.
InterPro; IPR005387; Fractalkiner.
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42102 MW;
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69.2%;
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nes 9; Conservative
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35
367 AA;
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SOLUTION OF THE TENEFORM OF THE STANDARD OF TH
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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30-WAY-2000 (Rel. 39, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
CX3C chemokine receptor 1 (C-X3-C CKR-1) (CX3CR1) (Fractalkine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 58; DB 1; Length 354;
Pred. No. 0.017;
1; Mismatches 6; Indels
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EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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7 (POTENTIAL)
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                                                                                                                                                 PROSITE; PS00237; G PROTEIN RECEP F1 1; 1. PROSITE; PS50262; G PROTEIN RECEP F1 2; 1. G-protein coupled receptor; Transmembrane.
InterPro, IPR000276; GPCR_Rhodpsn
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                                     Pfam; PF00001; 7tm 1; 1.
PRINTS; PR01562; FRACTALKINER.
PRINTS; PR00237; GPCRRHODOPSN.
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ses 11; Conservative
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SEQUENCE
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
R. Halton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahen J., Helton E., Ketreman M., Madan A., Rodrigues S., Sanchez A.,
Rhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Raterfield Y.S.M., Krzywinski M.I., Schautz J., Marra M.A.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Redriguez A.C., Grimwood J., Schmutz J., Job G.J., Schmutz J., G., Protecin coupled receptors.
C. I. STMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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3 (POTENTIAL).

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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
BY SIMILAPTWY
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PRINTS; PR00237; GPCRRHODOPSN.
PROGITE; PS00237; G PROTEIN RECEP_F1_1; 1.
PROSITE; PROSIES; G PROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane.
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
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P49238;
01-FEB-1996 (Rel. 33, Created)
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C3X1 HUMAN
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A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Strausberg R.L., Feingold E.A., Grouse L.H., Schemen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schemer C.F., Bhat N.K.,
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B Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gibbs R.A.,
B Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
N. Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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CX3C chemokine receptor 1 (C-X3-C CKR-1) (CX3CR1) (FractalKine receptor) (GPR13) (V28) (Beta chemokine receptor-like 1) (CMK-BRL-1)
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MEDILNE-20196025; PubMed=10731151;
Faure S., Meyer L., Costagliola D., Vaneensberghe C., Genin E.,
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variant of the chemokine receptor CX3CR1."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Coloning, chromosomal localization, and RNA expression of a human beta chemokine receptor-like gene.";
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                                                                                                                                  Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                  CX3CR1 OR GPR13
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                                                                                                   CMKBLR1
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Science 287:2274-2277 (2000).

-!- FUNCTION: Receptor for the CX3C chemokine fractalkine and mediates both its adhesive and migratory functions. Acts as co-receptor with CD4 for HIV-1 virus envelope protein (in viro).

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- TISSUB SPECIFICITY: Expressed in lymphoid and neural tissues.

-!- DISEASE: Increased susceptibility to HIV infection and rapid progression to AIDS are associated with the Ile-249/Met-280 haplotype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V -> I (common polymorphism in Caucasian population). /FIId=VAR_010043.
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R MIM; 60470; -..

R GO; GO:0005887; C:integral to plasma membrane; TAS.

GO; GO:0005887; C:chemokine receptor activity; TAS.

R GO; GO:0005895; F:cell adhesion; TAS.

R GO; GO:000698; P:cellular defense response; TAS.

R GO; GO:000583; P:cellular defense response; TAS.

R GO; GO:000583; P:cellular defense response; TAS.

R GO; GO:000186; P:G-protein coupled receptor protein signalin. ..;

R InterPro; IPR000277; Fractalkiner.

DR RINTS; PR00017; 7tm 1; 1.

DR PRINTS; PR00127; FRACTALKINER.

DR PRINTS; PR00127; GPCREHODOPEN.

DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.

DR ROSITE; PS00237; G-PROTEIN_RECEP_F1_2; 1.

R G-protein coupled receptor; Transmembrane; Polymorphism.

FORMAIN 1 31 EXTRACELLULAR (POTENTAL).
                                                                                                                                                                                                                                               -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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C59DC5F4C4312F22 CRC64;
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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EMBL; U28934; AAA87032.1; -.
EMBL; BC028078; AAH28078.1; -.
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Best Local Similarity 61.1%;
Matches 11; Conservative
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Genew; HGNC:2558; CX3CR1.
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Inngjerdingen M., Damaj B., Maghazachi A.A.;
Inngjerdingen M., Damaj B., Maghazachi A.A.;
"Human NK cells express CC chemokine receptors 4 and 8 and respond to thymus and activation-regulated chemokine, macrophage-derived chemokine, and I-309.";
J. Immunol. 164.4094-4054(2000).
-!- FUNCTION: High affinity receptor for the C-C type chemokines TARC/SCYA17 and MDC/SCYA22. The activity of this receptor is mediated by G(i) proteins which activate a phosphatidylinositol-
                                                                                                                                                                                                                                                          TISSUE-Spleen,
MEDLINE-95370289; PubMed=7642634;
MEDLINE-95370289; PubMed=7642634;
Prower C.A., Meyer A., Nemeth K., Bacon K.B., Hoogewerf A.J.,
Proudfoot A.E.I., Wells T.N.C.;
"Mollecular clothing and functional expression of a novel CC chemokine receptor cDNA from a human bacophilic cell line.",
J. Biol. Chem. 270:19495-19500(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99394604; PubMed=10466728; Campbell J.J., Qin S., Ponath P., Andrew D.P., Warnke R., Ruffing N., Kassam N., Wu L., Butcher B.C.; The chemokine receptor CCR4 in vascular recognition by cutaneous b. not intestinal memory T cells."; Nature 400:776-780(1999).
                                                                  CKR4 HUMAN STANDARD; PRT; 360 AA.

901LY6; 901LX6; 901LX7;
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 4), Last sequence update)
01-0CT-1996 (Rel. 4), Last cannotation update)
01-0CT chemokine receptor type 4 (C-C CKR-4) (CCR-4) (CCR-4)
(KS-5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97313486, PubMed=9169480;
Imai T., Baba M., Nishimura M., Kakizaki M., Takagi S., Yoshie O.;
"The T cell-directed CC chemokine TARC is a highly specific
biological ligand for CC chemokine receptor 4.";
J. Biol. Chem. 272:15036-15042(1997).
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND VARIANTS VAL-130 AND SER-178.
MEDLINE=21040311; PubMed=11196669;
Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki Hirai K., Tokunaga K.;
"New variations of human CC-chemokine receptors CCR3 and CCR4.";
Genes Immun. 1:97-104(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98104168; PubMed-9430724; mod C.L., Nishimura M., Godiska Mana T., Chantry D., Raport C.J., Wood C.L., Nishimura M., Godiska Yoshie O., Gray P.W.; "Macrophage-derived chemokine is a functional ligand for the CC
                                                                                                                                                           CCR4 OR CMKBR4.
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Kopatz S.A., Aronstam R.S., Sharma S.V.,
"CDNA clones of human proteins involved in signal transduction
sequenced by the Guthrie cDNA resource center (www.cdna.org).";
Submitted (UUN-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chemokine receptor 4.";
J. Biol. Chem. 273:1764-1768(1998)
    293 YAFAGEKFRYLYHLYGK 310
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                        CKR4 HUMAN
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calcium second messenger system. Can function as a chemoattractant homing receptor on circulating memory lymphocytes and as a coreceptor for some primary HIV-2 isolates. In the CNS, could mediate hippocampal-neuron survival.

--- SUBCENTURAR LOCATION: Integral membrane protein.

--- INSUE SPECIFICITY: Predominantly expressed in the thymus, in peripheral blood Leukocytes, including T cells, mostly cd4+ cells, and him platelets at lower levels, in the spleen and basophils, and in platelets at lower levels, in La-2-activated natural killer cells and skin-homing memory T cells, mostly the ones expressing the cutaneous lymphocyte antigen (CLA). Expressed in brain microvascular and coronary artery endothelial cells.

--- PTM: IN NATURAL KILLER CELLS, SCYA22 BINING INDUCES PROBABLY BY BENTA-ADRENBERGIC RECEPTOR KINASSE 1 AND 2.

--- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIN, 604836; -.
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0004950; F:chemokine receptor activity; TAS.
GO; GO:0004955; F:chemotaxis; TAS.
GO; GO:0000595; P:chemotaxis; TAS.
GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
GO; GO:0006955; P:immune response; TAS.
InterPro: IPR000256; GPCR_Rhodpsn.
Ffam; PF00001; 7tm_1: 1.
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CYTOPIASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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PROSITE; PS00237; G PROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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EMBL; AB02388; BAA86965.1; -...
EMBL; AB02389; BAA86966.1; -...
EMBL; AB023891; BAA86967.1; -...
EMBL; AB023891; BAA86968.1; -...
EMBL; AB023892; BAA86969.1; -...
EMBL; AS023892; BAA86969.1; -...
PIR.; A57160; A57160.
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Gaps

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Indels

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Mismatches

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Conservative

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CKR3_CAVPO
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                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                           AIDS Res. Hum. Retroviruses 17:981-986(2001).
-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA, RANTES, MOP-3 AND, LESS BFFICKENTLY, TO MIP-1-BETA OR MCP-1 AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCHUM IONS LEVEL. RESPONSIBLE FOR AFFECTING STEM CELL PROLIFERATION.
                     Gaps
                                                                                                                                                        15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
C-C chemokine receptor type 1 (C-C CKR-1) (CC-CKR-1) (CCR1)
                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=21354176; PubMed=11461684; Margulies B.J., Hauer D.A., Clements J.E.; macaque chemokine "Identification and comparison of eleven rhesus macaque chemokine
                                                                                                                                                                                                  Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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Pred. No. 0.039;
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InterPro; IPR00276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHODDSN.
PRINTS; PR00237; GPROTEIN RECEP F1 1; 1.
PROSITE; PS00262; GPROTEIN RECEP F1 2; 1.
PROSITE; PS00262; GPROTEIN TRADSMENDEAR;
G-protein coupled receptor; Transmendrane; Glycoprotein.
                    Indels
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
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; Mismatches
                                                                                                                        355 AA.
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                                                                                                                       PRT;
58.8%; PIE
                                                      304 YFFLGEKFRKYILQLFK 320
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28-FEB-2003 (Rel. 41, Last ann
                                         1 YAFVGEKFRNYLLVFFQ 17
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                   Conservative
                                                                                                                       STANDARD;
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NCBI_TaxID=9544;
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239
264
       Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                   receptors."
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                                                                                                                                                                                                                                                                                                                                                                                                                                  TI SEQUENCE FROM N.A.

WEDLINE-99049845; PubMed=9834099;

WEDLINE-99049845; PubMed=9834099;

WEDLINE-99049845; PubMed=9834099;

A Sabroe I., Conroy D.M., Gerard N.P., Li Y., Collins P.D., Post T.W.,

A Gose P.J., Williams T.J., Gerard C.J., Ponath P.D.;

T "Cloning and characterization of the guinea pig eosinophil ectaxin

T "Cloning and characterization of the guinea pig eosinophil ectaxin

T "Cloning and characterization of the guinea pig eosinophil ectaxin

T "Cloning and characterization of the guinea pig eosinophil ectaxin

T "Cloning and characterization of the guinea membrane protein.

T "Cloning and characterization of the guinear protein.

C "Increasing the intracellular calcium ions level (By similarity).

C "I SUBCELLULAR LOCATION: Integral membrane protein.

SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3) (CCR-3)
                                                                                                                                                                                                                                                                                                                              Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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7873FAB7A38C3670 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL). POTENTIAL.
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PRINTS, PROGEST; GFORRHODDERN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

G-Protein coupled receptor; Transmembrane.

DOMAIN

TRANSMEM

44

67
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301 YAFAGERFRKYLROLFHR 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41623 MW;
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                                                                                                                                 STANDARD;
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358 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                              CCR3 OR CMKBR3.
                                                                                                                            CKR3 CAVPO
Q9Z2I3;
30-MAY-2000 (
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
RANTES, AND LESS EFFICIENTLY, TO MIP-1-BETA OR MCP-1 AND
SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING STEM CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Detected in the heart, spleen, lung,
peritoneal exudate cells and leukocytes.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                   951675; 091VP9; 01-07-1996 (Rel. 34, Created) 01-07-1996 (Rel. 34, Last sequence update) 10-077-2003 (Rel. 44, Last annotation update) 0-07-2003 (Rel. 44, Last annotation update) 0-07-07-2003 (Rel. 47, Last annotation update) (CC chemokina receptor type 1 (C-C CKR-1) (CC-CKR-1) (CCR-1) (CCR1) (Macrophage inflammatory protein-1 alpha receptor) (MIP-lalpha-R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jerard C.;
"Molecular characterization of two murine eosinophil beta chemokine
                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRALIB129/Sv. TISSUE-Peritoneal macrophage;
MEDLINE=96072806; PubMed=1594543;
Post I.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gao J.-L., Murphy P.M.;
"Cloning and differential tissue-specific expression of three receptor-like genes, including the gene for a beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor."; J. Biol. Chem. 270:17494-17501(1995).
                                                                                                                                  355 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=129/SvJ;
MEDLINE=95340546; PubMed=7542241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptors.";
J. Immunol. 155:5299-5305(1995).
304 YAFVGERFOKYLRHFLHR 321
                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                             (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Breast;
                                                                                                                                                                                                                                                                                                                  CCR1 OR CMKBR1
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                                                                                                                                    CKR1 MOUSE
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95340546; PubMed=7542241;
Gao d'-L., Murphy P.N.;
"Cloning and differential tissue-specific expression of three mouse
beta chemokine receptor-like genes, including the gene for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 41, Last annotation update)
C-C chemokine receptor 1-like protein 1 (Macrophage inflammatory protein-1 alpha receptor-like 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                          EMBL; U29678; AAA86119.1; -...
EMBL; U28404; AAA89153.1; -...
EMBL; U28404; AAA89153.1; -...
EMBL; U28404; AAA89153.1; -...
EMBL; U28404; AAH1092.1; -...
EMBL; U28404; Ccrl.
AGD; MGI:104618; Ccrl.
AGO; GO:0005515; F:protein binding; IPI.
AGO; GO:0005515; F:protein binding; IPI.
AGO; GO:0005515; F:protein binding; IPI.
AGO; GO:0005519; F:mmune cell chemotaxis; IDA.
AGO; GO:0005519; F:mreliammatcry response; IMP.
AGO; GO:000576; GFCR Rhodpsn.
AGO; GO:000576; GFCR Rhodpsn.
AFAM; PFC0001; 7tm 1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                6 (POTENTIAL).
EXTRACELLUAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
M -> V (IN REF. 3).
L -> P (IN REF. 3).
H -> Q (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                       3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                   1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                   PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane.
DOMAIN 34 1 (POTENTIAL).
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Best Local Similarity 55.6
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278
355 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=129/SvJ;
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65
130
147
172
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P51676;
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DOMAIN
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functional macrophage inflammatory protein-1 alpha receptor.";
J. Biol. Chem. 270:17494-17501(1995).
--- FUNCTION: Probable receptor for a C-C type chemokine.
--- SUBCELLULAR LOCATION: Integral membrane protein.
--- TISSUE SPECIFICITY: Detected in the spleen, liver and leukocytes.
--- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                    RMEL, 198405; AAA88154.1; -.

RMEL, 198405; Carll.

RMGD; MGI:104617; Carll.

RMGD; MGI:104617; Carll.

REAM: PRO0017 7tm.1; 1.

RPKNITS; PRO0237; GPCRRHODOPSN.

RPKNITS; PRO0237; GPCRHOLIA.

RAG-Drotein coupled receptor; Transmembrane.

DOWAIN 1 32 EXTRACELLULAR (POTENTIAL).

TRANSMEM 68 92 2 (POTENTIAL).

TRANSMEM 109 130 3 (POTENTIAL).

TRANSMEM 109 130 3 (POTENTIAL).

TRANSMEM 199 224 (POTENTIAL).

TRANSMEM 199 224 (POTENTIAL).

TRANSMEM 199 224 CYTOPLASMIC (POTENTIAL).

TRANSMEM 199 224 CYTOPLASMIC (POTENTIAL).

TRANSMEM 199 224 CYTOPLASMIC (POTENTIAL).

TRANSMEM 241 265 6 (POTENTIAL).

TRANSMEM 241 265 6 (POTENTIAL).

TRANSMEM 283 306 7 (POTENTIAL).

TRANSMEM 283 306 7 (POTENTIAL).

TRANSMEM 281 8NS SMILERITY.

TRANSMEM 281 8NS SMILERITY.

TRANSMEM 281 8NS SMILERITY.
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356 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S:
Matches
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302 YVFVGKRFRKYLWQLFRR 319 g

1 YAFVGEKFRNYLLVFFQK 18

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Gaps ö

Search completed: September 28, 2004, 09:04:08
Job time : 6.625 secs

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Tue Sep 28 15:50:00 2004
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Name	GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	្ត ទេសសស ទេសសស
1971.199 Million cell updates/sec   1971.199 Million cell update	- protein search, using sw model	. w w w
Section   Sect	25, 2004, 00:30:10 (Without alignments) 197.199 Million cell updates)	0 0 0
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1017041 seqs, 315518202 residues	BLOSUM62 Gapop 10.0 , Gapext 0.	0 0 0 0 0 0 0 0 0 0
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### Minimum March 10% ### Minimum March 10% #### Minimum March 10% ####################################	of hits satisfying chosen parameters:	9 Q Q
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## Supported by chance to have a greater than or equal to the score distribution.  ## Support	 	1 4694; 4694; 7AN-199; 7AN-199; 7AN-200; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-199; 7AN-19
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100.0   33   4   014694   0014694   home sapien   DR   100.0   33   4   094024   094024   home sapien   DR   100.0   339   4   094024   094025   home sapien   DR   100.0   339   4   094023   094025   home sapien   DR   100.0   339   4   094025   094025   home sapien   DR   100.0   339   4   094025   094025   home sapien   RW   100.0   339   4   094025   094025   home sapien   RW   100.0   339   4   094025   094025   094025   home sapien   RW   100.0   339   4   094029   094025   094025   home sapien   SQ   100.0   339   6   0970W1   0940W2   09	SUMWARIES Query Query Anarch Length DB ID	
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100.0 339 6 Q9TUW8 Q9tuw8 gorilla gor 100.0 339 6 Q9TUT4 Q9tut4 macaca neme 100.0 339 6 Q9TUW9 Q9tuw9 hylobates c	100.0 339 6 Q9TQM0 Q9tQM0 100.0 339 6 Q9TQX1 Q9tux1 100.0 339 6 Q9TQU9 Q9tux3	Query Match Best Local Similarit Matches 18; Conse
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Q9TSQ1	SOLLOR	Q9TQW4	Q9TUW4	Q9TQU7	O9TUQ5	Q9TUU3	Q9TUR9	Q9TQT0	Q9TUT9	O9TSN2	Q9TUR6	9VQT6Q	Q9TUW6	09TU09	O9TSN3	Q9TUU7	Q9TUR2	Q9TQV0	9TU16	Q9TQU5	Q9TUS7	Q9TUW7	Q9TUW3	O9TUS5	ODTU0	O9TOV2	Q9TQV3	80nl60	
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## ALIGNMENTS

pes, co-receptor usage, and CCR5 polymorphism.";

m. Retroviruses 0:0-0(1997).

14; AAB657041.1; -.

15; C:integral to membrane; IEA.

15; F:receptor activity; IEA.

16; F:rhodopsin-like receptor activity; IEA.

17; F:receptor activity; IEA.

18; F:rhodopsin-like receptor protein signalin. .; IEA.

18; F:rhodopsin-like receptor protein signalin. .; IEA.

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18; Tear 100.0%; Score 95; DB 4; Length 333; tty 100.0%; Pred. No. 1.1e-07; servative 0; Mismatches 0; Indels 0; Gaps A. hers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B., mman). coa, Chordata, Craniata, Vertebrata, Buteleostomi, ria, Primates, Catarrhini, Hominidae, Homo. 333 AA; 38174 MW; AEFBA07A67893AEB CRC64; MBLrel. 05, Created) MBLrel. 05, Last sequence update) MBLrel. 24, Last annotation update) Fragment). PRT; 333 AA. IMINARY;

KFRNYLLVFFQK 18

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278 YAFVGEKFRNYLLVFFQK 295

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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF161919; AAD47676.1; -.

GO; GO:0001887; F:receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                       Erythrocebus patas (Red guenon) (Hussar).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Erythrocebus.
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCR5 genes from diverse simian and prosimian species.";
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
C-C. chemokine receptor 5 (Fragment).
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PRINTS; PR00237; GPCRAHODOPSN.
PROSITE; PS0237; G PROTEIN RECEP_F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP_F1_2; 1.
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les 18; Conservative (
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161916, AAD477673.1;
GO; GO:00166021; C:integral to membrane; IEA.
GO; GO:0016872; F:receptor activity; IEA.
GO; GO:0001884; F:rhodopain-like receptor activity; IEA.
GO; GO:000186; F:G-protein coupled receptor protein signalin. .; IEA.
InterPro; IPR000276; GPCR Rhodpsn.
PRINTS; PR000277; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kulken C., Marx P., Wolinksy S.;

"Sequences of the CCR5 genes from diverse simian and prosimian
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                                                                                                                                             100.0%; Score 95; DB 4; Length 339; 100.0%; Pred. No. 1.1e-07; tive 0; Mismatches 0; Indels
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339 AA, 39066 MW, 8BAF02E19423BF79 CRC64;
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339 339
339 AA, 39162 MW, A56369FE0529F4AB CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment)
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Local Similarity 100.0%; Pred. No. 1.1e-07;
les 18; Conservative 0; Mismatches 0;
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         PEAM, PF00001, 7tm 1, 1.
PRINTS, PR00237, GPCRRHODOPSN.
PROSITE, PS00237, G PROTEIN RECEP F1 1, 1.
PROSITE, PS50262, G PROTEIN RECEP F1 2, 1.
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InterPro; IPR000276; GPCR_Rhodpsn
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290 YAFVGEKFRNYLLVFFQK 307
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es 18; Conservative
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Homo sapiens (Human)

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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibara R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
Shibara R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
Sequences of the CCR5 genes from diverse simian and prosimian
species.";
Submitted (ULL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; API61920; AAD47677.1;
SCO, GO:0016021; C:integral to membrane; IEA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:001684; F:receptor activity; IEA.

GO; GO:00186; P:G-protein coupled receptor protein signalin. . .; IEA.

InterPro; IPR000276; GPCR_Rhodpsn.

Pfam; PR0001; 7tm 1; 1.

PROSITE; PS00237; GFRRHODDEN.

PROSITE; PS00237; GFRRHODDEN.

PROSITE; PS00262; G_PROTEIN_RECEP_FI_2; 1.
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Kunstnan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pilai S., Kuiken C., Marx P., Wolinksy S.;

Shibata R., Yoder A., Pilai S., Kuiken C., Marx P., Wolinksy S.;

"Sequences of the CCR5 genes from diverse simian and prosimian species.";

"Sequences of the EMBL/GenBank/DDBJ databases.

"Species.";

Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AFIG1921; AAD47678.1; -.

EMBL; AAD4767
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 95; DB 4; Length 339; 100.0%; Pred. No. 1.1e-07; live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      339 AA; 39115 MW; 3C6369F922C91AA7 CRC64;
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hes 18; Conservative
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Q9UBJ7
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GO; GO:0001881; Fireceptor activity; IEA.
GO; GO:0001884; Fireceptor activity; IEA.
GO; GO:0001886; Fireceptor activity; IEA.
GO; GO:0001886; Fireceptor activity; IEA.
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCR5 genes from diverse simian and prosimian
species.";
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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100.0%; Pred. No. 1.1e-07;
wiematches 0; Indels
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EMBL; AF161914; AAD47671.1; -
GO; GO:0016021; C.integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
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339 339
339 AA; 39146 MW; 10FE05FE5371D4B3 CRC64;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                     01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNAY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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PROSTITE; PRO0237; GPCRRADODSN.
PROSTITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSTITE; PS0262; G PROTEIN RECEP F1_2; 1.
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                                  290 YAFVGEKFRNYLLVFFQK 307
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1 YAFVGEKFRNYLLVFFOK 18
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es 18; Conservative
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                                                                                                                                                                                                                          PRELIMINARY;
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Homo sapiens (Human)
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Matches

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EMBL; AF162024; AAD47779.11; --
EMBL; AF162024; AAD47646.1; --
EMBL; AF161889; AAD47646.1; --
EMBL; AF161889; AAD47646.1; --
GO; GO:00016021; C:integral to membrane; IEA.
GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001884; F:rhodopsin-like receptor protein signalin. . .;
InterPro; IPR000276; GPCR_Rhodopsn.
                                                                                                                                                                                                                                                                                              species.";
Submitted (ULL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161913; AAD47670.1;
GO; GO:0016621; C:integral to membrane; IEA.
GO; GO:001684; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor protein signalin.
Interpro; IPR000276; GPCR_Rhodpsn.
FRIMTS; PR00137; GPCRHODOPSN.
PROSITE; PS00237; GPCRHODOPSN.
PROSITE; PS500262; G_PROTEIN_RECEP_F1_1; 1.
                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hylobates concolor (crested gibbon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibaen R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.,
"Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy N
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 95; DB 4; Length 339; 100.0%; Pred. No. 1.1e-07; Aztive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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339 339
339 AA; 39183 MW; 56C819F92D6DB1A6 CRC64;
    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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Q9TQWO;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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PRINTS; PR00237; GPCRANDODSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS0262; G PROTEIN RECEP F1 2; 1.
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                                                                                                           (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor.
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Submitted (JUL-1999) to the EWBL/GenBank/DDBJ databases.
EWBL; AF161915; AAD47666.1;
EWBL; AF161909; AAD47666.1;
EWBL; AF161910; AAD47668.1;
EWBL; AF161911; AAD47668.1;
EWBL; AF161912; AAD47669.1;
EWBL; AF161912; AAD47669.1;
EWBL; AF161912; AAD47669.1;
GO; GO:0001671; F:receptor activity; IEA.
GO; GO:0001887; F:receptor activity; IEA.
GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001886; F:rhodopsin-like receptor protein signalin. .; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
PRINTS; PR00237; GPCRHODOPSN.
PRINTS; PR00237; GPCRHODOPSN.
PROSITE; PS50227; G PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Kunstman K., Stanton J., Agy M., Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCRS genes from diverse simian and prosimian
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                                                                                                                                                                                                                                                        100.0%; Score 95; DB 4; Length 33
100.0%; Pred. No. 1.1e-07;
rative 0; Mismatches 0; Indels
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339 339
339 AA; 39086 MW; 88AD8B44E2CB4EC2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-VMN-2003 (TrEMBLrel. 24, Last annotation update)
C-C Chemokine receptor 5 (Fragment).
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PRINTS, PR00237; GPCRHODOSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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                                                                                                                                                                                                                                                                                                  18; Conservative
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les 18; Conserv
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RESULT 10 Q9UN28 ID Q9UN2: AC Q9UN2:

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Gaps

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Submitted (ULL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF161948; AAD47704.1; -..GENBANK/DDBJ databases.

EMBL; AF161948; AAD47704.1; -..GENBANK/DDBJ databases.

EMBL; AF161948; AAD47704.1; -..GENBANGANG, ISA.

GO; GO:0010612; F:receptor activity; IEA.

GO; GO:0001188; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001188; F:rhodopsin-like receptor protein signalin. ..; IEA.

InterPro; IPR000276; GFORE Rhodopsn.

PROSITE; PR00021; GFORE RECEP FIL; 1.

PROSITE; PS00237; GFORHEN RECEP FIL; 1.
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy ?
"Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     339 AA
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PROSITE; PS00237; G PROTEIN RECEP F1 1;
PROSITE; PS50262; G PROTEIN RECEP_F1_2;
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Best Local Similarity 100.
Matches 18; Conservative
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Submitted (JUL-199) to the EMBL/GenBank/DDBJ databases.

EMBL; AR161887; AAD47644.1;
GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016842; F:receptor activity; IEA.

GO; GO:0001884; F:receptor activity; IEA.

GO; GO:0001886; F:receptor activity; IEA.

FINTERPROPOSITY: TRM 1; 1.

PRINTS; PRO00237; GFCRRHODORN.

PROSITE; PSO0237; GPRRHODORN.

PROSITE; PSO0262; G_PROTEIN_RECEP_F1_2; 1.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae, Cercopithecidae, Cercopithecidae, Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hylobates concolor (crested gibbon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
MCBI_TaxID=29089;
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
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                                                              Query Match 100.0%; Score 95; DB 6; Length 339; Best Local Similarity 100.0%; Pred. No. 1.1e-07; Matches 18; Conservative 0; Mismatches 0; Indels
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  339
39036 MW; 5555FEAF2614D35C CRC64;
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39075 MW; 09257FBFBB34C4AE CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C_chemokine receptor 5 (Fragment).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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100.0%; Pred. No. 1.1e-07;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                      339 AA
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Best Local Similarity 100.
Matches 18; Conservative
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFI61949; AAD47651.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0001894; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001894; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
InterPro; IPR000276; GPCR_Rhodopsn.
Pfam; PF00001; 7tm 1: 1.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCRS genes from diverse simian and prosimian
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                                                                                                                                   Length 339;
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                                                                                                                                100.0%; Score 95; DB 6; Length 33
100.0%; Pred. No. 1.1e-07;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.1e-07;
iive 0; Mismatches 0; Indels
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339 339
339 AA, 39015 MW, 6D1A91546270F70D CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Cercopithecus.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Best Local Similarity 100.
Matches 18; Conservative
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10 20 17 SQ
10 00 1 SQ
10 00 1 SQ
10 10 SQ
10 10 SQ
10 10 SQ
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161979; AAD47734.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0001891; F:receptor activity; IEA.
GO; GO:0001896; F:receptor activity; IEA.
GO; GO:0001896; F:receptor activity; IEA.
GO; GO:0001896; F:receptor activity; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
PROSITE; PS00037; GPCRRHODPSN.
PROSITE; PS00037; GPROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF161890; AAD47671;
GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:001584; F:receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:000186; P:Grotein coupled receptor protein signalin. ..; IEA.

InterPro; IPR000276; GPCR_Rhodpsn.

Pfam; PR0001; 7fm 1; PR00278;
PFam; PR00217; GPCRRHODOPSN.

PROSITE; PS00237; G_ROTEIN_RECEP_F1_1; 1.
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                                                                                                                                                                                                                                                                                        Macaca nemestrina (Pig-tailed macaque).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bammalia; Butheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Macaca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; "Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hylobates concolor (crested gibbon).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hylobatidae, Hylobates.
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339 339
339 AA, 39092 MW, 84B51B9548B0703C CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 13, Last sequence update)
01-JUM-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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                                           PRELIMINARY;
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                                               Q9TUT4
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O9TUW9
AC 09TUW9
DT 01-MADT 
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Bukaryota, Metazooa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates; Catarrhini, Cercopithecidae;
Cercopithecinae; Cercopithecus.
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                                                                100.0%; Score 95; DB 6; Length 339;
100.0%; Pred. No. 1.1e-07;
tive 0; Mismatches 0; Indels
1 1
339 339
339 AA, 39024 MW, EC4CE48DEEEF107E CRC64,
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                                                                                                                                                                                                                                                                                               01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNAY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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01-WAY-2000 (TrEMBirel. 13, Last sequence update)
01-WAY-2003 (TrEMBirel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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1 YAFVGEKFRNYLLVFFQK 18
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Q9TUW4;
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GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0001849; F:rhodopsin-like receptor activity; IEA.

GO; GO:000186; P:G-protein coupled receptor protein signalin. .; IEA.

InterPro; IPR000276; GPCR_Rhodopsn.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_1; 1.

Receptor.
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EMBL; AF161905; AAD47652.1; -.

EMBL; AF161808; AAD47655.1; -.

EMBL; AF161904; AAD47658.1; -.

EMBL; AF161904; AAD47658.1; -.

EMBL; AF161904; AAD47661.1; -.

EMBL; AAD47661.1; -.

EMBL
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                                                    SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
Shibatences of the CGRS genes from diverse simian and prosimian
species.";
Shibitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCR5 genes from diverse simian and prosimian
species.";
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
NCBI_TaxID=9598;
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100.0%; Pred. No. 1.1e-07;
tive 0; Mismatches 0; Indels
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339 339
339 AA, 39049 MW; 6D1A93F66270F3ED CRC64;
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339 AA; 39129 MW; 4A88F8BB601D46A4 CRC64;
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PROSITE; PS00237; G PROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; G PROTEIN RECEP_F1_2; 1.
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Pan troglodytes (Chimpanzee)
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nes 18; Conservative
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NCBI_TaxID=36224;
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Q9TQW4;
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A Shibara R., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
A Shibara R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;

"Sequences of the CCR5 genes from diverse simian and prosimian
species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF161903; AAD47660.1;
CO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016021; F:receptor activity; IEA.

GO; GO:0001884; F:rhodopsin-like receptor protein signalin. .; II

InterPro; IPR000276; GPCR_Rhodpsn.

R Pfam; PF00001; 7tm 1, 1.

R PRINTS; PR00137; GPCRRHODPSN.

R PRINTS; PR001237; GPCRRHODPSN.

R PROSITE; PS50262; G_PROTEIN_RBGEP_F1_2; 1.
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Eukaryota, Metazoa, Chordata, Craniata, Vortebrata, Euteleostomi,

Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,

Cercopithecinae, Cercopithecus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 95; DB 6; Length 339; 100.0%; Pred. No. 1.1e-07; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF162047; AAD47802.1; -.
EMBL; AF162042; AAD47797.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 1
339 339
339 AA, 39159 MW, 8E699E882BAC0E84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UMAY-2003 (TEMBLrel. 24, Last annotation update)
C-C Chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                    339 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 339 AA
                                                                                                                                                                                    PRT;
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290 YAFVGEKFRNYLLVFFQK 307
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                                                                                                                                                                                                                                                                                                                                                                               CCR5.
Pan troglodytes (Chimpanzee)
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Matches

RESULT 22

g

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01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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es 18; Conservative
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Q9TUR9
     SOTT THE STATE OF 
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                       GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:000184; F:receptor activity; IEA.
GO; GO:000186; F:receptor activity; IEA.
GO; GO:0007186; F:receptor coupled receptor protein signalin. . .; IEA.
InterPro; IPR:00276; GPCR_Rhodpsn.
PETam; PF:00001; Tam 1.
PR:00017; GPCR-RHODPSN.
PROSITE; PS:00237; G_PROTEIN_RECEP_FI_1; 1.
PROSITE; PS:00237; G_PROTEIN_RECEP_FI_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; "Sequences of the CCR5 genes from diverse simian and prosimian species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Erythrocebus patas (Red guenon) (Hussar).
Enythrocebus patas (Red guenon) (Hussar) (Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae, Cercopithecidae, Erythrocebus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF162054; AAD47809.1; -...
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001864; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
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                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 95; DB 6; Length 339; 100.0%; Pred. No. 1.1e-07; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                       339 AA; 39150 MW; 847D5F92BB03E6E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         339 AA; 39048 MW; 1A2E19E3A6A5A52A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          339 AA.
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PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G-PROTEIN RECEP_F1 1; 1.

PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
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     EMBL; AF162044; AAD47799.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18; Conservative
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les 18; Conserv
                                                                                                                                                                                                                                                                                      Receptor.
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Q9TUU3
ID Q9TUU3
AC Q9TUU3;
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Best Loc Matches

g

·; IEA Gaps Saguinus sp. Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Platyrrhini; Callitrichidae; Saguinus. NCBI\_TaxID=100754; A KUNDACE FROM N.A.

A KUNDACA R., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,

Kunbata R., Yoder A., Pillais S., Kuiken C., Marx P., Wolinksy S.;

Shibata R., Yoder A., Pillais S., Kuiken C., Marx P., Wolinksy S.;

I "sequences of the CCRS genes from diverse simian and prosimian

I Secies."

Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF161961; AAD47716.1; -. EMBL, AF161961; AAD47716.1; -.

EMBL, AF161961; AAD47716.1; -.

RGJ, GO:0001881; F:raceptor activity, IEA.

RGJ, GO:0001861; F:raceptor activity, IEA.

RGJ, GO:0001786; P:C-Protein coupled receptor protein signalin. ..;

R PRINTS; PRO1377; GPCRHODOPSN.

R PROSITE; PS50227; G-PROTEIN RECEP F1\_1; 1.

R PROSITE; PS502251; G-PROTEIN RECEP F1\_2; 1. Σ. Ω. Σ. Ω. Macaca mulatta (Rhesus macaque).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca. . Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy P. Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S. "Sequences of the CCR5 genes from diverse simian and prosimian 100.0%; Score 95; DB 6; Length 339; 100.0%; Pred. No. 1.1e-07; ative 0; Mismatches 0; Indels 339 339 339 AA; 39121 MW; AFB6E3EE4D6D3484 CRC64; Q9TUR9 PRELIMINARY; PRT; 339 AA.
Q9TUR9;
01-MAY-2000 (TZEMBLrel. 13, Created)
01-MAY-2003 (TZEMBLrel. 13, Last sequence update)
01-UUN-2003 (TZEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment). 

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Query Match
Best Local Similarity
     [1]
SEQUENCE FROM N.A.
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                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Walkaryota; Metacoca; Chordata; Craniata; Vertebrata; Euteleostomi;
Mamalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macaca mulatta (Rhesus macaque).
Bukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi,
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
NCBI_TaxID=9544;
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinkey S.; "Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species.";
Submitted (ULL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF161954; AAD47710.1;
EMBL, AF161952; AAD47706.1;
EMBL, AF161952; AAD47708.1;
EMBL, AF161952; AAD47708.1;
EMBL, AF161952; AAD47708.1;
EMBL, AF161952; AAD47708.1;
EMBL, FECOPORT CONDISOR (CONDISOR)
GO, GO:0001684; F:rhodopsin-like receptor activity; IEA.
GO, GO:0001584; F:rhodopsin-like receptor protein signalin.
FECOPORT (CONDISOR (CONDISOR
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                                                                                100.0%; Score 95; DB 6; Length 33
100.0%; Pred. No. 1.1e-07;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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339
39097 MW; C576E7AA492D7080 CRC64;
  339 339 39063 MW; 78BCE7A84B877085 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-WAY-2000 (TrEMBLrel. 13, Created)
1-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                    339 AA.
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PROSITE; PSO0237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
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Best Local Similarity 100.
Matches 18, Conservative
                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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339 3
339 AA;
                                                                          Query Match
Best Local Similarity
Matches 18; Conserv
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OSTOTO
DIO 09107
DT 001-MA
DT 01-MA
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Q9TUT9
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                      ENEMI, AF161972; AAAP1727.1; -
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0001884; F:racceptor activity; IEA.
GO; GO:0001886; F:racceptor activity; IEA.
GO; GO:0001886; F:racceptor activity; IEA.
GO; GO:0007186; F:racceptor activity; IEA.
FO; GO:0007186; F:racceptor activity; IEA.
FINEMENTO: PRO00276; GPCR.Rhodpsn.
FEAM; PRO00277; Ten 1; 1.
FRINTS; PRO0237; GFCRHODDEN.
FROSITE; PSG0227; GFCRHODDEN.
FROSITE; PSG0227; GFROTEIN_RECEP_FI_1; 1.
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Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
"Sequences of the CCRS genes from diverse simian and prosimian
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy P
Kunstman K., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
"Sequences of the CCRS genes from diverse simian and prosimian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 95; DB 6; Length 33
100.0%; Pred. No. 1.1e-07;
tive 0; Mismatches 0; Indels
                                                                                 species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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339 339
339 AA; 39067 MW; SBFCBCSBA96C2F9E CRC64;
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Best Local Similarity 100.
Matches 18; Conservative
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NCBI_TaxID=9541;
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Matches
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Q9TUW6
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:000186; F:rhodopsin-like receptor activity; IEA.
GO; GO:000186; P:rhodopsin-like receptor protein signalin. . .; IEA.
Interpro; IPR000276; GPCR_Rhodpsn.
PFam; PR00037; GPCRRHODDSN.
PROSITE; PS000237; GPCRRHODDSN.
PROSITE; PS500262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Colobus guereza (Black-and-white colobus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                          Cercopithecus aethiops vervet.

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Bummalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; "Sequences of the CCRS genes from diverse simian and prosimian species.";
                                                                                                                                                                                                           Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCR5 genes from diverse simian and prosimian
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Submitter.";
Submitter(JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF162005; AAD47760.1; -.
EMBL; AF162001; AAD47755.1; -.
EMBL; AF162001; AAD47756.1; -.
                                                                                                                                                                                                                                              species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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YAFVGEKFRNYLLVFFQK 307
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                                                      PRELIMINARY;
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EMBL, AF162003; AAD47758.1; -.
EMBL, AF162004; AAD47759.1; -.
EMBL, AF162004; AAD47759.1; -.
EMBL, AF162004; AAD47759.1; -.
EMBL, AF162004; AAD47759.1; -.
GO, GO:001607; C:integral to membrane; IEA.
GO, GO:0001684; F:rceeptor activity; IEA.
GO, GO:0001188; F:rceeptor activity; IEA.
GO, GO:0001188; P:rchodopsin-like receptor activity; IEA.
InterPro; IPR000276; PGPCR Rhodpsn.
PFAMP: PRO0001; 7tm 1; 1.
PROMITE: PRO00217; GPCRHODOPSN.
PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
NCBI_TaxID=9598;
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SEQUENCE FROM N.A.
KUNGERMAN K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M
KUNGERMAN K., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S
"Sequences of the CCR5 genes from diverse simian and prosimian
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                      339 339 MW; 6A4BF72FEBFF566F CRC64;
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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339 339 378 WW, F0132E8BC44EF829 CRC64;
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nes 18; Conservative
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NCBI_TaxID=9542;
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF161911; AAD47707.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004812; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-liver receptor activity; IEA.
GO; GO:0001186; P:Grotein coupled receptor protein signalin. . .; IEA.
InterPro; IPR000276; GPGR_Rhodpsn.
Ffam; PF00001; 7tm_1; 1......
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Bukaryota, Metacoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
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K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                              Eukarzycka; Metazzoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. Kunstman K., Chan Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinksy S.; "Sequences of the CCRS genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 95; DB 6; Length 33 100.0%; Pred. No. 1.1e-07; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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339 339
339 AA; 39019 MW; 7176F940AF11F3ED CRC64;
    01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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PROSITE, PS00237, GPROTEIN RECEP_F1 1, 1.
PROSITE, PS50262, GPROTEIN RECEP_F1_2, 1.
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                                                                                                                                                                                                                                 Cercopithecus mona.
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Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=36226;
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SEQUENCE
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Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates; Catarrhini; Cercopithecidae;
NCBI_TaxID=9538;
[1]
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                          Macaca fuscata (Japanese macaque).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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    Length 339;
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100.0%; Pred. No. 1.1e-07;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                339 AA; 39097 MW; C576E7AA492D7080 CRC64;
                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
C-C Chemokine receptor 5 (Fragment).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
100.0%; Score 95; DB 6; I 100.0%; Pred. No. 1.1e-07; ive 0; Mismatches 0;
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290 YAFVGEKFRNYLLVFFQK 307

FROM N.A.

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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9542;
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                                                                                                                                                                Q9TUU6
Q9TUU6;
                                                                                                  RESULT 36
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161989; AAD47744.1;
EMBL; AF161988; AAD47744.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
InterPro; IPR000276; GPCR_Rhodopsn.
                             Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S., "Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Papio.
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                                                                                                                        pecies.";
species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AR1620134; AAD47799.1;
GO; GO:0016021; C.integral to membrane; IEA.
GO; GO:0018472; F:receptor activity; IEA.
GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001886; F:G-protein coupled receptor protein signalin.
InterPro; IPR000276; GPCR_Rhodpsn.
FROM: PR00017; Tem 1; 1.
PRINTS; PR000237; GPCRHODOPSN.
PROSITE; PS000237; GPCRHODOPSN.
PROSITE; PS500237; GPROTEIN RECEP_FI_1; 1.
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; Pred. No. 1.1e-07;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 339;
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339 339
339 AA; 39113 MW; 7F9803EAOE0AF9ED CRC64;
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339 339
339 AA; 39138 WW; AD31455EBBC69499 CRC64;
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 95; DB 6; L
100.0%; Pred. No. 1.1e-07;
ative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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Best Local Similarity 100.0
....hes 18; Conservative
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nes 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor.
NON TER
NON TER
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Q9TQV0
RAPATA RAPATA PARAPA PA
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YAFVGEKFRNYLLVFFQK 18

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species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF161956; AAA4712.1;
GO; GO:00016021; C:integral to membrane; IEA.
GO; GO:0001887; F:receptor activity; IEA.
GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.
GO; GO:000186; F:rhodopsin-like receptor protein signalin. . ; IEA.
InterPro.; IPRO00276; GFCR_Rhodopsin.
PRINTS; PRO00217; GFCR_RHODOPSN.
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EMBL, AF162046, AAD47801.1; --
EMBL, AF162043, AAD477801.1; --
GO, GO:0016021; C:integral to membrane; IEA.

GO, GO:0016021; C:integral to membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M., Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.; "Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cercopithecus nictitans (white-nosed guenon).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Cercopithecus.
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                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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OSTQUS;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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Pred. No. 1.1e-07;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                   Macaca fuscata (Japanese macaque)
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Les 18; Conservative
PRELIMINARY;
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Score 95; DB 6; I
Pred. No. 1.1e-07;
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339
339 AA;
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Best Local Similarity
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                                                                                                                                           species.";
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GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_l; 7tm_l; PR0001; 7tm_l; PR0001; PR00175; PR00175; PR00175; PR00175; GPCRHODOPSN.
PROSITE; PS00237; GPROTEIN_RECEP_FI_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_FI_2; 1.
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates; Catarrhini, Cercopithecidae,
Cercopithecinae, Papio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCRS genes from diverse simian and prosimian
species.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
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.339 339
339 AA, 39068 MW, 84EB018085DC0A62 CRC64;
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339 339 339 378 MW; 847F8F936B00E6E2 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C-C_chemokine receptor 5 (Fragment).
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PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Best Local Similarity 10v.v.
And 18; Conservative
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Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinkey S.,
"Sequences of the CCR5 genes from diverse simian and prosimian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
Shibata R., Yoder A., Pillal S., Kuiken C., Marx P., Wolinksy S.;
"Sequences of the CCR5 genes from diverse simian and prosimian
Pan troglodytes (Chimpanzee).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukāryotā, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pongo.
                                                                                                                                                                                                                                                                                         Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF161899; AAD47656.1; -.

EMBL, AF161899; AAD47656.1; -.

EMBL, AF161899; AAD47656.1; -.

GO; GO:001681; C:integral to membrane; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor protein signalin.

INTERPRO (1007186; P:G-PRODOSIN.

PRINTS; PRO0023; GFCR.Rhodpsn.

PRINTS; PRO0023; GFCR.Rhodpsn.

PROSITE; PSO0023; GFCR.Rhodpsn.

PROSITE; PSO0023; GFCR.Rhodpsn.
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339 339
339 AA; 39157 MW; 4A9EBAD183E8E72D CRC64;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2003 (TrEMBLrel. 24, Last annotation update)
C-C chemokine receptor 5 (Fragment).
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Search completed: September 28, 2004, 09:06:20 Job time : 28.8 secs